

PT (ESTs), useful in diagnostic, forensic, gene therapy or chromosome
PT mapping procedures, or for designing expression vectors and secretion
PT vectors.
XX
XX
PS Disclosure; Fig 5; 163pp; English.
XX
XX
CC The invention relates to purified nucleic acids, which comprise sequences
CC selected from any of more than 50000 sequences not defined in the
CC specification. The polynucleotide sequences are useful in making cDNA,
CC polypeptides and promoter DNA, and in diagnostic, forensic, gene therapy
CC or chromosome mapping procedures. The nucleic acid sequences are also
CC useful for designing expression vectors and secretion vectors. This
CC polynucleotide sequence represents a P15B4 promoter transcription binding
CC site of the invention
XX
SQ Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TCGCCCTTCC 19
DB 1 TCCACCTTCC 11

RESULT 717
ABK99454
ID ABK99454 standard; DNA; 11 BP.
XX
AC ABK99454;
XX
XX
DT 21-OCT-2002 (first entry)
XX
DE Human CYP3A5 gene polymorphic reference DNA sequence #40.
XX
XX Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
KW AIDS; African American; forensic marker; pharmacological; cytostatic;
KW antidiabetic; anti-HIV; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200253775-A2.
XX
XX 11-JUL-2002.
XX
XX
XX 21-DEC-2001; 2001WO-EP015290.
XX
XX 28-DEC-2000; 2000EP-00128627.
XX
XX 28-DEC-2000; 2000US-0258684P.
XX
XX 29-DEC-2000; 2000US-0258952P.
XX
XX 16-JAN-2001; 2001EP-00100172.
XX
XX 18-JAN-2001; 2001US-0262859P.
XX
XX 16-AUG-2001; 2001EP-00118884.
XX
XX 16-AUG-2001; 2001US-0312825P.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX
XX Wojnowski L, Haberl M, Hustert E;
XX
XX WPI; 2002-583628/62.
XX
XX
XX Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer,
PT cardiovascular diseases, diabetes and AIDS, and for identifying
PT polymorphisms.
XX
XX
XX Example 2; Page 51; 138pp; English.
XX
XX The present invention relates to a new CYP3A5 polynucleotide encoding a
CC polypeptide, where the polynucleotide is capable of hybridising to a
CC CYP3A5 gene. The invention is useful in an in vitro method for
CC identifying a polymorphism. The invention is also useful for useful for
CC diagnosing a disorder related to the presence of a molecular variant of a

CC CYP3A5 or susceptibility to such a disorder, where the disorder is
CC cancer, or diseases including cardiovascular diseases, diabetes and AIDS.
CC The invention can further be used for the preparation of a diagnostic
CC composition for diagnosing a disease in a subject having a genome
CC comprising a variant allele of the CYP3A5 gene, where the subject is an
CC African American. The molecules of the invention are as forensic markers
CC and in pharmacological studies. The present nucleic acid sequence
CC represents a human CYP3A5 gene polymorphism reference DNA sequence, as
CC described in the invention
XX
SQ Sequence 11 BP; 2 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTCATCGCCC 14
DB 1 CATCATTCGCC 11

RESULT 718
ADG28157/C
ID ADG28157 standard; DNA; 11 BP.
XX
AC ADG28157;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human Myo/V1 protein-related NfkappaB regulation site SeqID161.
XX
XX cardiac-associated protein; Myo/V1 protein; MP; cardiant; vasotropic;
KW immunosuppressive; vulnery; NfkappaB p50; NfkappaB p65;
KW cardiovascular disease; cardiac hypertrophy; myocardial infarction;
KW ischaemia; reperfusion injury; heart transplantation;
KW anti-ageing treatment; human; ds.
XX
XX Homo sapiens.
OS
XX WO200245659-A2.
XX
XX 13-JUN-2002.
XX
XX 26-OCT-2001; 2001WO-US051272.
XX
XX 27-OCT-2000; 2000US-0243985P.
XX
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX Sivasubramanian N, Knuefermann P, Mann DL;
XX
XX WPI; 2002-537532/57.
XX
XX Novel dominant negative mutant sequence or constitutively active mutant
PT sequence of Myo/V1 polypeptide, useful for treating cardiovascular
PT disorders and inhibiting formation of NfkappaB homodimers.
XX
XX
XX Example 21; SEQ ID NO 161; 217pp; English.
XX
XX This invention relates to a novel dominant negative or constitutively
CC active mutant sequence of the cardiac-associated Myo/V1 protein (MP). The
CC invention may be useful for the development of compounds with a cardiant,
CC vasotropic, immunosuppressive or vulnery activity through the
CC inhibition of formation of NfkappaB p50 or NfkappaB p65 homodimers. The
CC invention may be useful for the development of treatments for
CC cardiovascular disease including cardiac hypertrophy, myocardial
CC infarction, ischaemia/reperfusion injury and heart transplantation, in a
CC mammal, for anti-ageing treatment, for inhibiting formation of NfkappaB
CC p50 homodimers or NfkappaB p65 homodimers in a cell of a mammal and for
CC reducing formation of NfkappaB p65 homodimers in a cell of a mammal.
XX
XX Sequence 11 BP; 3 A; 3 C; 5 G; 0 T; 0 U; 0 Other;
SQ

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCCCTTCCT 20
Db 11 CGCGGCTTCCT 1

RESULT 719

ADCG6432

ID ADCG6432 standard; DNA; 11 BP.

XX AC

XX ADCG6432;

XX DT 18-DEC-2003 (first entry)

XX DE

XX DE Signalling aptamer complex related oligonucleotide.

XX KW

XX KW signalling aptamer complex; detection; target binding domain;

XX KW target complementary region; duplex structure; aptamer; ss.

XX OS

XX Synthetic.

XX PN

XX WO2003062422-A1.

XX PD

XX 31-JUL-2003.

XX PF

XX 22-JAN-2003; 2003WO-CA000086.

XX PR

XX 22-JAN-2002; 2002US-0349340P.

XX PA

XX (UYMC-) UNIV MCMASTER.

XX PI

XX Li Y, Nutiu R;

XX DR

XX WPI; 2003-748010/70.

XX PT

XX PT A signaling aptamer complex having a fluorophore and a quencher where
XX PT fluorescent signal is quenched when the aptamer is not bound to a target
XX PT molecule is useful to detect target molecules including nucleic acids and
XX PT proteins in a sample.

XX PS

XX Example 8; Fig 7A; 59pp; English.

XX CC

XX CC The present invention describes a signalling aptamer complex (I) for
XX CC detecting a target. (I) comprises a first oligonucleotide (ON1) having a
XX CC target binding domain and at least a second oligonucleotide (ON2) having a
XX CC a sequence complementary to a region of ON1, where in the absence of
XX CC target complementary regions of ON1 and ON2 form a duplex structure, and
XX CC in the presence of target the duplex dissociates and a reporter signal is
XX CC generated. The signalling aptamer complex (I) can be used to detect target
XX CC molecules in a sample. Aptamers can bind to nucleic acid molecules,
XX CC proteins, small organic compounds or entire organisms. Aptamers are
XX CC easier and more cost-effective to make than other recognition molecules
XX CC such as antibodies. The present sequence represents an oligonucleotide
XX CC which is used in the exemplification of the present invention.

SQ

Sequence 11 BP; 1 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

Query Match

Best Local Similarity 30.0%; Score 7.8; DB 1; Length 11;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCCCTAAGCA 25
Db 1 CTTCCCTCCGCA 11

RESULT 720

ADH77013

ID ADH77013 standard; DNA; 11 BP.

XX

AC

XX ADH77013;

XX DT 22-APR-2004 (first entry)

XX DE

XX DE SOX18 wild type DNA sequencing fragment #2.

XX KW

XX KW Mouse; ds; SOX18; cell differentiation; vasculogenesis; angiogenesis;
XX KW hair follicle development; MEF2C; atherosclerosis; cancer; restenosis;
XX KW pulmonary disease; tissue injury; hair loss; tumorigenesis;
XX KW subgroup F SOX; HMG domain; trans-activation domain;
XX KW conserved C terminal domain; arterial wall; vascular smooth muscle;
XX KW blood supply; cardiovascular disorder; ischaemic heart injury;
XX KW neo-vascularisation; atherosclerotic plaque;
XX KW double balloon intravascular catheter; gene transfer;
XX KW fibroblast growth factor-1; FGF-1; platelet derived growth factor; PDGF;
XX KW femoral artery; intimal hyperplasia; matrix deposition; gene therapy;
XX KW cytostatic; antiarteriosclerotic; vasotropic.

XX OS

XX Mus sp.

XX XX

XX US2002142415-A1.

XX PN

XX 03-OCT-2002.

XX PD

XX 23-MAR-2001; 2001US-00814777.

XX PF

XX 24-MAR-2000; 2000AU-00006457.

XX PR

XX (KOOP/) KOOPMAN P A.

XX PA

XX (MUSC/) MUSCAT G E O.

XX XX

XX Koopman PA, Muscat GEO;

XX PI

XX WPI; 2003-155943/15.

XX DR

XX Novel SOX18 polypeptide useful for modulating cell differentiation,

XX PT

XX PT vasculogenesis, angiogenesis, hair follicle development, cell

XX PT proliferation and tumorigenesis.

XX PT

XX Disclosure; Fig 13A; 148pp; English.

XX CC

XX CC The invention discloses an isolated SOX18 polypeptides, given in the
XX CC specification, and biologically active fragments having at least 6 amino
XX CC acids in length, or variants having at least 85% sequence identity. Also
XX CC claimed are isolated polynucleotides encoding the polypeptides; isolated
XX CC polynucleotides encoding polypeptides which modulates an activity
XX CC selected from cell differentiation, vasculogenesis, angiogenesis, hair
XX CC follicle development; detecting a specific polypeptide or polynucleotide
XX CC sequence; detecting a SOX18 polypeptide, by contacting a test polypeptide
XX CC with a MEF2C polypeptide in a biological sample; an antigen-binding
XX CC molecule that is specifically immuno-interactive; detecting the activity
XX CC selected from cell differentiation, vasculogenesis, angiogenesis and hair
XX CC follicle development; a composition for treatment and/or prophylaxis of
XX CC at least one condition selected from atherosclerosis, cancer, restenosis,
XX CC pulmonary disease, tissue injury and hair loss, comprising a SOX18
XX CC polypeptide and an agent that enhances the level and/or functional
XX CC activity of the polypeptide, together with a carrier; a composition for
XX CC treatment and/or prophylaxis of tumorigenesis, comprising an agent that
XX CC reduces the level and/or functional activity of at least one subgroup F
XX CC SOX polypeptide, together with a carrier and a composition comprising one
XX CC or more agents that enhances the level and/or functional activity of at
XX CC least two subgroup F SOX polypeptides. The biologically active fragment
XX CC is at least 8 amino acids in length and comprises a SOX18 HMG domain,
XX CC SOX18 trans-activation domain, SOX18 conserved C terminal domain, or a
XX CC portion of the domain having at least 6 amino acids in length. Delivery
XX CC of recombinant Sox18 into arterial walls had use in the stimulation of
XX CC vascular smooth muscle cells to improve blood supply and flow in a
XX CC several cardiovascular disorders including ischaemic heart injury and the
XX CC neo-vascularisation of atherosclerotic plaques. This was achieved using a
XX CC similar double balloon intravascular catheter mediated gene transfer
XX CC approach of fibroblast growth factor (FGF)-1 and platelet derived growth
XX CC factor (PDGF) into the femoral arteries resulted in induced intimal
XX CC hyperplasia, angiogenesis and matrix deposition. The polynucleotides may

CC be used in gene therapy. The sequence presented is wild-type mouse SOX18
 CC fragment.

XX Sequence 11 BP; 0 A; 6 C; 3 G; 2 T; 0 U; 0 Other;
 SQ Best Local Similarity 30.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 3.2e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 30.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 3.2e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
 DB 1 CGCCCTTCCT 11

RESULT 721

ID ADQ36146
 ADQ36146 standard; DNA; 11 BP.

XX AC ADQ36146;

XX 23-SEP-2004 (first entry)

XX Human hair-bearing skin-associated DNA fragment SEQ ID NO 963.

XX hair-bearing skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; cosmetic; pharmaceutical; biochip; ds.

XX Homo sapiens.

XX DE10260931-A1.

XX 08-JUL-2004.

XX 20-DEC-2002; 2002DE-01060931.

XX 20-DEC-2002; 2002DE-01060931.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;

XX WPI; 2004-518857/50.

XX In vitro identification of genes important for hair-bearing skin, useful
 PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 4; SEQ ID NO 963; 250pp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for hair-bearing skin in humans. The method
 CC comprises recovering, from hair-bearing skin, a first mixture of
 CC genetically expressed (transcribed and optionally translated) factors
 CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
 CC mixture from skin on which hair does not grow and subjecting both
 CC mixtures to serial analysis of gene expression (SAGE) to identify those
 CC genes for which expression is markedly different between the two types of
 CC skin. The invention also describes in vitro methods for determining
 CC homeostasis of human hair-bearing skin and for determining activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
 CC a test kit comprising a solid support (flexible or rigid) with
 CC immobilised probes are also described for determining homeostasis. The
 CC hair-bearing skin is from the scalp and the other skin is from the face.
 CC The method allows identification of as many as possible of the genes
 CC important for hair-bearing skin, and therefore, of a very wide range of
 CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
 CC human DNA tag fragments used to identify genes associated with hair-
 CC bearing skin.

XX Sequence 11 BP; 2 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 3.2e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTCATGCCCC 15
 DB 1 CTCATGCCCC 11

RESULT 722

ID ADQ35222
 ADQ35222 standard; DNA; 11 BP.

XX AC ADQ35222;

XX 23-SEP-2004 (first entry)

XX Human hair-bearing skin-associated DNA fragment SEQ ID NO 39.

XX hair-bearing skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; cosmetic; pharmaceutical; biochip; ds.

XX Homo sapiens.

XX DE10260931-A1.

XX 08-JUL-2004.

XX 20-DEC-2002; 2002DE-01060931.

XX 20-DEC-2002; 2002DE-01060931.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;

XX WPI; 2004-518857/50.

XX In vitro identification of genes important for hair-bearing skin, useful
 PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 9; SEQ ID NO 39; 250pp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for hair-bearing skin in humans. The method
 CC comprises recovering, from hair-bearing skin, a first mixture of
 CC genetically expressed (transcribed and optionally translated) factors
 CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
 CC mixture from skin on which hair does not grow and subjecting both
 CC mixtures to serial analysis of gene expression (SAGE) to identify those
 CC genes for which expression is markedly different between the two types of
 CC skin. The invention also describes in vitro methods for determining
 CC homeostasis of human hair-bearing skin and for determining activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
 CC a test kit comprising a solid support (flexible or rigid) with
 CC immobilised probes are also described for determining homeostasis. The
 CC hair-bearing skin is from the scalp and the other skin is from the face.
 CC The method allows identification of as many as possible of the genes
 CC important for hair-bearing skin, and therefore, of a very wide range of
 CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
 CC human DNA tag fragments used to identify genes associated with hair-
 CC bearing skin.

XX Sequence 11 BP; 3 A; 7 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 3.2e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22

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Db      1  CCCCCACCTAA 11
|||||  |||||
RESULT 723
ADQ35034/c
ID  ADQ35034 standard; DNA; 11 BP.
XX
AC  ADQ35034;
XX
DT  23-SEP-2004 (first entry)
XX
DE  Human facial skin-associated DNA fragment SEQ ID NO 3124.
XX
KW  facial skin; human; serial analysis of gene expression; SAGE;
KW  homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS  Homo sapiens.
XX
PN  DE10260928-A1.
XX
PD  08-JUL-2004.
XX
PF  20-DEC-2002; 2002DE-01060928.
XX
PR  20-DEC-2002; 2002DE-01060928.
XX
PA  (HENK ) HENKEL KGAA.
XX
PI  Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI  Conradt M, Hofmann K;
XX
WPI; 2004-518855/50.
XX
In vitro identification of genes important for facial skin, useful for
PT  assessing homeostasis and in screening for pharmaceutical or cosmetic
PT  agents, based on differential expression analysis.
XX
PS  Claim 4; SEQ ID NO 3124; 577pp; German.
XX
This invention describes a novel in vitro method for identifying genes
CC  that are significant for facial skin in humans. The method comprises
CC  recovering, from facial skin, a first mixture of genetically expressed
CC  (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC  their fragments), recovering a second, similar mixture from some other
CC  human tissue, preferably skin from a protected area, especially from the
CC  breast and subjecting the mixtures to serial analysis of gene expression
CC  (SAGE) to identify those genes for which expression is markedly different
CC  between facial skin and the other tissue. The invention also describes an
CC  in vitro method for determining homeostasis of human facial skin; a test
CC  kit which comprises a solid support (flexible or rigid) on which are
CC  immobilised probes that bind specifically to the factors of interest and
CC  a biochip for determining homeostasis of human facial skin. The products
CC  of the invention are also used in a method which determines activity of
CC  cosmetic and pharmaceutical agents for use against disorders or
CC  disturbances of the homeostasis of human skin and a screening method for
CC  identifying cosmetic and pharmaceutical agents. The method allows
CC  identification of as many as possible of the genes important for facial
CC  skin and thus of a very wide range of potential therapeutic and cosmetic
CC  agents. ADQ31911-ADQ35111 represent human DNA tag fragments used to
CC  identify the facial skin-associated genes described in the invention.
XX
SQ  Sequence 11 BP; 3 A; 2 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 TCATCGCCCT 16
||| |||||
Db 11 TCTGCGCCCT 1

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RESULT 724
ADQ34728
ID  ADQ34728 standard; DNA; 11 BP.
XX
AC  ADQ34728;
XX
DT  23-SEP-2004 (first entry)
XX
DE  Human facial skin-associated DNA fragment SEQ ID NO 2818.
XX
KW  facial skin; human; serial analysis of gene expression; SAGE;
KW  homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS  Homo sapiens.
XX
PN  DE10260928-A1.
XX
PD  08-JUL-2004.
XX
PF  20-DEC-2002; 2002DE-01060928.
XX
PR  20-DEC-2002; 2002DE-01060928.
XX
PA  (HENK ) HENKEL KGAA.
XX
PI  Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI  Conradt M, Hofmann K;
XX
WPI; 2004-518855/50.
XX
In vitro identification of genes important for facial skin, useful for
PT  assessing homeostasis and in screening for pharmaceutical or cosmetic
PT  agents, based on differential expression analysis.
XX
PS  Claim 4; SEQ ID NO 2818; 577pp; German.
XX
This invention describes a novel in vitro method for identifying genes
CC  that are significant for facial skin in humans. The method comprises
CC  recovering, from facial skin, a first mixture of genetically expressed
CC  (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC  their fragments), recovering a second, similar mixture from some other
CC  human tissue, preferably skin from a protected area, especially from the
CC  breast and subjecting the mixtures to serial analysis of gene expression
CC  (SAGE) to identify those genes for which expression is markedly different
CC  between facial skin and the other tissue. The invention also describes an
CC  in vitro method for determining homeostasis of human facial skin; a test
CC  kit which comprises a solid support (flexible or rigid) on which are
CC  immobilised probes that bind specifically to the factors of interest and
CC  a biochip for determining homeostasis of human facial skin. The products
CC  of the invention are also used in a method which determines activity of
CC  cosmetic and pharmaceutical agents for use against disorders or
CC  disturbances of the homeostasis of human skin and a screening method for
CC  identifying cosmetic and pharmaceutical agents. The method allows
CC  identification of as many as possible of the genes important for facial
CC  skin and thus of a very wide range of potential therapeutic and cosmetic
CC  agents. ADQ31911-ADQ35111 represent human DNA tag fragments used to
CC  identify the facial skin-associated genes described in the invention.
XX
SQ  Sequence 11 BP; 0 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 10 CGCCCTTCCT 20
||| |||||
Db 1 CGCCGCTTCT 11

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RESULT 725
ADQ32871
ID  ADQ32871 standard; DNA; 11 BP.
XX

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AC ADQ32871;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human facial skin-associated DNA fragment SEQ ID NO 961.
 XX
 KW facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX
 OS Homo sapiens.
 XX
 XX DE10260928-A1.
 XX
 XX 08-JUL-2004.
 XX
 XX 20-DEC-2002; 2002DE-01060928.
 XX
 XX 20-DEC-2002; 2002DE-01060928.
 XX
 XX (HENK) HENKEL KGAA.
 XX
 XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 PI
 XX WPI; 2004-518855/50.
 XX
 PT In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.
 XX
 PS Claim 5; SEQ ID NO 961; 577pp; German.
 XX
 CC This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.
 XX
 SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 30.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 3.2e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 4 CCTCATGCCCC 14
 Db 1 CCTCATTTCCC 11
 RESULT 726
 ADQ33165/c
 ID ADQ33165 standard; DNA; 11 BP.
 XX
 AC ADQ33165;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 KW Human facial skin-associated DNA fragment SEQ ID NO 1867.
 KW facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.

DE Human facial skin-associated DNA fragment SEQ ID NO 1255.
 XX facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX
 OS Homo sapiens.
 XX
 XX DE10260928-A1.
 XX
 XX 08-JUL-2004.
 XX
 XX 20-DEC-2002; 2002DE-01060928.
 XX
 XX 20-DEC-2002; 2002DE-01060928.
 XX
 XX (HENK) HENKEL KGAA.
 XX
 XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 PI
 XX WPI; 2004-518855/50.
 XX
 PT In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.
 XX
 PS Claim 5; SEQ ID NO 1255; 577pp; German.
 XX
 CC This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.
 XX
 SQ Sequence 11 BP; 3 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 30.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 3.2e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 12 CCCCTTCCTAA 22
 Db 11 CCCCTTCCTAA 1
 RESULT 727
 ADQ33777/c
 ID ADQ33777 standard; DNA; 11 BP.
 XX
 AC ADQ33777;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human facial skin-associated DNA fragment SEQ ID NO 1867.
 KW facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.

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XX OS Homo sapiens.
XX PN DE10260928-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060928.
XX PR 20-DEC-2002; 2002DE-01060928.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PN Conradt M, Hofmann K;
XX WPI; 2004-518855/50.
XX In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX Claim 5; SEQ ID NO 1867; 577pp; German.
XX This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to a serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX SQ Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TCGCCCTTCC 19
Db 11 TCGACCTGCC 1

RESULT 728
ADY89233/C
ID ADY89233 standard; RNA; 11 BP.
XX AC ADY89233;
XX 16-JUN-2005 (first entry)
XX DE VEGF siRNA SEQ ID NO 2269.
XX ss; siRNA; short interfering RNA; RNA interference; gene silencing; VEGF;
KW pharmaceutical; cancer; neoplasm; Cytostatic.
XX OS Synthetic.
XX PN WO2005028649-A1.

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XX PD 31-MAR-2005.
XX PF 16-SEP-2004; 2004WO-US030488.
XX PR 16-SEP-2003; 2003US-00664767.
XX PR 16-SEP-2003; 2003US-00685255.
XX PR 23-SEP-2003; 2003US-00670011.
XX PR 23-OCT-2003; 2003US-00693059.
XX PR 24-NOV-2003; 2003US-00720448.
XX PR 03-DEC-2003; 2003US-00727780.
XX PR 14-JAN-2004; 2004US-00757803.
XX PR 26-JAN-2004; 2004US-00764957.
XX PR 10-FEB-2004; 2004US-0543480P.
XX PR 13-FEB-2004; 2004US-00780447.
XX PR 16-APR-2004; 2004US-00826966.
XX PR 23-APR-2004; 2004US-00831620.
XX PR 30-APR-2004; 2004US-00013456.
XX PR 11-MAY-2004; 2004US-00844076.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX Jadhav V, Kossen K, Zinnen S, Vaish N, Mcswiggen J;
XX WPI; 2005-254128/26.
XX New multifunctional siNA molecule that directs cleavage of the first and
PT second VEGF or VEGFR target sequences via RNA interference, useful in
PT preparing a composition for treating cell proliferative disorders e.g.
PT cancers.
XX Disclosure; SEQ ID NO 2269; 396pp; English.
XX The invention relates to a multifunctional siNA molecule comprising a
CC structure having Formula MP-III and which directs cleavage of the first
CC and second VEGF or VEGFR target sequences via RNA interference. The
CC multifunctional siNA molecule is useful in preparing a pharmaceutical
CC composition for treating cell proliferative disorders, e.g. cancer. The
CC present sequence represents a VEGF siRNA.
XX SQ Sequence 11 BP; 5 A; 0 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
Db 11 CTCCTTCCT 1

RESULT 729
AEA14699/C
ID AEA14699 standard; DNA; 11 BP.
XX AC AEA14699;
XX 14-JUL-2005 (first entry)
XX DE Immunostimulatory oligonucleotide - SEQ ID 14.
XX Immune stimulation; viral infection; virucide; bacterial infection;
KW antibacterial; fungal infection; fungicide; parasitic infection;
KW antiparasitic; allergy; antiallergic; asthma; antiasthmatic; cancer;
KW cytostatic; ss.
XX OS Unidentified.
XX WO2005042018-A2.
XX 12-MAY-2005.
XX 29-OCT-2004; 2004WO-US036240.

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XX 30-OCT-2003; 2003US-0516193P.
XX (COLE-) COLEY PHARM GMBH.
XX (COLE-) COLEY PHARM GROUP INC.
XX Uhlmann E, Vollmer J, Krieg AM, Noll BO;
XX WPI; 2005-333611/34.
XX
XX New composition comprising an immunostimulatory nucleic acid molecule
XX useful for manufacturing a medicament for the treatment of an infection
XX (e.g. viral or bacterial), allergic condition (e.g. allergic asthma) or
XX cancer.
XX
XX Claim 29; SEQ ID NO 14; 113pp; English.
XX
XX The invention comprises a composition that contains an immunostimulatory
XX nucleic acid. The immunostimulatory nucleic acid of the invention is
XX useful for manufacturing a medicament for the treatment of an infection
XX (e.g. viral, bacterial, fungal or parasitical), an allergic condition
XX (e.g. allergic asthma), or cancer. The present DNA sequence represents an
XX immunostimulatory oligonucleotide of the invention.
XX
XX Sequence 11 BP; 2 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
XX
Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 ACCTCATCGCC 13
Db 11 ACCTCCTCGAC 1

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Search completed: May 9, 2006, 16:57:18
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:59:40 ; Search time 0.001 Seconds
(without alignments)
203.528 Million cell updates/sec

Title: US-09-904-968A-4-COPY
Perfect score: 26
Sequence: 1 ccacccatcgccctcccaagcat 26

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 309 seqs, 3914 residues

Total number of hits satisfying chosen parameters: 618

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 309 summaries

Database : pubmaindb4.*

Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	12.8	49.2	18	1	US-10-697-527-11
5	12.2	46.9	17	1	US-09-866-108-242
6	12.2	46.9	17	1	US-09-866-108-7555
7	12.2	46.9	17	1	US-09-780-533A-2547
8	12.2	46.9	17	1	US-10-723-361-242
9	12.2	46.9	17	1	US-10-723-361-7555
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11	11.4	43.8	13	1	US-10-257-017B-109216
12	11.2	43.1	16	1	US-10-604-944-105
13	10.8	41.5	15	1	US-10-056-414-33
14	10.8	41.5	15	1	US-10-056-414-126
15	10.8	41.5	15	1	US-10-056-414-153
16	10.8	41.5	15	1	US-10-056-414-158
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C 180	9.4	36.2	13	1	US-10-257-017B-171152	Sequence 171152,
C 181	9.4	36.2	13	1	US-10-257-017B-171713	Sequence 171713,
C 182	9.4	36.2	13	1	US-10-257-017B-171714	Sequence 171714,
C 183	9.4	36.2	13	1	US-10-257-017B-180561	Sequence 180561,
C 184	9.4	36.2	13	1	US-10-257-017B-180562	Sequence 180562,
C 185	9.4	36.2	13	1	US-10-257-017B-180569	Sequence 180569,
C 186	9.4	36.2	13	1	US-10-257-017B-187479	Sequence 187479,
C 187	9.4	36.2	13	1	US-10-257-017B-187480	Sequence 187480,
C 188	9.4	36.2	13	1	US-10-257-017B-193135	Sequence 193135,
C 189	9.4	36.2	13	1	US-10-257-017B-193136	Sequence 193136,
C 190	9.4	36.2	13	1	US-10-257-017B-205334	Sequence 205334,
C 191	9.4	36.2	13	1	US-10-257-017B-212563	Sequence 212563,
C 192	9.4	36.2	13	1	US-10-257-017B-212564	Sequence 212564,
C 193	9.4	36.2	13	1	US-10-257-017B-240965	Sequence 240965,
C 194	9.4	36.2	13	1	US-10-257-017B-240966	Sequence 240966,
C 195	9.4	36.2	13	1	US-10-257-017B-244719	Sequence 244719,
C 196	9.4	36.2	13	1	US-10-257-017B-244720	Sequence 244720,
C 197	9.4	36.2	13	1	US-10-257-017B-263651	Sequence 263651,
C 198	9.4	36.2	13	1	US-10-257-017B-263652	Sequence 263652,
C 199	9.4	36.2	13	1	US-10-984-919-1297	Sequence 1297, Ap
C 200	9.4	36.2	13	1	US-11-116-252-2	Sequence 2, Appl1
C 201	9.4	36.2	10	1	US-09-783-338A-2	Sequence 2, Appl1
C 202	9.4	36.2	10	1	US-09-978-333B-1	Sequence 1, Appl1
C 203	9.4	36.2	10	1	US-10-033-145-1976	Sequence 1976, Ap
C 204	9.4	36.2	10	1	US-10-055-713-51	Sequence 51, Appl
C 205	9.4	36.2	10	1	US-10-055-713-51	Sequence 51, Appl
C 206	9.4	36.2	10	1	US-10-418-552-37	Sequence 37, Appl
C 207	9.4	36.2	10	1	US-10-650-454-56	Sequence 56, Appl
C 208	9.4	36.2	10	1	US-10-470-180-51	Sequence 51, Appl
C 209	9.4	36.2	11	1	US-09-783-338A-1	Sequence 1, Appl
C 210	9.4	36.2	11	1	US-10-450-797-877	Sequence 877, Ap
C 211	9.4	36.2	11	1	US-10-257-017B-270857	Sequence 270857,
C 212	9.4	36.2	12	1	US-10-257-017B-271330	Sequence 271330,
C 213	9.4	36.2	12	1	US-10-257-017B-292022	Sequence 292022,
C 214	9.4	36.2	12	1	US-10-257-017B-292650	Sequence 292650,
C 215	9.4	36.2	12	1	US-10-257-017B-296570	Sequence 296570,
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C 222	9.4	36.2	12	1	US-10-257-017B-319501	Sequence 319501,
C 223	9.4	36.2	12	1	US-10-257-017B-321861	Sequence 321861,
C 224	9.4	36.2	12	1	US-10-257-017B-323643	Sequence 323643,
C 225	9.4	36.2	12	1	US-10-257-017B-324895	Sequence 324895,
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C 227	9.4	36.2	12	1	US-10-257-017B-331318	Sequence 331318,
C 228	9.4	36.2	12	1	US-10-257-017B-336647	Sequence 336647,
C 229	9.4	36.2	12	1	US-10-257-017B-339949	Sequence 339949,
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C 231	9.4	36.2	12	1	US-10-257-017B-351281	Sequence 351281,
C 232	9.4	36.2	12	1	US-10-257-017B-362364	Sequence 362364,
C 233	9.4	36.2	12	1	US-10-257-017B-368993	Sequence 368993,
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C 235	9.4	36.2	12	1	US-10-257-017B-372951	Sequence 372951,
C 236	9.4	36.2	12	1	US-10-257-017B-376095	Sequence 376095,
C 237	9.4	36.2	12	1	US-10-257-017B-379937	Sequence 379937,
C 238	9.4	36.2	12	1	US-10-661-165-565	Sequence 565, Ap
C 239	9.4	36.2	12	1	US-10-836-670-34	Sequence 34, Appl
C 240	9.4	36.2	12	1	US-10-257-017B-268660	Sequence 268660,
C 241	9.4	36.2	12	1	US-10-257-017B-269228	Sequence 269228,
C 242	9.4	36.2	12	1	US-10-257-017B-270998	Sequence 270998,
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C 244	9.4	36.2	12	1	US-10-257-017B-277116	Sequence 277116,
C 245	9.4	36.2	12	1	US-10-257-017B-278152	Sequence 278152,
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C 247	9.4	36.2	12	1	US-10-257-017B-280327	Sequence 280327,
C 248	9.4	36.2	12	1	US-10-257-017B-281811	Sequence 281811,
C 249	9.4	36.2	12	1	US-10-257-017B-286583	Sequence 286583,
C 250	9.4	36.2	12	1	US-10-257-017B-287738	Sequence 287738,
C 251	9.4	36.2	12	1	US-10-257-017B-290339	Sequence 290339,
C 252	9.4	36.2	12	1	US-10-257-017B-292113	Sequence 292113,

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279 8.8 33.8 12 1 US-10-257-017B-329701 Sequence 329701,
280 8.8 33.8 12 1 US-10-257-017B-334701 Sequence 334701,
281 8.8 33.8 12 1 US-10-257-017B-335615 Sequence 335615,
282 8.8 33.8 12 1 US-10-257-017B-337282 Sequence 337282,
283 8.8 33.8 12 1 US-10-257-017B-339583 Sequence 339583,
284 8.8 33.8 12 1 US-10-257-017B-344435 Sequence 344435,
285 8.8 33.8 12 1 US-10-257-017B-344822 Sequence 344822,
286 8.8 33.8 12 1 US-10-257-017B-348072 Sequence 348072,
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288 8.8 33.8 12 1 US-10-257-017B-349377 Sequence 349377,
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307 8.8 33.8 12 1 US-10-257-017B-378396 Sequence 378396,
308 8.8 33.8 12 1 US-10-257-017B-381325 Sequence 381325,
309 8.8 33.8 12 1 US-10-257-017B-381966 Sequence 381966,

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ALIGNMENTS

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RESULT 1
US-09-904-968A-4
; Sequence 4, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMING, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHAKDEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2

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; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer BPR9
US-09-904-968A-4
Query Match 100.0%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.52; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCACCTATGCGCCCTTCTTAAGCAT 26
Db 1 CCACCTATGCGCCCTTCTTAAGCAT 26

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RESULT 2
US-10-455-229-6/c
; Sequence 6, Application US/10455229
; Publication No. US20040016030A1
; GENERAL INFORMATION:
; APPLICANT: LOWE, BRENDA A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF MAIZE LINES
; FILE REFERENCE: DEKM:195US
; CURRENT APPLICATION NUMBER: US/10/455,229
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 60/386,522
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-455-229-6
Query Match 55.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 6 TCATCGCCCTTCTTA 21
Db 20 TCATCGCCCTTCTTA 5

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RESULT 3
US-08-983-605-11
; Sequence 11, Application US/08983605A
; Publication No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum aestivum and Triticum Triticum and the Use of
; FILE REFERENCE: 2936.10400
; CURRENT APPLICATION NUMBER: US/08/983,605A
; CURRENT FILING DATE: 1998-05-01
; EARLIER APPLICATION NUMBER: DE 195 25 284.5
; EARLIER FILING DATE: 1995-06-28

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; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-11

Query Match          49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTGATGCCCCCT 16
Db      2 CGACCTGATGCCCCCT 17

RESULT 4
US-10-697-527-11
; Sequence 11, Application US/10697527
; Publication No. US20040146898A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: MICROSATELLITE MARKERS FOR PLANTS OF THE SPECIES TRITICUM AESTIVUM
; FILE REFERENCE: US 08/983,605
; CURRENT APPLICATION NUMBER: US/10/697,527
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: PCT/DE96/01185
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: DE 195 25 284.5
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Triticum sp.
US-10-697-527-11

Query Match          49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTGATGCCCCCT 16
Db      2 CGACCTGATGCCCCCT 17

RESULT 5
US-09-866-108-242
; Sequence 242, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 242
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-242

Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 CCTCATGCCCCCTTCTCT 20
Db      1 CATCTCGCCCCCTCTCT 17

RESULT 6
US-09-866-108-7555/C
; Sequence 7555, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7555
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7555

Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 TCGCCCTTCTTAAGCA 25
DB 17 TGGCCCGCTCATAGCA 1

RESULT 7
US-09-780-533A-2547/c
; Sequence 2547, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowitra, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2547
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2547

Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTCATGCCCCCTTCTTA 21
DB 17 CTCATGCGCTTCTCAT 1

RESULT 8
US-10-723-361-242
; Sequence 242, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
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; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 242
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-242

Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTCATGCCCCCTTCTT 20
DB 1 CATCTGCGCCCTCTCT 17

RESULT 9
US-10-723-361-7555/c
; Sequence 7555, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 7555
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7555

Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      9 TCGCCCTTCTATAGCA 25
Db      17 TGGCCCGTCATAGCA 1

RESULT 10
US-10-257-017B-109215/c
; Sequence 109215, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 109215
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027329
US-10-257-017B-109215

Query Match          43.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 67;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCCC 15
Db      13 ACCTCATCCCCC 1

RESULT 11
US-10-257-017B-109216
; Sequence 109216, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
;

; SEQ ID NO 109216
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027329
US-10-257-017B-109216

Query Match          43.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 67;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCCC 15
Db      1 ACCTCATCCCCC 13

RESULT 12
US-10-604-944-105/c
; Sequence 105, Application US/10604944
; Publication No. US20040219515A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL HIV REGULATORY GENES
; FILE REFERENCE: 55008
; CURRENT APPLICATION NUMBER: US/10/604,944
; CURRENT FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus 1
US-10-604-944-105

Query Match          43.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 69;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCACCTCATCGCCCT 16
Db      16 CAACATCATCTCCCT 1

RESULT 13
US-10-056-414-33
; Sequence 33, Application US/10056414
; Publication No. US20030003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; RELATED TO LEVELS OF
; NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 613 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-056-414-33

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 79;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACCTCATGCGCC 14
Db 2 CCACCTCATGCGCC 15

RESULT 14
US-10-056-414-126
Sequence 126, Application US/10056414
Publication No. US2003003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
McSwigen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
Street: 633 West Fifth Street
Suite 4700
City: Los Angeles
State: California
Country: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-10-056-414-126

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 79;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GCCCCTTCTTAAGC 24
Db 1 GUCCCTUCUACG 14

RESULT 15
US-10-056-414-153
Sequence 153, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
McSwigen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
Street: 633 West Fifth Street
Suite 4700
City: Los Angeles
State: California
Country: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 153:
US-10-056-414-153

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 79;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCTTACG 24
Db 1 GUCCCUCCUCACG 14

RESULT 16
US-10-056-414-158
Sequence 158, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 158:
US-10-056-414-158

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 79;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCTTACG 24
Db 2 GUCCCUCCUCACG 15

RESULT 17
US-10-056-414-162
Sequence 162, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-10-056-414-162

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATGCCCTTCTCT 20
Db 2 CAUGGUCUCCUCCU 15

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RESULT 18
US-10-257-017B-303995/c
; Sequence 303995, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303995
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020735
US-10-257-017B-303995

Query Match      40.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 92;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 CCCCTTCTAG 23
Db      12 CCCCTCTCTAG 1

RESULT 19
US-10-257-017B-308420/c
; Sequence 308420, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 308420
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023007
US-10-257-017B-308420

Query Match      40.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 92;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      14 CCTTCTTAACA 25
Db      12 CCTTCTTAACA 1

RESULT 20
US-10-257-017B-2227/c
; Sequence 2227, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

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; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 2227
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC000901
US-10-257-017B-2227

Query Match      40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      14 CCTTCTTAACA 25
Db      12 CCTTCTTAACA 1

RESULT 21
US-10-257-017B-2228
; Sequence 2228, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 2228
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC000901
US-10-257-017B-2228

Query Match      40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      14 CCTTCTTAACA 25
Db      2 CCTTCTTAACA 13

RESULT 22
US-10-257-017B-11629/c
; Sequence 11629, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 11629
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC000901
US-10-257-017B-11629
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; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 11629
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002818
US-10-257-017B-11629

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15
Db 13 CCTCATCGCCCC 2

RESULT 23
US-10-257-017B-11630
; Sequence 11630, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 11630
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002818
US-10-257-017B-11630

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15
Db 1 CCTCATCGCCCC 12

RESULT 24
US-10-257-017B-63253/c
; Sequence 63253, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 63253
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016710
US-10-257-017B-63253

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15
Db 12 CCTCATCGCCCC 1

RESULT 25
US-10-257-017B-63254
; Sequence 63254, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 63254
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016710
US-10-257-017B-63254

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15
Db 2 CCTCATCGCCCC 13

RESULT 26
US-10-257-017B-86351/c
; Sequence 86351, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 86351
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021689
US-10-257-017B-86351

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      4 CCTCATGCCCC 15
      |||||
Db      13 CCTCACCGCCCC 2

RESULT 27
US-10-257-017B-86352
; Sequence 86352, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 86352
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021689
US-10-257-017B-86352

Query Match      40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCTCATGCCCC 15
      |||||
Db      1 CCTCACCGCCCC 12

RESULT 28
US-10-257-017B-171701/c
; Sequence 171701, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171701
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042797
US-10-257-017B-171701

Query Match      40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCTCATGCCCC 15
      |||||
Db      12 CCTCATCTCCCC 1

RESULT 29
US-10-257-017B-171702
; Sequence 171702, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171702
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042797
US-10-257-017B-171702

Query Match      40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCTCATGCCCC 15
      |||||
Db      2 CCTCATCTCCCC 13

RESULT 30
US-10-257-017B-182255/c
; Sequence 182255, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 182255
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045047
US-10-257-017B-182255

Query Match      40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 CATGCCCCCTTC 18
      |||||
Db      13 CATGCCCCCTTC 2

RESULT 31
US-10-257-017B-182256
; Sequence 182256, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
```

```

; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 182256
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045047
US-10-257-017B-182256

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CATGCCCTTC 18
Db      1 CATGCCCTTC 12

RESULT 32
US-10-257-017B-209367/C
; Sequence 209367, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 209367
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0051131
US-10-257-017B-209367

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TCGCCCTTCCT 20
Db      13 TCACCCCTTCCT 2

RESULT 33
US-10-257-017B-209368
; Sequence 209368, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 209368
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0051131
US-10-257-017B-209368

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TCGCCCTTCCT 20
Db      13 TCACCCCTTCCT 2

RESULT 34
US-10-257-017B-303994/C
; Sequence 303994, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303994
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020735
US-10-257-017B-303994

Query Match          38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCTA 21
Db      12 CCCCTTCCTA 3

RESULT 35
US-10-257-017B-307435
; Sequence 307435, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307435
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022495
US-10-257-017B-307435
```


Query Match 38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 CCCCTTCTTA 21
DB 3 CCCCTTCTTA 12

RESULT 36
US-10-257-017B-315233
; Sequence 315233, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 315233
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026790
US-10-257-017B-315233

Query Match 38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCACCTATC 10
DB 2 CCACCTATC 11

RESULT 37
US-10-257-017B-321799/C
; Sequence 321799, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 321799
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030498
US-10-257-017B-321799

Query Match 38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CCCTTCTTAA 22
DB 13 CCCTTCTTAA 22

DB 12 CCCTTCTTAA 3

RESULT 38
US-10-257-017B-322509
; Sequence 322509, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322509
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide-primer
US-10-257-017B-322509

Query Match 38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CCCTTCTTAA 22
DB 1 CCCTTCTTAA 10

RESULT 39
US-10-257-017B-348675/C
; Sequence 348675, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 348675
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045700
US-10-257-017B-348675

Query Match 38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CCCTTCTTAA 22
DB 12 CCCTTCTTAA 3

RESULT 40
US-10-257-017B-357467
; Sequence 357467, Application US/10257017B
; Publication No. US20040241651A1

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 357467
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050637
US-10-257-017B-357467

Query Match      38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
Db      1 CCCTTCCTAA 10

RESULT 41
US-10-257-017B-374592
; Sequence 374592, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 374592
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060789
US-10-257-017B-374592

Query Match      38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
Db      3 CCCTTCCTAA 12

RESULT 42
US-10-257-017B-381693
; Sequence 381693, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 381693
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064489
US-10-257-017B-381693

Query Match      38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCTA 21
Db      2 CCCCTTCCTA 11

RESULT 43
US-10-257-017B-1599/C
; Sequence 1599, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 1599
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0000579
US-10-257-017B-1599

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
Db      13 CCCTTCCTAA 4

RESULT 44
US-10-257-017B-1600
; Sequence 1600, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 1600
; LENGTH: 13
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC000579
US-10-257-017B-1600
```

```
Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          13 CCCTTCTCTAA 22
              |||||
Db           1 CCGTTCCTTA 10
```

```
RESULT 45
US-10-257-017B-24289/c
; Sequence 24289, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 24289
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0005767
US-10-257-017B-24289
```

```
Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY          11 GCCCCTTCTTAA 22
              :|||
Db           13 RCCCCATCTTA 2
```

```
RESULT 46
US-10-257-017B-24290
; Sequence 24290, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 24290
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0005767
US-10-257-017B-24290
```

```
Query Match          38.5%; Score 10; DB 1; Length 13;
```

```
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY          11 GCCCCTTCTTAA 22
              :|||
Db           1 RCCCCATCTTA 12
```

```
RESULT 47
US-10-257-017B-30023/c
; Sequence 30023, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 30023
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009041
US-10-257-017B-30023
```

```
Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          7 CATGCCCCCT 16
              |||||
Db           13 CATGCCCCCT 4
```

```
RESULT 48
US-10-257-017B-30024
; Sequence 30024, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 30024
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009041
US-10-257-017B-30024
```

```
Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          7 CATGCCCCCT 16
              |||||
Db           1 CATGCCCCCT 10
```

```
RESULT 49
US-10-257-017B-51035/c
; Sequence 51035, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 51035
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014276
US-10-257-017B-51035

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
      |||||
Db      10 CCCTTCCTAA 1

RESULT 50
US-10-257-017B-51036
; Sequence 51036, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 51036
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014276
US-10-257-017B-51036

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
      |||||
Db      4 CCCTTCCTAA 13

RESULT 51
US-10-257-017B-78483/c
; Sequence 78483, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 78483
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019989
US-10-257-017B-78483

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACCTCATC 10
      |||||
Db      11 CCACCTCATC 2

RESULT 52
US-10-257-017B-78484
; Sequence 78484, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 78484
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019989
US-10-257-017B-78484

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACCTCATC 10
      |||||
Db      3 CCACCTCATC 12

RESULT 53
US-10-257-017B-80875/c
; Sequence 80875, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 80875
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019989
US-10-257-017B-80875/c

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACCTCATC 10
      |||||
Db      3 CCACCTCATC 12
```

```

; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 80875
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020490
US-10-257-017B-80875

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
DB      10 CCCTTCCTAA 1

RESULT 54
US-10-257-017B-80876
; Sequence 80876, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 80876
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020490
US-10-257-017B-80876

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
DB      4 CCCTTCCTAA 13

RESULT 55
US-10-257-017B-133103/C
; Sequence 133103, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 133103
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033208
US-10-257-017B-133103

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
DB      11 CCCTTCCTAA 2

RESULT 56
US-10-257-017B-133104
; Sequence 133104, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 133104
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033208
US-10-257-017B-133104

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
DB      3 CCCTTCCTAA 12

RESULT 57
US-10-257-017B-133107/C
; Sequence 133107, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 133107
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033208
US-10-257-017B-133107

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 13 CCCTTCCTAA 22
| | | | |
Db 11 CCCTTCCTAA 2

RESULT 58

US-10-257-017B-133108
; Sequence 133108, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 133108
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033208
US-10-257-017B-133108

Query Match

Best Local Similarity 38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
| | | | |
Db 3 CCCTTCCTAA 12

RESULT 59

US-10-257-017B-193907/c
; Sequence 193907, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 193907
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047683
US-10-257-017B-193907

Query Match

Best Local Similarity 38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
| | | | |
Db 13 CCCTTCCTAA 4

RESULT 60

US-10-257-017B-193908
; Sequence 193908, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 193908
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047683
US-10-257-017B-193908

Query Match

Best Local Similarity 38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
| | | | |
Db 1 CCCTTCCTAA 10

RESULT 61

US-10-257-017B-237207/c
; Sequence 237207, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 237207
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0057853
US-10-257-017B-237207

Query Match

Best Local Similarity 38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
| | | | |
Db 12 CCCTTCCTAA 3

RESULT 62

US-10-257-017B-237208
; Sequence 237208, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

```

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 237208
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0057853
US-10-257-017B-237208

Query Match      38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13  CCCTTCCTAA 22
Db      2  CCCTTCCTAA 11

RESULT 63
US-09-997-672-39/c
; Sequence 39, Application US/09997672
; Publication No. US20030061632A1
; GENERAL INFORMATION:
; APPLICANT: Weterings, Koen
; APPLICANT: Apuya, Nestor R.
; APPLICANT: Tatarinova, Tatiana
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Polynucleotides Useful for Modulating Transcription
; FILE REFERENCE: 023070-115810US
; CURRENT APPLICATION NUMBER: US/09/997,672
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,672
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:H-AP56 forward
US-09-997-672-39

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      14  CCTTCTAGCAT 26
Db     13  CCTTCATAGCTT 1

RESULT 64
US-10-257-017B-5801/c
; Sequence 5801, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
```

```

; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 5801
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001882
US-10-257-017B-5801

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CCTCATGCCCCCT 16
Db     13  CCTCATGCTACTT 1

RESULT 65
US-10-257-017B-5802
; Sequence 5802, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 5802
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001882
US-10-257-017B-5802

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CCTCATGCCCCCT 16
Db     13  CCTCATGCTACTT 13

RESULT 66
US-10-257-017B-16407/c
; Sequence 16407, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 16407
; LENGTH: 13
```

```
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003579
US-10-257-017B-16407
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATGCCCCCTTCCT 20
Db 13 ATCTCCCCCTTCCT 1

```
RESULT 67
US-10-257-017B-16408
Sequence 16408, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 16408
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003579
US-10-257-017B-16408
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATGCCCCCTTCCT 20
Db 1 ATCTCCCCCTTCCT 13

```
RESULT 68
US-10-257-017B-31007/c
Sequence 31007, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 31007
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009549
US-10-257-017B-31007
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;

Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCTTAAGCAT 26
Db 13 CCTTCTTAATCCAT 1

```
RESULT 69
US-10-257-017B-31008
Sequence 31008, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 31008
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009549
US-10-257-017B-31008
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCTTAAGCAT 26
Db 1 CCTTCTTAATCCAT 13

```
RESULT 70
US-10-257-017B-58775/c
Sequence 58775, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 58775
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015747
US-10-257-017B-58775
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACCTATCGCCC 14
Db 13 CACCCATCCCCC 1


```
RESULT 71
US-10-257-017B-58776
; Sequence 58776, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 58776
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015747
US-10-257-017B-58776

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CACCTCATGCCCC 14
Db      1 CACCCCATCCCCC 13

RESULT 72
US-10-257-017B-103101/c
; Sequence 103101, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103101
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025784
US-10-257-017B-103101

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 CATGCCCCCTTCC 19
Db      13 CATCCCCCATCC 1

RESULT 73
US-10-257-017B-103102
; Sequence 103102, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

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; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103102
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025784
US-10-257-017B-103102

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 CATGCCCCCTTCC 19
Db      1 CATCCCCCATCC 13

RESULT 74
US-10-257-017B-109217/c
; Sequence 109217, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 109217
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027329
US-10-257-017B-109217

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 ACCTCATGCCCC 15
Db      13 ACCTCAACCCCC 1

RESULT 75
US-10-257-017B-109218
; Sequence 109218, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
```

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; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 109218
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027329
US-10-257-017B-109218

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  ACCTCATCGCCCC 15
DB      1  ACCTCAACCCCC 13

RESULT 76
US-10-257-017B-111859/c
; Sequence 111859, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111859
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027920
US-10-257-017B-111859

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10  CGCCCTTCTCTAA 22
DB      13  CCCCCCTACTCTAA 1

RESULT 77
US-10-257-017B-111860
; Sequence 111860, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111860
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027920
US-10-257-017B-111860

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10  CGCCCTTCTCTAA 22
DB      13  CCCCCCTACTCTAA 1

RESULT 78
US-10-257-017B-114403/c
; Sequence 114403, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 114403
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028646
US-10-257-017B-114403

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  ACCTCATCGCCCC 15
DB      13  ACCTCATCTCTCC 1

RESULT 79
US-10-257-017B-114404
; Sequence 114404, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 114404
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028646
US-10-257-017B-114404

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 3 ACCTCATGCCCC 15
|||
Db 1 ACCTCATCTCTCC 13

RESULT 80

US-10-257-017B-142679/C
; Sequence 142679, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 142679
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035782
US-10-257-017B-142679

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 CCTTCCTAAGCAT 26
|||||
Db 13 CCTTCATTAACAT 1

RESULT 81

US-10-257-017B-142680
; Sequence 142680, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 142680
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035782
US-10-257-017B-142680

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 CCTTCCTAAGCAT 26
|||||
Db 1 CCTTCATTAACAT 13

RESULT 82

US-10-257-017B-146283/C
; Sequence 146283, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 146283
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036653
US-10-257-017B-146283

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 CCTTCCTAAGCA 25
|||||
Db 13 CCTTCCCAACA 1

RESULT 83

US-10-257-017B-146284
; Sequence 146284, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 146284
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036653
US-10-257-017B-146284

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 CCTTCCTAAGCA 25
|||||
Db 1 CCTTCCCAACA 13

RESULT 84

US-10-257-017B-160217/C
; Sequence 160217, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160217
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040348
US-10-257-017B-160217

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCTCTAA 22
      ||| ||| ||| |||
Db      13 CACTCTTCTCTAA 1

RESULT 85
US-10-257-017B-160218
; Sequence 160218, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160218
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040348
US-10-257-017B-160218

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCTCTAA 22
      ||| ||| ||| |||
Db      1 CACTCTTCTCTAA 13

RESULT 86
US-10-257-017B-178305/c
; Sequence 178305, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008146

; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 178305
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044162
US-10-257-017B-178305

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 CCTTCTCTAGCA 25
      ||| ||| ||| |||
Db      13 CCTTCTCTAGCA 1

RESULT 87
US-10-257-017B-178306
; Sequence 178306, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 178306
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044162
US-10-257-017B-178306

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 CCCTTCTCTAGCA 25
      ||| ||| ||| |||
Db      1 CTTTCTCTAGCA 13

RESULT 88
US-10-257-017B-205671/c
; Sequence 205671, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 205671
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008146
```

```
US-10-257-017B-205671
Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      14 CCTTCTTAAGCAT 26
      ||| ||| ||| |||
Db      13 CCTCCTTAATCAT 1

RESULT 89
US-10-257-017B-205672
; Sequence 205672, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 205672
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008146
US-10-257-017B-205672

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      14 CCTTCTTAAGCAT 26
      ||| ||| ||| |||
Db      1 CCTCCTTAATCAT 13

RESULT 90
US-10-257-017B-220613/c
; Sequence 220613, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 220613
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053694
US-10-257-017B-220613

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      13 CCTTCTTAAGCA 25
```

```
Db      13 CCTTACTAAGCA 1

RESULT 91
US-10-257-017B-220614
; Sequence 220614, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 220614
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053694
US-10-257-017B-220614

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      13 CCTTCTTAAGCA 25
      ||| ||| ||| |||
Db      1 CCTTACTAAGCA 13

RESULT 92
US-10-257-017B-230287/c
; Sequence 230287, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 230287
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0056170
US-10-257-017B-230287

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      14 CCTTCTTAAGCAT 26
      ||| ||| ||| |||
Db      13 CCTCCTTAACCAT 1

RESULT 93
US-10-257-017B-230288
; Sequence 230288, Application US/10257017B
```

```
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 230288
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0056170
US-10-257-017B-230288

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCTTAAGCAT 26
DB      1 CTTCCCTTAACCAT 13

RESULT 94
US-10-257-017B-263207/C
; Sequence 263207, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 263207
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000489
US-10-257-017B-263207

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCTTAAGCAT 26
DB      13 CATTCTTAACAT 1
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 263208
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000489
US-10-257-017B-263208

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCTTAAGCAT 26
DB      1 CATTCTTAACAT 13

RESULT 96
US-10-984-919-1296
; Sequence 1296, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiefen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1296
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1296

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 CCCCTTCTTAAGC 24
DB      1 CTCCTCTTAAGC 13

RESULT 97
US-10-836-670-18
; Sequence 18, Application US/10836670
; Publication No. US20040235031A1
; GENERAL INFORMATION:
; APPLICANT: Schultz, Gregory Scott
; APPLICANT: Lewin, Alfred Samuel
; APPLICANT: Bialock, Timothy D.
; TITLE OF INVENTION: ANTI-SCARRING RIBOZYMES AND METHODS
; FILE REFERENCE: 5853-303
; CURRENT APPLICATION NUMBER: US/10/836,670
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 57
```

```
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 12
TYPE: DNA
ORGANISM: Human adenovirus type 1
US-10-836-670-18
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy          4 CCTCATCGCCC 14
            |||||
Db          1 CCTCCTCGCCC 11
```

```
RESULT 98
US-10-257-017B-276286
Sequence 276286, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 276286
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004140
US-10-257-017B-276286
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy          5 CTGATCGCCC 15
            |||||
Db          2 CTCATCGCCC 12
```

```
RESULT 99
US-10-257-017B-283032/c
Sequence 283032, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 283032
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004140
US-10-257-017B-283032
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy          4 CCTCATCGCCC 14
            |||||
Db          12 CCTCATCGCAC 2
```

```
RESULT 100
US-10-257-017B-283033/c
Sequence 283033, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 283033
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011109
US-10-257-017B-283033
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy          4 CCTCATCGCCC 14
            |||||
Db          12 CCTCATCGCCG 2
```

```
RESULT 101
US-10-257-017B-288035
Sequence 288035, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 288035
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013344
US-10-257-017B-288035
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy          4 CCTCATCGCCC 14
            |||||
Db          1 CCTCACC GCC 11
```

```
RESULT 102
US-10-257-017B-290681/c
; Sequence 290681, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290681
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014470
US-10-257-017B-290681

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CCTTCCTAGC 24
Db      12 CCTTCCTAAC 2

RESULT 103
US-10-257-017B-291350/c
; Sequence 291350, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 291350
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014761
US-10-257-017B-291350

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 TTCCTAGCAT 26
Db      12 TTCCTAACAT 2

RESULT 104
US-10-257-017B-300973
; Sequence 300973, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300973
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019284
US-10-257-017B-300973

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCTAA 22
Db      2 CCCCTTCTTA 12

RESULT 105
US-10-257-017B-305394
; Sequence 305394, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 305394
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021425
US-10-257-017B-305394

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCTAA 22
Db      2 CCCCTTCTTA 12

RESULT 106
US-10-257-017B-306843/c
; Sequence 306843, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306843
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021425
US-10-257-017B-306843/c

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCTAA 22
Db      2 CCCCTTCTTA 12
```



```

; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306843
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022198
US-10-257-017B-306843

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTCTAA 22
DB 11 CTCCTTCTCTAA 1

RESULT 107
US-10-257-017B-307267
; Sequence 307267, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307267
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022406
US-10-257-017B-307267

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCTTAGCAT 26
DB 2 TTCTTAGCAT 12

RESULT 108
US-10-257-017B-307408/c
; Sequence 307408, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307408
; LENGTH: 12
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022484
US-10-257-017B-307408

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTCTAA 22
DB 11 CCCCTTCTCTAA 1

RESULT 109
US-10-257-017B-313315/c
; Sequence 313315, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 313315
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025663
US-10-257-017B-313315

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTCTAA 22
DB 12 CCTCTTCTCTAA 2

RESULT 110
US-10-257-017B-316732
; Sequence 316732, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 316732
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027582
US-10-257-017B-316732

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTTCTTACCA 25
| | | | | | | | | |
Db 2 CTTCTTACCA 12

RESULT 111

```
US-10-257-017B-317750/c
; Sequence 317750, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317750
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028225
US-10-257-017B-317750
```

Query Match 36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTTAA 22
| | | | | | | | | |
Db 12 CCCCTTCTTAA 2

RESULT 112

```
US-10-257-017B-324000/c
; Sequence 324000, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 324000
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031723
US-10-257-017B-324000
```

Query Match 36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTTAA 22
| | | | | | | | | |
Db 12 CCCCTTCTTAA 2

RESULT 113

```
US-10-257-017B-324164
; Sequence 324164, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 324164
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031842
US-10-257-017B-324164
```

Query Match 36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CTTCTTCTTAA 24
| | | | | | | | | |
Db 1 CTTCTTCTTAA 11

RESULT 114

```
US-10-257-017B-330982
; Sequence 330982, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 330982
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0035890
US-10-257-017B-330982
```

Query Match 36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTTAA 22
| | | | | | | | | |
Db 2 CCCCTTCTTAA 12

RESULT 115

```
US-10-257-017B-341250
; Sequence 341250, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341250
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0041948
US-10-257-017B-341250

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 CATGCGCCCTT 17
Db      1 CATGCGCTCTT 11

RESULT 116
US-10-257-017B-341938/C
; Sequence 341938, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341938
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042302
US-10-257-017B-341938

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      15 CTTCCTAACA 25
Db      12 CTTCCTAACA 2

RESULT 117
US-10-257-017B-344659
; Sequence 344659, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 344659
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043651
US-10-257-017B-344659

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      14 CCTTCCTAAC 24
Db      1 CCTTCCTAAC 11

RESULT 118
US-10-257-017B-349772
; Sequence 349772, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 349772
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046308
US-10-257-017B-349772

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCTCATGCCC 14
Db      2 CCTCATGCCC 12

RESULT 119
US-10-257-017B-351147
; Sequence 351147, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 351147
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0047122
US-10-257-017B-351147

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CTCATCGCCCC 15
DB 1 CTCCTCGCCCC 11

RESULT 120
US-10-257-017B-353448
; Sequence 353448, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353448
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048524
US-10-257-017B-353448

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTTAA 22
DB 1 CACCTTCTTAA 11

RESULT 121
US-10-257-017B-376045
; Sequence 376045, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 376045
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061586
US-10-257-017B-376045

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATCGC 12
DB 2 CACCTCATCTC 12

RESULT 122
US-10-257-017B-377399
; Sequence 377399, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 377399
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010447
US-10-257-017B-377399

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTTAA 22
DB 1 CCCCTTCTTAA 11

RESULT 123
US-10-994-626-31
; Sequence 31, Application US/10994626
; Publication No. US20050112677A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A substrate having an oxide layer, method for detecting a target
; FILE REFERENCE: P051212
; CURRENT APPLICATION NUMBER: US/10/994,626
; CURRENT FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 31
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe oligonucleotide
US-10-994-626-31

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGCCCTTCTCT 20
DB 2 CGCCCTTCTTCT 12

RESULT 124
US-11-078-601-53
; Sequence 53, Application US/11078601
; Publication No. US20050202492A1
; GENERAL INFORMATION:
```

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; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A microarray having probe polynucleotide spots binding to a same
; TITLE OF INVENTION: Target polynucleotide fragment maximally apart therebetween and
; FILE REFERENCE: PNO52961
; CURRENT APPLICATION NUMBER: US/11/078,601
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Kopacentic 1.71
; SEQ ID NO 53
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe polynucleotide
US-11-078-601-53

Query Match      36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 CGCCCTTCTT 20
Db      2 CGCCCTTCTT 12

RESULT 125
US-10-257-017B-5883/C
; Sequence 5883, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 5883
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001890
US-10-257-017B-5883

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CACCTATCGC 12
Db      11 CACCTATCGC 1

RESULT 126
US-10-257-017B-5884
; Sequence 5884, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 5884
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001890
US-10-257-017B-5884
```

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; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 5884
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001890
US-10-257-017B-5884

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CACCTATCGC 12
Db      3 CACCTATCGC 13

RESULT 127
US-10-257-017B-11473/C
; Sequence 11473, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 11473
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002797
US-10-257-017B-11473

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CACCTATCGC 12
Db      11 CACCTATCGC 1

RESULT 128
US-10-257-017B-11474
; Sequence 11474, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 11474
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002797
US-10-257-017B-11474
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC002797
US-10-257-017B-11474

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATCGC 12
DB 3 CACTCATCGC 13

RESULT 129
US-10-257-017B-33623/C
; Sequence 33623, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 33623
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010714
US-10-257-017B-33623

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCT 16
DB 11 TCATCGCTCT 1

RESULT 130
US-10-257-017B-33624
; Sequence 33624, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 33624
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010714
US-10-257-017B-33624

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCTTAAGCAT 26
DB 1 TTCTTAACCAT 11

RESULT 132
US-10-257-017B-37116
; Sequence 37116, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 37116
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011591
US-10-257-017B-37116

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCTTAAGCAT 26
DB 1 TTCTTAACCAT 11

RESULT 133
US-10-257-017B-47113/C

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCTTAAGCAT 26
DB 1 TTCTTAACCAT 11

RESULT 133
US-10-257-017B-47113/C
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; Sequence 47113, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 47113
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013556
US-10-257-017B-47113

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
DB 11 CCCCTTACTAA 1

RESULT 134
US-10-257-017B-47114
; Sequence 47114, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 47114
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013556
US-10-257-017B-47114

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
DB 3 CCCCTTACTAA 13

RESULT 135
US-10-257-017B-55917/c
; Sequence 55917, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 55917
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015221
US-10-257-017B-55917

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; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 55917
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015221
US-10-257-017B-55917

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CTCATCGCCCC 15
DB 13 CTCCTCGCCCC 3

RESULT 136
US-10-257-017B-55918
; Sequence 55918, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 55918
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015221
US-10-257-017B-55918

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CTCATCGCCCC 15
DB 1 CTCCTCGCCCC 11

RESULT 137
US-10-257-017B-74019/c
; Sequence 74019, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 74019
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015221
US-10-257-017B-74019/c

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```
; SEQ ID NO 74019
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019042
US-10-257-017B-74019

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCCC 15
Db      13 RCTCTCTCCCCC 1

RESULT 138
US-10-257-017B-74020
; Sequence 74020, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 74020
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019042
US-10-257-017B-74020

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCCC 15
Db      1 RCTCTCTCCCCC 13

RESULT 139
US-10-257-017B-87741/c
; Sequence 87741, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 87741
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022068
US-10-257-017B-87741

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCTCATCGCCC 14
Db      13 CCTCATCGCCC 3

RESULT 140
US-10-257-017B-87742
; Sequence 87742, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 87742
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022068
US-10-257-017B-87742

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCTCATCGCCC 14
Db      1 CCACATCGCCC 11

RESULT 141
US-10-257-017B-87751/c
; Sequence 87751, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 87751
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022068
US-10-257-017B-87751

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCTCATCGCCC 14
Db      1 CCTCATCGCCC 14
```



```
Db          13 CCGCATCGCCC 3

RESULT 142
US-10-257-017B-87752
; Sequence 87752, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 87752
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022068
US-10-257-017B-87752

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          4 CCTCATCGCCC 14
Db          1 CCGCATCGCCC 11

RESULT 143
US-10-257-017B-88487/C
; Sequence 88487, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88487
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022233
US-10-257-017B-88487

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TCGCCCTTCC 19
Db          13 TCTCCCTTCC 3

RESULT 144
US-10-257-017B-88488
; Sequence 88488, Application US/10257017B
; Publication No. US20040241651A1

; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88488
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022233
US-10-257-017B-88488

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TCGCCCTTCC 19
Db          13 TCTCCCTTCC 3

RESULT 145
US-10-257-017B-97321/C
; Sequence 97321, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 97321
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024141
US-10-257-017B-97321

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          12 CCCCTTCTTCA 22
Db          12 CCCCTTCTTCA 2

RESULT 146
US-10-257-017B-97322
; Sequence 97322, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
```

	CURRENT APPLICATION NUMBER:	US-10-257,017B
	PRIOR FILING DATE:	2002-10-07
	PRIOR APPLICATION NUMBER:	DE 10019173.8
	PRIOR FILING DATE:	2000-04-07
	NUMBER OF SEQ ID NOS:	382046
	SEQ ID NO	97322
	LENGTH:	13
	TYPE:	DNA
	ORGANISM:	Artificial Sequence
	FEATURE:	
	OTHER INFORMATION:	Oligonucleotide for detection of SNP TSC0024141
	US-10-257-017B-97322	
	Query Match	Best Local Similarity Score 9.4; DB 1; Length 13; Pred. No. 1.2e+02;
	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	2 CACCTCATCGC 12 1 CCCCTCCAAA 12	
Db	2 CCCCTCCAAA 12	
	RESULT 147	
	US-10-257-017B-97389/C	
	Sequence 97389, Application US/10257017B	
	Publication No. US20040241651A1	
	GENERAL INFORMATION:	
	APPLICANT: Alexander Olek	
	APPlicant: Christian Piepenbrock	
	TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine	
	TITLE OF INVENTION: methylation	
	FILE REFERENCE: E01/1193/WO	
	CURRENT APPLICATION NUMBER: US/10/257,017B	
	PRIOR FILING DATE: 2002-10-07	
	PRIOR APPLICATION NUMBER: DE 10019173.8	
	PRIOR FILING DATE: 2000-04-07	
	NUMBER OF SEQ ID NOS: 382046	
	SEQ ID NO 97389	
	LENGTH: 13	
	TYPE: DNA	
	ORGANISM: Artificial Sequence	
	FEATURE:	
	OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024174	
	US-10-257-017B-97389	
	Query Match	Best Local Similarity Score 9.4; DB 1; Length 13; Pred. No. 1.2e+02;
	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	2 CACCTCATCGC 12 13 CACTCATCTC 3	
Db	13 CACTCATCTC 3	
	RESULT 148	
	US-10-257-017B-97390	
	Sequence 97390, Application US/10257017B	
	Publication No. US20040241651A1	
	GENERAL INFORMATION:	
	APPLICANT: Alexander Olek	
	AppLicant: Christian Piepenbrock	
	ApPlicAnt: Kurt Berlin	
	TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine	
	TITLE OF INVENTION: methylation	
	FILE REFERENCE: E01/1193/WO	
	CURRENT APPLICATION NUMBER: US/10/257,017B	
	PRIOR FILING DATE: 2002-10-07	
	PRIOR APPLICATION NUMBER: DE 10019173.8	
	PRIOR FILING DATE: 2000-04-07	
	NUMBER OF SEQ ID NOS: 382046	
	SEQ ID NO 97390	
	LENGTH: 13	
	TYPE: DNA	
	ORGANISM: Artificial Sequence	
	FEATURE:	
	OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024611	
	US-10-257-017B-99114	
	Query Match	Best Local Similarity Score 9.4; DB 1; Length 13; Pred. No. 1.2e+02;
	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	9 TCGCCCTTTC 19 12 TCCCCCTTC 2	
Db	12 TCCCCCTTC 2	
	RESULT 150	
	US-10-257-017B-99114	
	Sequence 99114, Application US/10257017B	
	Publication No. US20040241651A1	
	GENERAL INFORMATION:	
	APPLICANT: Alexander Olek	
	appLIcAnT: Christian Piepenbrock	
	APlIcAnT: Kurt Berlin	
	TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytozin	
	TITLE OF INVENTION: methylation	
	FILE REFERENCE: E01/1193/WO	
	CURRENT APPLICATION NUMBER: US/10/257,017B	
	PRIOR FILING DATE: 2002-10-07	
	PRIOR APPLICATION NUMBER: DE 10019173.8	
	PRIOR FILING DATE: 2000-04-07	
	NUMBER OF SEQ ID NOS: 382046	
	SEQ ID NO 99114	
	LENGTH: 13	
	TYPE: DNA	
	ORGANISM: Artificial Sequence	
	FEATURE:	
	OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024611	
	US-10-257-017B-99114	
	Query Match	Best Local Similarity Score 9.4; DB 1; Length 13; Pred. No. 1.2e+02;
	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	2 CACCTCATCGC 12 1 CACCTCATCTC 11	
Db	1 CACCTCATCTC 11	
	RESULT 149	
	US-10-257-017B-99113/C	
	Sequence 99113, Application US/10257017B	
	Publication No. US20040241651A1	
	GENERAL INFORMATION:	
	APPLICANT: Alexander Olek	
	AppLICanT: Christian Piepenbrock	
	ApPLICAnt: Kurt Berlin	
	TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin	
	TITLE OF INVENTION: methylation	
	FILE REFERENCE: E01/1193/WO	
	CURRENT APPLICATION NUMBER: US/10/257,017B	
	PRIOR FILING DATE: 2002-10-07	
	PRIOR APPLICATION NUMBER: DE 10019173.8	
	PRIOR FILING DATE: 2000-04-07	
	NUMBER OF SEQ ID NOS: 382046	
	SEQ ID NO 99113	
	LENGTH: 13	
	TYPE: DNA	
	ORGANISM: Artificial Sequence	
	FEATURE:	
	OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024611	
	US-10-257-017B-99113	
	Query Match	Best Local Similarity Score 9.4; DB 1; Length 13; Pred. No. 1.2e+02;
	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	9 TCGCCCTTTC 19 12 TCCCCCTTC 2	
Db	12 TCCCCCTTC 2	
	RESULT 150	
	US-10-257-017B-99114	
	Sequence 99114, Application US/10257017B	
	Publication No. US20040241651A1	
	GENERAL INFORMATION:	

Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCTTCC 19
| | | | |
| | | | |
Db 2 TCGCCCTTCC 12

RESULT 151

US-10-257-017B-100941/c
; Sequence 100941, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 100941
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025123
US-10-257-017B-100941

Query Match 36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGCCCTTCTCCT 20
| | | | |
| | | | |
Db 11 CTCCCTTCTCCT 1

RESULT 152
US-10-257-017B-100942
; Sequence 100942, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 100942
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025123
US-10-257-017B-100942

Query Match 36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGCCCTTCTCCT 20
| | | | |
| | | | |
Db 3 CTCCCTTCTCCT 13

RESULT 153
US-10-257-017B-109443/c
; Sequence 109443, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 109443
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027383
US-10-257-017B-109443

Query Match 36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCTATGATCAT 26
| | | | |
| | | | |
Db 11 TTCTATGATCAT 1

RESULT 154
US-10-257-017B-109444
; Sequence 109444, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 109444
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027383
US-10-257-017B-109444

Query Match 36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCTATGATCAT 26
| | | | |
| | | | |
Db 3 TTCTATGATCAT 13

RESULT 155
US-10-257-017B-112773/c
; Sequence 112773, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 112773
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028182
US-10-257-017B-112773

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      12 CACCTTCCTAA 2

RESULT 156
US-10-257-017B-112774
; Sequence 112774, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 112774
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028182
US-10-257-017B-112774

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      2 CACCTTCCTAA 12

RESULT 157
US-10-257-017B-117647/c
; Sequence 117647, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 126495
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029417
US-10-257-017B-117648

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      1 CCACTTCCTAA 11

RESULT 158
US-10-257-017B-117648
; Sequence 117648, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117648
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029417
US-10-257-017B-117648

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      13 CCACTTCCTAA 3

RESULT 159
US-10-257-017B-126495/c
; Sequence 126495, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 126495
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029417
US-10-257-017B-117647

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      13 CCACTTCCTAA 3
```

```
FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0031652
US-10-257-017B-126495

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      15 CTTCTTAAGCA 25
      |||||
Db      13 CTTCTTAATCA 3

RESULT 160
US-10-257-017B-126496
; Sequence 126496, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 126496
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0031652
US-10-257-017B-126496

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      15 CTTCTTAAGCA 25
      |||||
Db      1 CTTCTTAATCA 11

RESULT 161
US-10-257-017B-131503/c
; Sequence 131503, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131503
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032822
US-10-257-017B-131503

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 CACCTCATCGC 12
      |||||
Db      12 CACCTCATCAC 2

RESULT 162
US-10-257-017B-131504
; Sequence 131504, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131504
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032822
US-10-257-017B-131504

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CACCTCATCGC 12
      |||||
Db      2 CACCTCATCAC 12

RESULT 163
US-10-257-017B-131881/c
; Sequence 131881, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131881
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032929
US-10-257-017B-131881

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      8 ATCGCCCTTCTT 20
      :|||
Db      13 RTCTCACCTTCTT 1

RESULT 164
```

```
US-10-257-017B-131882
; Sequence 131882, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131882
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032929
US-10-257-017B-131882

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      8 ATGCCCTTCCT 20
Db      1 RTCTCGCTTCCT 13

RESULT 165
US-10-257-017B-131885/c
; Sequence 131885, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131885
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032929
US-10-257-017B-131885

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      8 ATGCCCTTCCT 20
Db      1 RTCTCGCTTCCT 1

RESULT 166
US-10-257-017B-131886
; Sequence 131886, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131886
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032929
US-10-257-017B-131886

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      8 ATGCCCTTCCT 20
Db      1 RTCTCGCTTCCT 1

RESULT 167
US-10-257-017B-149605/c
; Sequence 149605, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 149605
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037765
US-10-257-017B-149605

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      13 CCACTTCCTAA 3

RESULT 168
US-10-257-017B-149606
; Sequence 149606, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 149606
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037765
US-10-257-017B-149606

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      13 CCACTTCCTAA 3
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 149606
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037765
US-10-257-017B-149606

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12  CCCCTTCCTTA 22
Db      1  CCACCTCCTTA 11

RESULT 169
US-10-257-017B-154545/C
; Sequence 154545, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 154545
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0039062
US-10-257-017B-154545

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3  ACCTCATCGCCCC 15
Db      13 RCTCATCTCTCCC 1

RESULT 170
US-10-257-017B-154546
; Sequence 154546, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 154546
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0039062
```

```
US-10-257-017B-154546

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3  ACCTCATCGCCCC 15
Db      1  RCTCATCTCTCCC 13

RESULT 171
US-10-257-017B-160177/C
; Sequence 160177, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160177
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040333
US-10-257-017B-160177

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  CACCTCATCGC 12
Db      11 CACCTCATCAG 1

RESULT 172
US-10-257-017B-160178
; Sequence 160178, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160178
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040333
US-10-257-017B-160178

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  CACCTCATCGC 12
```

```
Db          3 CACCTCATCAG 13

RESULT 173
US-10-257-017B-160495/c
; Sequence 160495, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160495
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040405
US-10-257-017B-160495

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TCGCCCTTCC 19
Db          13 TCCGCCCTTCC 3

RESULT 174
US-10-257-017B-160496
; Sequence 160496, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160496
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040405
US-10-257-017B-160496

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TCGCCCTTCC 19
Db          1 TCCGCCCTTCC 11

RESULT 175
US-10-257-017B-167797/c
; Sequence 167797, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 167797
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010656
US-10-257-017B-167797

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          12 CCCCTTCTTAA 22
Db          12 CCCATTCTTAA 2

RESULT 176
US-10-257-017B-167798
; Sequence 167798, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 167798
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010656
US-10-257-017B-167798

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          12 CCCCTTCTTAA 22
Db          2 CCCATTCTTAA 12

RESULT 177
US-10-257-017B-169489/c
; Sequence 169489, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 169489
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010656
US-10-257-017B-169489
```



```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 169489
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042339
US-10-257-017B-169489

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CCTTCCTAGC 24
Db      11 CCTTCCTATC 1

RESULT 178
US-10-257-017B-169490
; Sequence 169490, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 169490
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042339
US-10-257-017B-169490

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CCTTCCTAGC 24
Db      3 CCTTCCTATC 13

RESULT 179
US-10-257-017B-171151/C
; Sequence 171151, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171151
```

```
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009084
US-10-257-017B-171151

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTCTCTAA 22
Db      12 CCTCTCTCTAA 2

RESULT 180
US-10-257-017B-171152
; Sequence 171152, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171152
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009084
US-10-257-017B-171152

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTCTCTAA 22
Db      2 CCTCTCTCTAA 12

RESULT 181
US-10-257-017B-171713/C
; Sequence 171713, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171713
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042804
US-10-257-017B-171713
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CGCCCTTCTCT 20
Db      13 CTCCTCTCTCT 3

RESULT 182
US-10-257-017B-171714
; Sequence 171714, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171714
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044693
US-10-257-017B-171714

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CGCCCTTCTCT 20
Db      1 CTCCTCTCTCT 11

RESULT 183
US-10-257-017B-180561/C
; Sequence 180561, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 180561
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044693
US-10-257-017B-180561

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCTCTAA 22
Db      13 CCCCTTCTCTAA 3

RESULT 184
US-10-257-017B-180562
; Sequence 180562, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 180562
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044693
US-10-257-017B-180562

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCTCTAA 22
Db      1 CCCCTTCTCTAA 11

RESULT 185
US-10-257-017B-187479/C
; Sequence 187479, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187479
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046214
US-10-257-017B-187479

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCTCTAA 22
Db      12 CCCCTTCTCTAA 2

RESULT 186
US-10-257-017B-187480
; Sequence 187480, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187480
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046214
US-10-257-017B-187480

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 CCCCTTCCTAA 22
Db      2 CCCTTTCCTAA 12

RESULT 187
US-10-257-017B-193135/C
; Sequence 193135, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 193135
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047508
US-10-257-017B-193135

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ACCTCATCGCC 13
Db      11 ACCTCATCTCC 1

RESULT 188
US-10-257-017B-193136
; Sequence 193136, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 205334
; LENGTH: 13
; TYPE: DNA

```

```

; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 193136
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047508
US-10-257-017B-193136

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ACCTCATCGCC 13
Db      3 ACCTCATCTCC 13

RESULT 189
US-10-257-017B-205333/C
; Sequence 205333, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 205333
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0050342
US-10-257-017B-205333

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      16 TTCTTANGCAT 26
Db      13 TTCTTATCAT 3

RESULT 190
US-10-257-017B-205334
; Sequence 205334, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 205334
; LENGTH: 13
; TYPE: DNA

```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0050342
US-10-257-017B-205334
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      16 TTCCTAAGCAT 26
      |||||
Db      1 TTCCTATCAT 11
```

```
RESULT 191
US-10-257-017B-212563/c
; Sequence 212563, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 212563
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0051772
US-10-257-017B-212563
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      15 CTCCTAAGCA 25
      |||||
Db      11 CTCCTAACA 1
```

```
RESULT 192
US-10-257-017B-212564
; Sequence 212564, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 212564
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0051772
US-10-257-017B-212564
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
```

```
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      15 CTCCTAAGCA 25
      |||||
Db      3 CTCCTAACA 13
```

```
RESULT 193
US-10-257-017B-240965/c
; Sequence 240965, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 240965
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0058763
US-10-257-017B-240965
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 CATGCCCTT 17
      |||||
Db      11 CATGCCCTT 1
```

```
RESULT 194
US-10-257-017B-240966
; Sequence 240966, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 240966
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0058763
US-10-257-017B-240966
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 CATGCCCTT 17
      |||||
Db      3 CATGCCCTT 13
```

```
RESULT 195
US-10-257-017B-244719/c
; Sequence 244719, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 244719
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059747
US-10-257-017B-244719

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CCTTCCTAAC 24
DB 12 CCTTCCTAAC 2

RESULT 196
US-10-257-017B-244720
; Sequence 244720, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 244720
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059747
US-10-257-017B-244720

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CCTTCCTAAC 24
DB 2 CCTTCCTAAC 12
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 263651
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063915
US-10-257-017B-263651

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATGC 12
DB 12 CACCTCATGC 2

RESULT 198
US-10-257-017B-263652
; Sequence 263652, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 263652
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063915
US-10-257-017B-263652

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATGC 12
DB 2 CACCTCATGC 12

RESULT 199
US-10-984-919-1297
; Sequence 1297, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiefen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
```

```

; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1297
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1297

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CCTTCTAAGC 24
Db      1 CCTCTTACGC 11

RESULT 200
; Sequence 2, Application US/11116252
; Publication No. US2005018632A1
; GENERAL INFORMATION:
; APPLICANT: KATOAKA, Kohsuke
; TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR
; FILE REFERENCE: 069817
; CURRENT APPLICATION NUMBER: US/11/116,252
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/10/129,192
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/JP00/00841
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: JP 1999-314335
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Maf recognition element
US-11-116-252-2

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      15 CTTCTTAAGCA 25
Db      3 CTTACTAAGCA 13

RESULT 201
US-09-783-338A-2/c
; Sequence 2, Application US/09783338A
; Patent No. US20020028922A1
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter M.
;           Havey, Pamela A.
; TITLE OF INVENTION: Chemically Modified Oligonucleotide for
;           Site-Directed Mutagenesis
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia

; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,338A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,088
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-783-338A-2

Query Match          34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
Db      9 CCCCTTCT 1

RESULT 202
US-09-978-333B-1/c
; Sequence 1, Application US/09978333B
; Publication No. US20030232768A1
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter M.
; TITLE OF INVENTION: Triple-Helix forming Oligonucleotides for Targeted Mutagenesis
; FILE REFERENCE: YU 132
; CURRENT APPLICATION NUMBER: US/09/978,333B
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 09/411,291
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 08/476,712
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AG10
US-09-978-333B-1

Query Match          34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
Db      9 CCCCTTCT 1
```

```
RESULT 203
US-10-033-145-1976
; Sequence 1976, Application US/10033145
; Publication No. US2002051515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1976
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1976

Query Match      34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTTCTTAG 23
DB      2 CTTCTTAG 10

RESULT 204
US-10-055-713-51/C
; Sequence 51, Application US/10055713
; Publication No. US20030044957A1
; GENERAL INFORMATION:
; APPLICANT: JAMIESON, Andrew
; APPLICANT: LI, Guofu
; TITLE OF INVENTION: ZINC FINGER PROTEINS FOR DNA BINDING AND GENE
; FILE REFERENCE: 8325-0026 / S26-US1
; CURRENT APPLICATION NUMBER: US/10/055,713
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/263,445
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/290,716
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP 5 target sequence
US-10-055-713-51

Query Match      34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
DB      10 CCCCTTCT 2

RESULT 205
US-10-055-711-55/C
; Sequence 55, Application US/10055711
; Publication No. US20030108880A1
; GENERAL INFORMATION:
```

```
; APPLICANT: REBAR, Edward
; APPLICANT: JAMIESON, Andrew
; TITLE OF INVENTION: MODIFIED ZINC FINGER BINDING PROTEINS
; FILE REFERENCE: 8325-0025
; CURRENT APPLICATION NUMBER: US/10/055,711
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP #5 target
US-10-055-711-55

Query Match      34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
DB      10 CCCCTTCT 2

RESULT 206
US-10-418-552-37/C
; Sequence 37, Application US/10418552
; Publication No. US20030233672A1
; GENERAL INFORMATION:
; APPLICANT: LI, Guofu
; APPLICANT: LIU, Qiang
; APPLICANT: JAMIESON, Andrew
; APPLICANT: REBAR, Edward
; APPLICANT: VAN BENENNAAM, Alison
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR REGULATION OF PLANT GAMMA-
; TITLE OF INVENTION: TOCOPHEROL METHYLTRANSFERASE
; FILE REFERENCE: 8325-0029 (S29-US1)
; CURRENT APPLICATION NUMBER: US/10/418,552
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/373,488
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/385,992
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/442,470
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: AGMTS target
US-10-418-552-37

Query Match      34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
DB      10 CCCCTTCT 2

RESULT 207
US-10-650-454-56/C
; Sequence 56, Application US/10650454
; Publication No. US20040091990A1
; GENERAL INFORMATION:
; APPLICANT: LI, Guofu
; APPLICANT: LIU, Qiang
```

```
APPLICANT: JAMIESON, Andrew
APPLICANT: REBAR, Edward
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION OF PLANT GAMMA-TOCOPHEROL
FILE REFERENCE: 8325-0029.30 (S29-US2)
CURRENT APPLICATION NUMBER: US/10/650,454
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: 60/406,849
PRIOR FILING DATE: 2002-08-29
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: ZFP5 target
US-10-650-454-56
```

Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCT 20
DB 10 CCCCTTCT 2

RESULT 208
US-10-470-180-51/c

```
Sequence 51, Application US/10470180
Publication No. US20040128717A1
GENERAL INFORMATION:
APPLICANT: JAMIESON, Andrew
APPLICANT: LI, Guofu
TITLE OF INVENTION: ZINC FINGER PROTEINS FOR DNA BINDING AND GENE
REGULATION IN PLANTS
FILE REFERENCE: 8325-0026.30 / S26-US2
CURRENT APPLICATION NUMBER: US/10/470,180
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: PCT/US02/01906
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/263,445
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/290,716
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ZFP 5 target sequence
US-10-470-180-51
```

Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCT 20
DB 10 CCCCTTCT 2

RESULT 209
US-09-783-338A-1/c

```
GENERAL INFORMATION:
APPLICANT: Glazer, Peter M.
APPLICANT: Havre, Pamela A.
TITLE OF INVENTION: Chemically Modified Oligonucleotide for
Site-directed Mutagenesis
NUMBER OF SEQUENCES: 13
```

```
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,338A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,088
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: YU109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 11
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-783-338A-1
```

Query Match 34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCT 20
DB 10 CCCCTTCT 2

```
RESULT 210
US-10-450-797-877
Sequence 877, Application US/10450797
Publication No. US20040142335A1
GENERAL INFORMATION:
APPLICANT: Petersohn, Dirk
APPLICANT: Conradt, Marcus
APPLICANT: Hofmann, Kay
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
FILE REFERENCE: HENK-0041
CURRENT APPLICATION NUMBER: US/10/450,797
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: PCT/EP01/15178
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: DE 101 00 121.5
PRIOR FILING DATE: 2001-01-03
NUMBER OF SEQ ID NOS: 1435
SOFTWARE: PatentIn version 3.2
SEQ ID NO 877
LENGTH: 11
TYPE: DNA
ORGANISM: Homo sapiens
US-10-450-797-877
```

Query Match 34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCT 20
DB 3 CCCCTTCT 11

RESULT 211


```

US-10-257-017B-270857
; Sequence 270857, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 270857
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002302
US-10-257-017B-270857

Query Match      34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CCTTCCTAA 22
DB      4 CCTTCCTAA 12

RESULT 212
US-10-257-017B-271330/c
; Sequence 271330, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 271330
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002471
US-10-257-017B-271330

Query Match      34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTCTCT 20
DB      11 CCCCTCTCT 3

RESULT 213
US-10-257-017B-292092/c
; Sequence 292092, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

```

```

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 292092
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015081
US-10-257-017B-292092

Query Match      34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CCTTCCTAA 22
DB      10 CCTTCCTAA 2

RESULT 214
US-10-257-017B-295660
; Sequence 295660, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295660
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016678
US-10-257-017B-295660

Query Match      34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CCTTCCTAA 22
DB      4 CCTTCCTAA 12

RESULT 215
US-10-257-017B-296570/c
; Sequence 296570, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 296570
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016678
US-10-257-017B-296570

Query Match      34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CCTTCCTAA 22
DB      4 CCTTCCTAA 12

```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 296570
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017152
US-10-257-017B-296570

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CGCCCTTC 18
Db      11 CGCCCTTC 3

RESULT 216
US-10-257-017B-302250/c
; Sequence 302250, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 302250
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019887
US-10-257-017B-302250

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CATGCCCC 15
Db      9 CATGCCCC 1

RESULT 217
US-10-257-017B-306989/c
; Sequence 306989, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306989
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022284
```

```
US-10-257-017B-306989

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CCTTCCTAA 22
Db      9 CCTTCCTAA 1

RESULT 218
US-10-257-017B-307276/c
; Sequence 307276, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307276
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022412
US-10-257-017B-307276

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
Db      12 CCCCTTCT 4

RESULT 219
US-10-257-017B-307786
; Sequence 307786, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307786
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022686
US-10-257-017B-307786

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTA 21
```

```
Db          2 CCTTCCTTA 10
|||||
RESULT 220
US-10-257-017B-317371/c
; Sequence 317371, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317371
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027956
US-10-257-017B-317371

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy          14 CCTTCCTTA 22
|||||
Db          12 CCTTCCTTA 4

RESULT 221
US-10-257-017B-318871
; Sequence 318871, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 318871
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028928
US-10-257-017B-318871

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy          12 CCTTCCT 20
|||||
Db          3 CCTTCCT 11

RESULT 222
US-10-257-017B-319500/c
; Sequence 319500, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 319500
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029262
US-10-257-017B-319500

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy          14 CCTTCCTTA 22
|||||
Db          10 CCTTCCTTA 2

RESULT 223
US-10-257-017B-321861
; Sequence 321861, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 321861
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030535
US-10-257-017B-321861

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy          1 CCACCTCAT 9
|||||
Db          1 CCACCTCAT 9

RESULT 224
US-10-257-017B-323643/c
; Sequence 323643, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323643
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030535
US-10-257-017B-323643/c

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy          1 CCACCTCAT 9
|||||
Db          1 CCACCTCAT 9
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323643
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031518
US-10-257-017B-323643

Query Match
Best Local Similarity 34.6%; Score 9; DB 1; Length 12;
100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCCCTTC 18
Db 9 CGCCCTTC 1

RESULT 225
US-10-257-017B-324895/c
; Sequence 324895, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 324895
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0032282
US-10-257-017B-324895

Query Match
Best Local Similarity 34.6%; Score 9; DB 1; Length 12;
100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCTTCTTA 22
Db 10 CCTTCTTA 2

RESULT 226
US-10-257-017B-331316
; Sequence 331316, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331316

; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036120
US-10-257-017B-331318

Query Match
Best Local Similarity 34.6%; Score 9; DB 1; Length 12;
100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACCTCATCG 11
Db 4 ACCTCATCG 12

RESULT 227
US-10-257-017B-331318
; Sequence 331318, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331318
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036120
US-10-257-017B-331318

Query Match
Best Local Similarity 34.6%; Score 9; DB 1; Length 12;
100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACCTCATCG 11
Db 4 ACCTCATCG 12

RESULT 228
US-10-257-017B-336647
; Sequence 336647, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 336647
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039455
US-10-257-017B-336647
```

Query Match 34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCCTTA 21
Db 1 CCCTTCCTTA 9

RESULT 229

US-10-257-017B-339949
; Sequence 339949, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 339949
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007933
US-10-257-017B-339949

Query Match 34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCCCTTC 18
Db 2 CGCCCTTC 10

RESULT 230

US-10-257-017B-347634/c
; Sequence 347634, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 347634
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045197
US-10-257-017B-347634

Query Match 34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCCTTA 21
Db 9 CCCTTCCTTA 1

RESULT 231
US-10-257-017B-351281/c

; Sequence 351281, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 351281
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0047204
US-10-257-017B-351281

Query Match 34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCCTTA 21
Db 10 CCCTTCCTTA 2

RESULT 232

US-10-257-017B-362364/c
; Sequence 362364, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 362364
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053186
US-10-257-017B-362364

Query Match 34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CCCCTTCCT 20
Db 11 CCCCTTCCT 3

RESULT 233

US-10-257-017B-368993
; Sequence 368993, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:

```

; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 368993
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057391
US-10-257-017B-368993

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13  CCCTTCCTA 21
Db      3  CCCTTCCTA 11

RESULT 234
US-10-257-017B-368994
; Sequence 368994, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 368994
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057391
US-10-257-017B-368994

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13  CCCTTCCTA 21
Db      3  CCCTTCCTA 11

RESULT 235
US-10-257-017B-372951
; Sequence 372951, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 372951
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057391
US-10-257-017B-372951

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13  CCCTTCCTA 21
Db      3  CCCTTCCTA 11
```

```

; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 372951
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0059746
US-10-257-017B-372951

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14  CCTTCCTAA 22
Db      4  CCTTCCTAA 12

RESULT 236
US-10-257-017B-376095/C
; Sequence 376095, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 376095
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061608
US-10-257-017B-376095

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCACCTCAT 9
Db      11 CCACCTCAT 3

RESULT 237
US-10-257-017B-379937
; Sequence 379937, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379937
; LENGTH: 12
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063546
US-10-257-017B-379937

Query Match
Best Local Similarity 34.6%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CCCCTTCTCT 20
Db 2 CCCCTTCTCT 10

RESULT 238
US-10-661-165-565/c
; Sequence 565, Application US/10661165
; Publication No. US20040137470A1
; GENERAL INFORMATION:
; APPLICANT: Dhaliyan, Ravinder S.
; TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
; FILE REFERENCE: 54331200420
; CURRENT APPLICATION NUMBER: US/10/661,165
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: PCT/US03/06198
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/378,354
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 10/093,618
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/360,232
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/US03/27308
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 10/376,770
; NUMBER OF SEQ ID NOS: 628
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 565
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-661-165-565

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCTCT 20
Db 12 TCGCCCTTCTCT 1

RESULT 239
US-10-836-670-34
; Sequence 34, Application US/10836670
; Publication No. US20040235031A1
; GENERAL INFORMATION:
; APPLICANT: Schultz, Gregory Scott
; APPLICANT: Bialock, Timothy D.
; TITLE OF INVENTION: ANTI-SCARRING RIBOZYMES AND METHODS
; FILE REFERENCE: 5853-303
; CURRENT APPLICATION NUMBER: US/10/836,670
; PRIOR FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 12
; TYPE: DNA
```

```

; ORGANISM: Human adenovirus type 1
US-10-836-670-34

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CCCCTTCTCTAG 23
Db 1 CCCCTTCTCTAG 12

RESULT 240
US-10-257-017B-268660/c
; Sequence 268660, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 268660
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001285
US-10-257-017B-268660

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 CTTCTTAGCAT 26
Db 12 CTTCTTAGCAT 1

RESULT 241
US-10-257-017B-269228
; Sequence 269228, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 269228
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001671
US-10-257-017B-269228

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 CTCATCGCCCT 16
Db      1 CTCATCTACCT 12

RESULT 242
US-10-257-017B-270998/c
; Sequence 270998, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 270998
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002355
US-10-257-017B-270998

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 TCGCCCTTCT 20
Db      12 TCGCCTTCT 1

RESULT 243
US-10-257-017B-276248/c
; Sequence 276248, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 276248
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004128
US-10-257-017B-276248

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 CATCGCCCTTC 18
Db      12 CTCGCCCCCTC 1

RESULT 244
US-10-257-017B-277116

; Sequence 277116, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 277116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004389
US-10-257-017B-277116

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCC 14
Db      1 ACCTCATATCCC 12

RESULT 245
US-10-257-017B-278152/c
; Sequence 278152, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 278152
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005715
US-10-257-017B-278152

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      11 GCCCTTCTCTAA 22
Db      12 GCCCTTCTCTTA 1

RESULT 246
US-10-257-017B-278353/c
; Sequence 278353, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
US-10-257-017B-277116
```



```

; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 278353
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005916
US-10-257-017B-278353

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 TCGCCCTTCTCT 20
Db      12 TCCCCCTACCT 1

RESULT 247
US-10-257-017B-280327
; Sequence 280327, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 280327
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008491
US-10-257-017B-280327

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      10 CGCCCTTCTCTA 21
Db      1 CCCCCCTACCTA 12

RESULT 248
US-10-257-017B-281811
; Sequence 281811, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 281811
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010079
US-10-257-017B-281811

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      14 CCTTCTACCA 25
Db      1 CCTTCCACCA 12

RESULT 249
US-10-257-017B-286583
; Sequence 286583, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 286583
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012738
US-10-257-017B-286583

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 ACCTCATCGCCC 14
Db      1 ACCTCATACCC 12

RESULT 250
US-10-257-017B-287738/c
; Sequence 287738, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 287738
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013227
US-10-257-017B-287738
```



```

; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299865
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018786
US-10-257-017B-299865

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCTCTA 21
Db      12 CTCCTCTTCCCA 1

RESULT 256
US-10-257-017B-300302/c
; Sequence 300302, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300302
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018963
US-10-257-017B-300302

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTCATCGC 12
Db      12 CAACCTCATCCC 1

RESULT 257
US-10-257-017B-302104/c
; Sequence 302104, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
```

```

; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 302104
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019796
US-10-257-017B-302104

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 CCCTTCTCTAAGC 24
Db      12 CCATCTCTAAGC 1

RESULT 258
US-10-257-017B-303551/c
; Sequence 303551, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303551
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020529
US-10-257-017B-303551

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCC 14
Db      12 ACCTTATCACCC 1

RESULT 259
US-10-257-017B-304348
; Sequence 304348, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 304348
; LENGTH: 12
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020881
US-10-257-017B-304348
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      10 CGCCCTCTCCTA 21
          |||||
Db       1 CTCCTTACTA 12
```

```
RESULT 260
US-10-257-017B-306913
; Sequence 306913, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306913
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022244
US-10-257-017B-306913
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 CCTCATCGCCCC 15
          |||||
Db       1 CTTATCTCCCC 12
```

```
RESULT 261
US-10-257-017B-313065/C
; Sequence 313065, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 313065
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025454
US-10-257-017B-313065
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
```

```
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 ACCTCATCGCCC 14
          |||||
Db       12 ACCACCTCGCCC 1
```

```
RESULT 262
US-10-257-017B-313798/C
; Sequence 313798, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 313798
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025975
US-10-257-017B-313798
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      7 CATCGCCCTTC 18
          |||||
Db       12 CATCTCCCTCC 1
```

```
RESULT 263
US-10-257-017B-314753
; Sequence 314753, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314753
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026548
US-10-257-017B-314753
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 ACCTCATCGCCC 14
          |||||
Db       1 ACATCATCGCAC 12
```

```
RESULT 264
US-10-257-017B-314756
; Sequence 314756, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314756
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026548
US-10-257-017B-314756

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCC 14
      |||||
Db      1 ACATCATCGCC 12

RESULT 265
US-10-257-017B-314759
; Sequence 314759, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314759
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026548
US-10-257-017B-314759

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCC 14
      |||||
Db      1 ACCTCATCGAC 12

RESULT 266
US-10-257-017B-314762
; Sequence 314762, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

```
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314762
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026548
US-10-257-017B-314762

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCC 14
      |||||
Db      1 ACCTCATCGCC 12

RESULT 267
US-10-257-017B-315110/c
; Sequence 315110, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 315110
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026719
US-10-257-017B-315110

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 CATGCCCTTC 18
      |||||
Db      12 CATTAACCTTC 1

RESULT 268
US-10-257-017B-315369
; Sequence 315369, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
```

```

; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 315369
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026872
US-10-257-017B-315369

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCTACGA 25
DB      1 CCTTCTACGA 12

RESULT 269
US-10-257-017B-315967
; Sequence 315967, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 315967
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027203
US-10-257-017B-315967

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTCATCGC 12
DB      1 CCACCTCATCAC 12

RESULT 270
US-10-257-017B-317533/c
; Sequence 317533, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317533
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028084
US-10-257-017B-317533

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 ATGCCCCCTTCC 19
DB      12 ATCTCCCATCC 1

RESULT 271
US-10-257-017B-319294
; Sequence 319294, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 319294
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029155
US-10-257-017B-319294

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 TCGCCCTTCTCT 20
DB      1 TCGCCCTTACT 12

RESULT 272
US-10-257-017B-320903
; Sequence 320903, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 320903
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029956
US-10-257-017B-320903

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 13 CCTTCTTAAGC 24
|||
Db 1 CCTTCTTAACC 12

RESULT 273

US-10-257-017B-322792/c
; Sequence 322792, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322792
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031068
US-10-257-017B-322792

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCTT 20
|||
Db 12 TCACCCTTCTT 1

RESULT 274

US-10-257-017B-323185
; Sequence 323185, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323185
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031247
US-10-257-017B-323185

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCTCATGCCCC 15
|||
Db 1 CCTCATGCCCC 12

RESULT 275

US-10-257-017B-323187
; Sequence 323187, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323187
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031247
US-10-257-017B-323187

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCTCATGCCCC 15
|||
Db 1 CCTCATGCCCC 12

RESULT 276
US-10-257-017B-326521/c
; Sequence 326521, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 326521
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031109
US-10-257-017B-326521

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 CCTTCTTAAGCA 25
|||
Db 12 CCATCTTAAGCA 1

RESULT 277

US-10-257-017B-327842/c
; Sequence 327842, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 327842
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033930
US-10-257-017B-327842

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCCTAAGCA 25
DB 12 CCTTCCCTAAGCA 1

RESULT 278
US-10-257-017B-328615
; Sequence 328615, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 328615
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034416
US-10-257-017B-328615

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCTCATGCGCCCC 15
DB 1 CCCCCCTGCCCC 12

RESULT 279
US-10-257-017B-329701
; Sequence 329701, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329701
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0038351
US-10-257-017B-334701

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATCGGCCCTTC 18
DB 1 CATCTCCCTTTC 12

RESULT 280
US-10-257-017B-334701
; Sequence 334701, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 334701
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0038351
US-10-257-017B-335615

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATCGGCCCTTC 18
DB 1 CATCTCCCTTTC 12

RESULT 281
US-10-257-017B-335615
; Sequence 335615, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 335615
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0038921
```


US-10-257-017B-335615

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATGCCCTTC 18
DB 1 CACGCCCTTC 12

RESULT 282

US-10-257-017B-337282/c
; Sequence 337282, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337282
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039782
US-10-257-017B-337282

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATGCCCTTC 18
DB 12 CATGCCCTTC 1

RESULT 283

US-10-257-017B-339583/c
; Sequence 339583, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 339583
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0041083
US-10-257-017B-339583

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATGCCCTTC 19

DB 12 ATCACCTTACC 1

RESULT 284

US-10-257-017B-344435/c
; Sequence 344435, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 344435
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043536
US-10-257-017B-344435

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCTTCTTAA 22
DB 12 GCCCACCTTAA 1

RESULT 285

US-10-257-017B-344922
; Sequence 344922, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 344922
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043771
US-10-257-017B-344922

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTCATGCCCT 16
DB 1 CTCATGCCCT 12

RESULT 286

US-10-257-017B-348072/c
; Sequence 348072, Application US/10257017B

```
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 348072
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010192
US-10-257-017B-348072

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCTCTA 21
DB      12 CTCCTCTCTCTA 1

RESULT 287
US-10-257-017B-349107/c
; Sequence 349107, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 349107
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045920
US-10-257-017B-349107

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CACCTCATGCC 13
DB      12 CACTTCATCTCC 1

RESULT 288
US-10-257-017B-349377
; Sequence 349377, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 349377
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046101
US-10-257-017B-349377
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 349377
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046101
US-10-257-017B-349377

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  ACCTCATGCC 14
DB      1  ACCTCATGCC 12

RESULT 289
US-10-257-017B-350201/c
; Sequence 350201, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350201
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046561
US-10-257-017B-350201

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14  CCTTCTAAGCA 25
DB      12  CCTCCTAATCA 1

RESULT 290
US-10-257-017B-350285/c
; Sequence 350285, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350285
```

```

; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046584
US-10-257-017B-350285
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy          3 ACCTCATGCCCC 14
             |||||
Db          12 ACCTCATGCCCC 1
```

RESULT 291

```
US-10-257-017B-350759
; Sequence 350759, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350759
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046864
US-10-257-017B-350759
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy          2 CACCTCATGCCC 13
             |||||
Db          1 CACCTCAACCCC 12
```

RESULT 292

```
US-10-257-017B-354578
; Sequence 354578, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 354578
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049156
US-10-257-017B-354578
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy          14 CCTTCCTAAGCA 25
             |||||
Db          1 CCTACCTAAGCA 12
```

RESULT 293

```
US-10-257-017B-356323/C
; Sequence 356323, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 356323
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050058
US-10-257-017B-356323
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy          3 ACCTCATGCCCC 14
             |||||
Db          12 ACCTCTTGCTC 1
```

RESULT 294

```
US-10-257-017B-357335/C
; Sequence 357335, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 357335
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050568
US-10-257-017B-357335
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy          15 CTTCCTAAGCAT 26
             |||||
Db          12 CTCCTTAACCAT 1
```

```
RESULT 295
US-10-257-017B-357650
; Sequence 357650, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 357650
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007066
US-10-257-017B-357650

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 CATGCCCCCTTC 18
Db      1 CATCTCCCTCTC 12

RESULT 296
US-10-257-017B-358254
; Sequence 358254, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358254
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007531
US-10-257-017B-358254

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCCTACGA 25
Db      1 CCTCCTTAACA 12

RESULT 297
US-10-257-017B-359463/c
; Sequence 359463, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359463
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051615
US-10-257-017B-359463

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 TCGCCCTTCCT 20
Db      12 TCCTCCTTCCT 1

RESULT 298
US-10-257-017B-360360/c
; Sequence 360360, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 360360
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052046
US-10-257-017B-360360

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACTCATGCG 12
Db      12 CCACCTCTCTC 1

RESULT 299
US-10-257-017B-362746/c
; Sequence 362746, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

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; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 362746
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053413
US-10-257-017B-362746

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 CCCTTCCTAAGC 24
Db 12 CACTTCCTAATC 1

RESULT 300
US-10-257-017B-364264
; Sequence 364264, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 364264
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC005484
US-10-257-017B-364264

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CACCTCATCGCC 13
Db 1 CACATCACCGCC 12

RESULT 301
US-10-257-017B-368210/c
; Sequence 368210, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 368210
; LENGTH: 12
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0056866
US-10-257-017B-368210

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 CTTCCTAAGCAT 26
Db 12 CTTCATTAACAT 1

RESULT 302
US-10-257-017B-370744
; Sequence 370744, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 370744
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0058361
US-10-257-017B-370744

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCCT 20
Db 1 TCCCTCTTCCT 12

RESULT 303
US-10-257-017B-371049
; Sequence 371049, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 371049
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0058537
US-10-257-017B-371049

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATGCCCCCTTCC 19
 ||| |||||
 Db 1 ATCTACCTTCC 12

RESULT 304

US-10-257-017B-372640/C
 ; Sequence 372640, Application US/10257017B
 ; Publication No. US20040241651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
 ; FILE REFERENCE: E01/1193/WO
 ; CURRENT APPLICATION NUMBER: US/10/257,017B
 ; PRIOR FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; NUMBER OF SEQ ID NOS: 382046
 ; SEQ ID NO 372640
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0059513
 US-10-257-017B-372640

Query Match 33.8%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCTAGCA 25
 |||||
 Db 12 CTTTCCTATCA 1

RESULT 305

US-10-257-017B-373933
 ; Sequence 373933, Application US/10257017B
 ; Publication No. US20040241651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
 ; FILE REFERENCE: E01/1193/WO
 ; CURRENT APPLICATION NUMBER: US/10/257,017B
 ; PRIOR FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 382046
 ; SEQ ID NO 373933
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060397
 US-10-257-017B-373933

Query Match 33.8%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACCTCATGCC 13
 |||||
 Db 1 CACCTCCTTCC 12

RESULT 306

US-10-257-017B-374652/C
 ; Sequence 374652, Application US/10257017B
 ; Publication No. US20040241651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
 ; FILE REFERENCE: E01/1193/WO
 ; CURRENT APPLICATION NUMBER: US/10/257,017B
 ; PRIOR FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; NUMBER OF SEQ ID NOS: 382046
 ; SEQ ID NO 374652
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060825
 US-10-257-017B-374652

Query Match 33.8%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATGCC 14
 |||||
 Db 12 ACCTCATCCAC 1

RESULT 307

US-10-257-017B-378396
 ; Sequence 378396, Application US/10257017B
 ; Publication No. US20040241651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
 ; FILE REFERENCE: E01/1193/WO
 ; CURRENT APPLICATION NUMBER: US/10/257,017B
 ; PRIOR FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 382046
 ; SEQ ID NO 378396
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC008704
 US-10-257-017B-378396

Query Match 33.8%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATGCCCCCTTCC 19
 |||||
 Db 1 ATCTCCCATCC 12

RESULT 308

US-10-257-017B-381325
 ; Sequence 381325, Application US/10257017B
 ; Publication No. US20040241651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock

```

; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 381325
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064280
US-10-257-017B-381325

```

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Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      14 CCTCCTAATCA 25
Db      1 CCATCCTAATCA 12

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RESULT 309
US-10-257-017B-381966
; Sequence 381966, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 381966
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064656
US-10-257-017B-381966

```

```

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      4 CCTCATGCCCC 15
Db      1 CTCACCCCCCC 12

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Search completed: May 9, 2006, 16:59:40
Job time : 0.001 secs

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RESULT 1
US-10-310-914A-1031100/c
; Sequence 1031100, Application US/10310914A

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; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 788791
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-788791

Query Match          56.9%; Score 14.8; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 5.3;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTC 18
    |||||:|||||:|
Db 1 CCACCUCACGCCCAUUC 18

RESULT 4
US-11-083-784-788791
; Sequence 788791, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 788791
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-788791

Query Match          56.9%; Score 14.8; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 5.3;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTC 18
    |||||:|||||:|
Db 1 CCACCUCACGCCCAUUC 18

RESULT 5
US-10-310-914A-1300864
; Sequence 1300864, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1300864
; LENGTH: 19
; TYPE: RNA
```

```
; ORGANISM: Human
US-10-310-914A-1300864

Query Match          54.6%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 6.1;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCTTCCTAA 22
    ||:|||||:|:|
Db 1 CCUCCUGGCCCAUCCUAA 19

RESULT 6
US-10-310-914A-74927/c
; Sequence 74927, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 74927
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-74927

Query Match          54.6%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCT 20
    |||||:|||||:|
Db 20 CCCCTCTCACCCCTTCCT 2

RESULT 7
US-10-310-914A-1166831/c
; Sequence 1166831, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1166831
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1166831

Query Match          54.6%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTC 19
    |||||:|||||:|
Db 19 CCACCTCTCTCGCCCGGCC 1

RESULT 8
US-10-310-914A-74926/c
; Sequence 74926, Application US/10310914A
```

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 74926
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-74926

Query Match          53.1%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.1;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCTCATCGCCCTTCCT 20
    ||||| ||||| |||||
Db 18 CCTCTCACCCCTTCCT 2

RESULT 9
US-10-310-914A-627529/c
; Sequence 627529, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 627529
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-627529

Query Match          53.1%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.1;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCTCATCGCCCTTCCT 20
    ||||| ||||| |||||
Db 17 CCTCTCGCCCTTCCT 1

RESULT 10
US-10-310-914A-258747/c
; Sequence 258747, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 258747
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
```

```
US-10-310-914A-258747

Query Match          51.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 7.7;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCATCGCCCC 15
    ||||| ||||| |||||
Db 16 CCACCTCACCGCCCC 2

RESULT 11
US-10-310-914A-258760/c
; Sequence 258760, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 258760
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-258760

Query Match          51.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 7.7;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCATCGCCCC 15
    ||||| ||||| |||||
Db 18 CCACCTCACCGCCCC 4

RESULT 12
US-10-310-914A-526385
; Sequence 526385, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 526385
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-526385

Query Match          51.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 7.7;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCATCGCCCC 15
    ||||| ||||| |||||
Db 2 CCACCUCAUCGCCCC 16

RESULT 13
US-10-310-914A-634307
; Sequence 634307, Application US/10310914A
; Publication No. US20060003322A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 634307
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-634307

Query Match          51.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 7.7;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCTTCCTTAAGCA 25
   |||||:|:|:|
Db 3 GCCCCUCCUCACGA 17

RESULT 14
US-10-310-914A-1117030
; Sequence 1117030, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1117030
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1117030

Query Match          51.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 7.7;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCTTC 18
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Db 1 CCUCAUGGCCCUCC 15

RESULT 15
US-10-310-914A-634308
; Sequence 634308, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 634308
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-634308
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; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 100792
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-100792

Query Match          51.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.3;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCTTCCT 20
   |||||:|:|:|
Db 19 TCATCGCCCTTCCT 5

RESULT 17
US-11-101-244-100799/c
; Sequence 100799, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 100799
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-100799
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Query Match      51.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.3;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TCATCGCCCTTCCT 20
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Db      18 TCATCGCCCTTCCT 4

RESULT 18
US-11-083-784-100792/c
; Sequence 100792, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 100792
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-100792

Query Match      51.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.3;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TCATCGCCCTTCCT 20
      ||||| ||||| |||||
Db      19 TCATCGCCCTTCCT 5

RESULT 19
US-11-083-784-100799/c
; Sequence 100799, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 100799
; LENGTH: 19
; TYPE: RNA
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; ORGANISM: Homo sapiens
US-11-083-784-100799

Query Match      51.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.3;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TCATCGCCCTTCCT 20
      ||||| ||||| |||||
Db      18 TCATCGCCCTTCCT 4

RESULT 20
US-10-310-914A-126258
; Sequence 126258, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126258
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-126258

Query Match      50.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 61.1%; Pred. No. 8.1;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCACCTCATCGCCCTTC 18
      ||||| :|||:|:|:|:|
Db      1 CAACCCUCCUCCUCCUCC 18

RESULT 21
US-10-310-914A-755151/c
; Sequence 755151, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 755151
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-755151

Query Match      50.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 CTCATCGCCCTTCCTAA 22
      ||||| ||||| |||||
Db      18 CTCACGGCCCTTCCTTA 1

RESULT 22
US-10-310-914A-1097078/c
; Sequence 1097078, Application US/10310914A
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1097078
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1097078

Query Match      50.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  CACCTCATGCGCCCTTCC 19
Db      18  CATCTCATTTGCCCTTCC 1

RESULT 23
US-10-310-914A-616514/c
; Sequence 616514, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 616514
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-616514

Query Match      49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 8.9;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      11  GCCCCTTCTCTAAGCAT 26
Db      17  GCCCCTTCTCTGAGCCT 2

RESULT 24
US-10-310-914A-1008058
; Sequence 1008058, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1008058
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
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US-10-310-914A-1008058

Query Match      49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 8.9;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      11  GCCCCTTCTCTAAGCAT 26
Db      2  GCCCCUUCUCCAGCCU 17

RESULT 25
US-11-035-105-31
; Sequence 31, Application US/11035105
; Publication No. US20050255498A1
; GENERAL INFORMATION:
; APPLICANT: Aerssens, Jeroen
; APPLICANT: Athanasiou, Maria
; APPLICANT: Brain, Carlos
; APPLICANT: Cohen, Nadine
; APPLICANT: Dain, Bradley
; APPLICANT: Denton, R. Rex
; APPLICANT: Judson, Richard S.
; APPLICANT: Ozdemir, Vural
; APPLICANT: Reed, Carol R.
; TITLE OF INVENTION: APOC1 Genetic Markers Associated with Age of Onset of Alzheimer's
; FILE REFERENCE: 2300.0120001
; CURRENT APPLICATION NUMBER: US/11/035,105
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: US 60/538,606
; PRIOR FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward Primer Extension Oligonucleotide for Detecting Alleles a
; OTHER INFORMATION: PSS in Haplotypes Comprising Preferred Embodiments of Age of
; OTHER INFORMATION: Onset Markers I and II
US-11-035-105-31

Query Match      34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12  CCCCTTCTCT 20
Db      1  CCCCTTCTCT 9

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Job time : 0.001 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 15:44:42 ; Search time 0.001 Seconds
(without alignments)
7.030 Million cell updates/sec

Title: US-09-904-968A-19-COPY
Perfect score: 19
Sequence: 1 ggtcgcgcgtgtacgaagg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 16 seqs, 185 residues

Total number of hits satisfying chosen parameters:	32
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 16

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Database : estdb19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	10.8	56.8	15	1	BM396199	ACCESSION: BM396199	
2	9.8	51.6	13	1	BM396884	ACCESSION: BM396884	
3	9.8	51.6	13	1	BM397041	ACCESSION: BM397041	
4	8.8	46.3	12	1	BM395931	ACCESSION: BM395931	
5	8.8	46.3	12	1	BM400317	ACCESSION: BM400217	
6	8.4	44.2	12	1	BM395540	ACCESSION: BM395540	
7	8	42.1	11	1	BM395226	ACCESSION: BM395226	
8	7.8	41.1	11	1	BM679435	ACCESSION: BM679435	
9	7.8	41.1	11	1	AJ681247	ACCESSION: AJ681247	
10	7.8	41.1	11	1	AJ683713	ACCESSION: AJ683713	
11	7.8	41.1	11	1	BM686459	ACCESSION: BM686459	
12	7.8	41.1	11	1	BM395786	ACCESSION: BM395786	
13	7.8	41.1	11	1	BM398154	ACCESSION: BM398154	
14	7.8	41.1	11	1	BM401300	ACCESSION: BM401300	
15	7.4	38.9	10	1	BM396011	ACCESSION: BM396011	
16	7.4	38.9	10	1	BM398849	ACCESSION: BM398849	

ALIGNMENTS

RESULT 1				
BM396199				
LOCUS	BM396199	15 bp	mRNA	linear EST 17-JAN-2002
DEFINITION	5099-0-18-C04.t.1 Chilcoat/turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.			

ACCESSION BM396199
VERSION BM396199.1 GI:18196252
KEYWORDS EST.

SOURCE	ORGANISM
Soi.	<i>Tetrahymena thermophila</i>
Seawater	<i>Tetrahymena thermophila</i>
	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE AUTHORS

REFERENCE	1 (bases 1 to 15)
AUTHORS	Turkewitz, A. P., Karrer, K. M., Jahn, C., Orias, E., Kirk, K. E., Frankel, J., and Klobutcher, L.
TITLE	EST from <i>Tetrahymena thermophila</i> , strain CU428.1, growing cells
JOURNAL	Unpublished (2002)
COMMENT	Contact: Turkewitz AP

Correspondence: Andrzej Pawlowski, Department of Molecular Genetics and Cell Biology, University of Chicago, 920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apawluk@midway.uchicago.edu
Seg primer: T3.

FEATURES

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source
1. 15
/locus="G4444116"
/organism="Tetrachyena thermophila"
/mol_type="mRNA"
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/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA
/notes="Vector: Bluescript SK+; Det-
preparation can be found in Chilcoat
Proc. Natl. Acad. Sci. USA. 98: 8709.

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Query Match	56.8%	Score 10.8;	DB 1;	Length 15;
Best Local Similarity	85.7%	Pred. No. 1.4;		
Matches 12; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 3 TCGCGCTGTGGCA 16
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Dβ 1 TCACGCGGTGGCGA 14

RESULT 2

BM396884	LOCUS	BM396884	13 bp	mRNA	linear	EST 17-JAN-2002
DEFINITION						
5009-0-26-C11.t.1 Chilcoat/Turkewitz CDNA (large fraction)						
Tetrahymena thermophila cDNA, mRNA sequence.						

ACCESSION BM396884
VERSION BM396884.1 GI:18196937
KEYWORDS EST.

SOURCE	ORGANISM
Tetrahymena thermophila	Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.	Tetrahymena thermophila

REFERENCE
1 (Bases 1 to 13)
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Ortas, B., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
TITLE
EST from *Tetrahymena thermophila*, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)

Organized by: 12/02/7
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172

FEATURES

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1. 13
source
/organism="Tetrahymena thermophila"
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/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes=vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2000)
Proc. Natl. Acad. Sci. USA. 98: 8709-8713.

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Query Match	51.6%	Score 9.8;	DB 1;	Length 13;
Best Local Similarity	84.6%	Pred. No. 2.2;		
Matches 11; Conservative	0;	Mismatches	2;	Indels

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QY 3 TCGCGCTGTGGCG 15
Db 1 TCACGCGGTGGCG 13

RESULT 3
BM397041
LOCUS 13 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-28-C12.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397041
VERSION BM397041.1 GI:18197094
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 13)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 2.2;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCG 15
Db 1 TCACGCGGTGGCG 13

RESULT 4
BM395931
LOCUS 12 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-14-D04.t.1 Chilcoat/turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395931
VERSION BM395931.1 GI:18195984
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 12)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..12
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
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/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGC 14
Db 1 TCACGCGGTGGC 12

RESULT 5
BM400217
LOCUS 12 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-7-B09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM400217
VERSION BM400217.1 GI:18200270
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 12)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..12
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGC 14
Db 1 TCACGCGGTGGC 12

RESULT 6
AJ655540
LOCUS 12 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ655540 KN277 Sus scrofa cDNA clone C0005190_G13, mRNA sequence.
ACCESSION AJ655540
VERSION AJ655540.1 GI:49339572

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Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
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/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGC 14
Db 1 TCACGCGGTGGC 12

RESULT 5
BM400217
LOCUS 12 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-7-B09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM400217
VERSION BM400217.1 GI:18200270
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 12)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..12
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGC 14
Db 1 TCACGCGGTGGC 12

RESULT 6
AJ655540
LOCUS 12 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ655540 KN277 Sus scrofa cDNA clone C0005190_G13, mRNA sequence.
ACCESSION AJ655540
VERSION AJ655540.1 GI:49339572

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KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
1 (bases 1 to 12)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled early embryos, from 8- cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1..12
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005190_G13"
/tissue_type="embryo"
/clone_lib="KN277"
/notes="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 4.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGAA 17
Db ||||| |||

RESULT 7
LOCUS BM395226 11 bp mRNA linear EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395226
VERSION BM395226.1 GI:18195279
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
REFERENCE
1 (bases 1 to 11)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..11
Location/Qualifiers
/organism="Tetrahymena thermophila"

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/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:9811"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 42.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGCG 15
Db ||||| |||

RESULT 8
LOCUS AJ679435 11 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ679435 CSEQAN04 Sus scrofa cDNA clone C0001779_B18, mRNA sequence.
ACCESSION AJ679435
VERSION AJ679435.1 GI:49412022
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 11)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1..11
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001779_B18"
/tissue_type="uterus"
/clone_lib="CSEQAN04"
/notes="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14
Db ||||| |||

RESULT 9
LOCUS AJ681247 11 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ681247 CSEQAN04 Sus scrofa cDNA clone C0001795_I24, mRNA sequence.
ACCESSION AJ681247

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VERSION      AJ681247.1  GI:49413837
KEYWORDS
SOURCE       Sus scrofa (pig)
ORGANISM     Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
              Eukaryota; Metazoa; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
              Sus.

REFERENCE    1 (bases 1 to 11)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE        Development of cDNA and EST resources for studying reproduction and
              embryo development in pigs and cattle
JOURNAL      Unpublished (2004)
COMMENT      Contact: Anderson SI
              Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
              Single pass sequencing. Bases called and trimmed with phred
              v0.020425.c. Vector identified by cross_match with the -minscore 20
              and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
              R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
              from pig uterus. Clones available from UK Centre for Functional
              Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
              EH25 9PS, www.arkgenomics.org.

FEATURES     Location/Qualifiers
              1..11
                /organism="Sus scrofa"
                /mol_type="mRNA"
                /db_xref="taxon:9823"
                /clone="C0001795_124"
                /tissue_type="uterus"
                /clone_lib="CSEQRAN04"
                /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:
                NotI; Single pass sequencing. Normalised library
                constructed from pig uterus."

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  CGCGCTGTGGC 14
        | | | | | | | |
Db      1  CCGCGGTGGC 11

RESULT 10
AJ683713
LOCUS      AJ683713 CSEQRAN04 Sus scrofa cDNA clone C0001802_O06, mRNA
DEFINITION
ACCESSION  AJ683713
VERSION    AJ683713.1  GI:49416303
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
              Eukaryota; Metazoa; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
              Sus.

REFERENCE    1 (bases 1 to 11)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE        Development of cDNA and EST resources for studying reproduction and
              embryo development in pigs and cattle
JOURNAL      Unpublished (2004)
COMMENT      Contact: Anderson SI
              Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
              Single pass sequencing. Bases called and trimmed with phred
              v0.020425.c. Vector identified by cross_match with the -minscore 20
              and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
              R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
              from pig uterus. Clones available from UK Centre for Functional
              Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
              EH25 9PS, www.arkgenomics.org.

FEATURES     Location/Qualifiers
              1..11
                /organism="Sus scrofa"
                /mol_type="mRNA"
                /db_xref="taxon:9823"
                /clone="C0001795_124"
                /tissue_type="uterus"
                /clone_lib="CSEQRAN04"
                /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:
                NotI; Single pass sequencing. Normalised library
                constructed from pig uterus."

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  CGCGCTGTGGC 14
        | | | | | | | |
Db      1  CCGCGGTGGC 11

RESULT 10
AJ683713
LOCUS      AJ683713 CSEQRAN04 Sus scrofa cDNA clone C0001802_O06, mRNA
DEFINITION
ACCESSION  AJ683713
VERSION    AJ683713.1  GI:49416303
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
              Eukaryota; Metazoa; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
              Sus.

REFERENCE    1 (bases 1 to 11)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE        Development of cDNA and EST resources for studying reproduction and
              embryo development in pigs and cattle
JOURNAL      Unpublished (2004)
COMMENT      Contact: Anderson SI
              Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
              Single pass sequencing. Bases called and trimmed with phred
              v0.020425.c. Vector identified by cross_match with the -minscore 20
              and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
              R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
              from pig uterus. Clones available from UK Centre for Functional
              Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
              EH25 9PS, www.arkgenomics.org.

FEATURES     Location/Qualifiers
              1..11
                /organism="Sus scrofa"
                /mol_type="mRNA"
                /db_xref="taxon:9823"
                /clone="C0001802_O06"
                /tissue_type="uterus"
                /clone_lib="CSEQRAN04"
                /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:
                NotI; Single pass sequencing. Normalised library
                constructed from pig uterus."

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  CGCGCTGTGGC 14
        | | | | | | | |
Db      1  CCGCGGTGGC 11

RESULT 11
AJ686459
LOCUS      AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811_K23, mRNA
DEFINITION
ACCESSION  AJ686459
VERSION    AJ686459.1  GI:49419049
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
              Eukaryota; Metazoa; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
              Sus.

REFERENCE    1 (bases 1 to 11)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE        Development of cDNA and EST resources for studying reproduction and
              embryo development in pigs and cattle
JOURNAL      Unpublished (2004)
COMMENT      Contact: Anderson SI
              Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
              Single pass sequencing. Bases called and trimmed with phred
              v0.020425.c. Vector identified by cross_match with the -minscore 20
              and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
              R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
              from pig uterus. Clones available from UK Centre for Functional
              Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
              EH25 9PS, www.arkgenomics.org.

FEATURES     Location/Qualifiers
              1..11
                /organism="Sus scrofa"
                /mol_type="mRNA"
                /db_xref="taxon:9823"
                /clone="C0001811_K23"
                /tissue_type="uterus"
                /clone_lib="CSEQRAN04"
                /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:
                NotI; Single pass sequencing. Normalised library
                constructed from pig uterus."

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  CGCGCTGTGGC 14
        | | | | | | | |
Db      1  CCGCGGTGGC 11

RESULT 12
BM395786

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LOCUS      BM395786                      11 bp  mRNA  linear  EST 17-JAN-2002
DEFINITION  5009-0-11-G09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION   BM395786
VERSION     BM395786.1  GI:18195839
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 11)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3  TCACGCGTGTGG 13
    |||||
Db   1  TCACGCGGTGG 11

RESULT 13
LOCUS      BM398154                      11 bp  mRNA  linear  EST 17-JAN-2002
DEFINITION  5009-0-41-D10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION   BM398154
VERSION     BM398154.1  GI:18198207
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 11)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3  TCACGCGTGTGG 13
    |||||
Db   1  TCACGCGGTGG 11

RESULT 14
LOCUS      BM401300                      11 bp  mRNA  linear  EST 17-JAN-2002
DEFINITION  5009-0-85-E01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION   BM401300
VERSION     BM401300.1  GI:18201353
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 11)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3  TCACGCGTGTGG 13
    |||||
Db   1  TCACGCGGTGG 11

RESULT 15
LOCUS      BM396011                      10 bp  mRNA  linear  EST 17-JAN-2002
DEFINITION  5009-0-15-E12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION   BM396011
VERSION     BM396011.1  GI:18196064
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 10)

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/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3  TCACGCGTGTGG 13
    |||||
Db   1  TCACGCGGTGG 11

```

```

RESULT 14
LOCUS      BM401300                      11 bp  mRNA  linear  EST 17-JAN-2002
DEFINITION  5009-0-85-E01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION   BM401300
VERSION     BM401300.1  GI:18201353
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 11)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3  TCACGCGTGTGG 13
    |||||
Db   1  TCACGCGGTGG 11

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RESULT 15
LOCUS      BM396011                      10 bp  mRNA  linear  EST 17-JAN-2002
DEFINITION  5009-0-15-E12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION   BM396011
VERSION     BM396011.1  GI:18196064
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 10)

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AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3

FEATURES
source
1..10
Location/Qualifiers
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
||| |||||
Db 2 CGCGGTGGC 10

RESULT 16
BM398849
LOCUS 10 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-5-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398849
VERSION BM398849.1 GI:18198902
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 10)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..10
Location/Qualifiers
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/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14

Db ||| |||||
2 CGCGGTGGC 10

Search completed: May 9, 2006, 15:44:42
Job time : 0.001 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 15:46:51 ; Search time 0.001 Seconds
(without alignments)
68.894 Million cell updates/sec

Title: US-09-904-968A-19-COPY
Perfect score: 19
Sequence: 1 ggtcgcgtgtggaagg 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 173 seqs, 1813 residues

Total number of hits satisfying chosen parameters: 346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 173 summaries
Database : gcl9:*

Genbank/EMBL

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	19	100.0	19	1	ACCESSION:AX440515
2	10.4	54.7	14	1	ACCESSION:AR364760
3	10.4	54.7	14	1	ACCESSION:AR408022
4	9.8	51.6	14	1	ACCESSION:AR408022
5	9.8	51.6	14	1	ACCESSION:AR408022
6	9	47.4	10	1	ACCESSION:AR349597
7	9	47.4	10	1	ACCESSION:AR103443
8	9	47.4	10	1	ACCESSION:BD223041
9	9	47.4	10	1	ACCESSION:AR201469
10	9	47.4	10	1	ACCESSION:AR201469
11	9	47.4	10	1	ACCESSION:AR562046
12	9	47.4	11	1	ACCESSION:AR590095
13	8.8	46.3	12	1	ACCESSION:AX630373
14	8.4	44.2	10	1	ACCESSION:AJ524760
15	8.4	44.2	10	1	BD161333
16	8.4	44.2	10	1	BD238832
17	8.4	44.2	10	1	BD238855
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21	8.4	44.2	11	1	Q833102
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26	8.4	44.2	11	1	Q838061
27	8.4	44.2	11	1	CS058641
28	8.4	44.2	11	1	AX301724
29	8.4	44.2	11	1	AX470439
30	8.4	44.2	11	1	AX471346
31	8.4	44.2	11	1	AX523088
32	8.4	44.2	11	1	AX624098
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	43	8.4	44.2	12	1	ACCESSION:AX71524
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	106	7.4	38.9	10	1	AR533687
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C 116	7.4	38.9	10	1	AX153110	ACCESSION:AX153110	TITLE						
C 117	7.4	38.9	10	1	AX153149	ACCESSION:AX153149	JOURNAL						
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C 119	7.4	38.9	10	1	AX301491	ACCESSION:AX301491	source						
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JOURNAL Patent: US 6632057-A 115 14-OCT-2003;
GFI Aerospace; Paris;

FBX;

FEATURES
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QY 8 CTGCGCGAGG 19

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1 CTGTGGAGAGG 12

RESULT 4

BD225399

LOCUS

BD225399

Targeting antisense library.

14 bp DNA linear PAT 17-JUL-2003

ACCESSION

BD225399

VERSION

BD225399.1

KEYWORDS

JP 2002509733-A/33.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

Ruffner,D.E., Pierce,M.L. and Chen,Z.

TARGETING

antisense library

TITLE

Patent: JP 2002509733-A 33 02-APR-2002;

JOURNAL

UNIVERSITY OF UTAH RESEARCH FOUNDATION

OS Herpes simplex virus

PN JP 2002509733-A/33

PD 02-APR-2002

PF 28-MAR-1998 JP 2000541344

PR 28-MAR-1998 US 60/079792, 06-NOV-1998 US

PI 60/107504

DUANE E RUFFNER, MICHAEL L PIERCE, ZHIDONG CHEN

PC C12N15/09, C12Q1/68//A61K48/00, C12N15/00

CC Targeting antisense library

FH Key

Location/Qualifiers

FT source

1. .14

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FEATURES
source

Location/Qualifiers
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||||| |||||

2 GTGCGCGCTGGC 14

RESULT 5

AR349597

LOCUS

AR349597

Sequence 33 from patent US 6586180.

14 bp DNA linear PAT 17-AUG-2003

ACCESSION

AR349597

VERSION

AR349597.1

KEYWORDS

GI:33750395

SOURCE

Unknown.

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 14)

Ruffner,D.E., Pierce,M.L. and Chen,Z.

TARGETING

antisense libraries

TITLE

Patent: US 6586180-A 33 01-JUL-2003;

JOURNAL

University of Utah; Salt Lake City, UT

FEATURES
source

Location/Qualifiers
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Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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||||| |||||

2 GTGCGCGCTGGC 14

RESULT 6

AR103443/c

LOCUS

AR103443

Sequence 18 from patent US 6087477.

10 bp DNA linear PAT 14-FEB-2001

ACCESSION

AR103443

VERSION

AR103443.1

KEYWORDS

GI:12815031

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 10)

AUTHORS

Falb,D.A. and Gimbrone,M.A. Jr.

TARGETING

compositions and methods for the treatment and diagnosis of

cardiovascular disease

TITLE

Patent: US 6087477-A 18 11-JUL-2000;

JOURNAL

Location/Qualifiers

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FEATURES

source

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10 GTGCGGAG 2

RESULT 7

BD223041/c

LOCUS

BD223041

Sequence 18 from patent US 6087477.

10 bp DNA linear PAT 17-JUL-2003

DEFINITION

Compositions and methods for the treatment and diagnosis of

cardiovascular disease.

ACCESSION

BD223041

VERSION

BD223041.1

KEYWORDS

JP 2002521679-A/12.

SOURCE

synthetic construct

ORGANISM

other sequences; artificial sequences.

REFERENCE

1 (bases 1 to 10)

AUTHORS

Falb,D.A.

TITLE

Compositions and methods for the treatment and diagnosis of

cardiovascular disease

JOURNAL

Patent: JP 2002521679-A 12 16-JUL-2002;

COMMENT

MILLENNIUM PHARMACEUTICALS INC

OS Artificial Sequence

PN JP 2002521679-A/12

PD 16-JUL-2002

PF 30-JUL-1999 JP 2000562059

PI 30-JUL-1998 US 09/126640

PC DEAN A FALB

PC

G01N33/50, A61K31/711, A61K39/395, A61K39/395, A61K45/00, A61K48/00, PC

A61P7/00,

PC

A61P9/08, A61P9/10, A61P9/12, A61P9/14, A61P27/02, A61P29/00, A61P35/00,

PC

G01N33/15, G01N33/566, G01N33/68//C12N15/09, C12N15/00 CC


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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7414 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 GCGCTGTGG 11

RESULT 13
LOCUS      ATH524760
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            081C08.
ACCESSION  AJ524760
VERSION    AJ524760.1 GI:26792996
KEYWORDS   left border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS     Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE       T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED     12446565
REFERENCE   2 (bases 1 to 12)
AUTHORS     Balzerque,S.
TITLE       Direct Submission
JOURNAL     Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://absap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
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DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION  BD161333
VERSION    BD161333.1 GI:27867091
KEYWORDS   JP 2002186482-A/155.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
            1 (bases 1 to 10)
REFERENCE   Nagai,S., Matsushima,K. and Hashimoto,S.
AUTHORS     Human activated Th1 and Th2 cell expression genes
TITLE       Patent: JP 2002186482-A 155 02-JUL-2002;
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002186482-A/155
            PD 02-JUL-2002
            PF 19-DEC-2000 JP 2000385816
            PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
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DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD238832
VERSION    BD238832.1 GI:33048602
KEYWORDS   JP 2002534056-A/250.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
            1 (bases 1 to 10)
REFERENCE   Roberts,B.L. and Shankara,S.
AUTHORS     Preparation and use of superior vaccines
TITLE       Patent: JP 2002534056-A 250 15-OCT-2002;
JOURNAL     GENZYME CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002534056-A/250
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749

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08-DEC-1998 US 60/111715
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTCGGCGTG 10
DB 10 GGGCGGCGTG 1
RESULT 16
LOCUS BD238855 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238855
VERSION BD238855.1 GI:33048625
KEYWORDS JP 2002534056-A/273.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 273 15-OCT-2002;
GENZIME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/273
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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08-DEC-1998 US 60/111715
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 10 GGGCGGCGTG 1
RESULT 16
LOCUS BD238855 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238855
VERSION BD238855.1 GI:33048625
KEYWORDS JP 2002534056-A/273.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 273 15-OCT-2002;
GENZIME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/273
PD 15-OCT-2002
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DB 10 GGGCGGCGTG 1
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LOCUS AX152988/c 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 903 from Patent WO0138577.
ACCESSION AX152988
VERSION AX152988.1 GI:14534639
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 903 31-MAY-2001;
The Johns Hopkins University (US)
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DB 10 GGGCGGCGTG 1
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LOCUS BD124474 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124474
VERSION BD124474.1 GI:23219419
KEYWORDS JP 2002503460-A/305.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)

19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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Best Local Similarity 90.0%; Pred. No. 34;
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DB 1 CGCTGTGGCG 10
RESULT 17
LOCUS AX152988/c 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 903 from Patent WO0138577.
ACCESSION AX152988
VERSION AX152988.1 GI:14534639
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 903 31-MAY-2001;
The Johns Hopkins University (US)
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DB 10 GGGCGGCGTG 1
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LOCUS BD124474 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124474
VERSION BD124474.1 GI:23219419
KEYWORDS JP 2002503460-A/305.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)

AUTHORS Katz,E.H.
 TITLE Compositions and method for healing wound
 JOURNAL Patent: JP 2002503460-A 305 05-FEB-2002;
 THE WISTAR INSTITUTE
 COMMENT OS Mus musculus (mouse)
 PN JP 2002503460-A/305
 PD 05-FEB-2002
 PF 12-FEB-1999 JP 2000531545
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 28-SEP-1998 US 60/102051
 PI ELLEN HEBER KATZ
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 Db |||||
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 RESULT 19
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 LOCUS CQ832827 11 bp DNA linear PAT 29-JUL-2004
 DEFINITION Sequence 198 from Patent WO2004059002.
 ACCESSION CQ832827
 VERSION CQ832827.1 GI:50832434
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
 Conradt,M. and Hofmann,K.
 TITLE Method for determining the homeostasis of hairy skin
 JOURNAL Patent: WO 2004059002-A 198 15-JUL-2004;
 Henkel Kommanditgesellschaft auf Aktien (DE)
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 LOCUS CQ833102/c 11 bp DNA linear PAT 29-JUL-2004
 DEFINITION Sequence 473 from Patent WO2004059002.
 ACCESSION CQ833102
 VERSION CQ833102.1 GI:50832709
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 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
 Conradt,M. and Hofmann,K.
 TITLE Method for determining the homeostasis of hairy skin
 JOURNAL Patent: WO 2004059002-A 473 15-JUL-2004;
 Henkel Kommanditgesellschaft auf Aktien (DE)
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 LOCUS CQ833458 11 bp DNA linear PAT 29-JUL-2004
 DEFINITION Sequence 829 from Patent WO2004059002.
 ACCESSION CQ833458
 VERSION CQ833458.1 GI:50833065
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
 Conradt,M. and Hofmann,K.
 TITLE Method for determining the homeostasis of hairy skin
 JOURNAL Patent: WO 2004059002-A 829 15-JUL-2004;
 Henkel Kommanditgesellschaft auf Aktien (DE)
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 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCGCTGTGCG 14
 Db |||||
 2 GGGCTGTGCG 11
 RESULT 22
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 LOCUS CQ835173/c 11 bp DNA linear PAT 29-JUL-2004
 DEFINITION Sequence 231 from Patent WO2004059001.
 ACCESSION CQ835173
 VERSION CQ835173.1 GI:50834707
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
 Conradt,M. and Hofmann,K.

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TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 231 15-JUL-2004;
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Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GGCCTGTGGC 14
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RESULT 23
LOCUS      CQ837127/c
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ACCESSION  CQ837127
VERSION     CQ837127.1 GI:50836661
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
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           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominoidea; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
           Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 2185 15-JUL-2004;
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QY      10 GTGGCGAAGG 19
Db      11 GTGGAGAAGG 2

RESULT 24
LOCUS      CQ838018
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ACCESSION  CQ838018
VERSION     CQ838018.1 GI:50837552
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
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           Hominoidea; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
           Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 3076 15-JUL-2004;
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TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 231 15-JUL-2004;
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RESULT 25
LOCUS      CQ838061
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ACCESSION  CQ838061
VERSION     CQ838061.1 GI:50837595
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           Hominoidea; Homo.
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AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
           Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 3119 15-JUL-2004;
           Henkel Kommanditgesellschaft auf Aktien (DE)
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           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CGCTGTGGCG 15
Db      1 CGCTGTGGCG 10

RESULT 26
LOCUS      CS058641/c
DEFINITION Sequence 538 from Patent WO2005028671.
ACCESSION  CS058641
VERSION     CS058641.1 GI:62551824
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominoidea; Homo.
REFERENCE  1
AUTHORS    Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
           Kessler-Becker,D.
TITLE      Method for determining hair cycle markers
JOURNAL    Patent: WO 2005028671-A 538 31-MAR-2005;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   source
           1. .11
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GGCCTGTGGC 14

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Db      11  GCGCGGTGC 2
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RESULT 27
AR301724
LOCUS      11 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 305 from patent US 6538173.
ACCESSION AR301724
VERSION   AR301724.1 GI:31689526
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS  Heber-Katz,E.
TITLE    Compositions and methods for wound healing
JOURNAL  Patent: US 6538173-A 305 25-MAR-2003;
        The Wistar Institute; Philadelphia, PA;
        WOX;
FEATURES
source
1..11
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCTGTGGCCA 16
|||||
Db 1 GCTGTGGCCA 10

RESULT 28
AX470439
LOCUS      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 16 from Patent WO02053773.
ACCESSION AX470439
VERSION   AX470439.1 GI:22205564
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS  Hofmann,K., Conradt,M. and Petersohn,D.
TITLE    Method for determining skin stress or skin ageing in vitro
JOURNAL  Patent: WO 02053773-A 16 11-JUL-2002;
        HENKEL KGAA (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GTGGCGAAGG 19
|||||
Db 1 GTGGCGAATG 10

RESULT 29
AX471346/c
LOCUS      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 923 from Patent WO02053773.
ACCESSION AX471346
VERSION   AX471346.1 GI:22206471
KEYWORDS

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SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS  Hofmann,K., Conradt,M. and Petersohn,D.
TITLE    Method for determining skin stress or skin ageing in vitro
JOURNAL  Patent: WO 02053773-A 923 11-JUL-2002;
        HENKEL KGAA (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GTGGCGAAGG 19
|||||
Db 11 GTGGAGAAGG 2

RESULT 30
AX623088
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 129 from Patent WO02053774.
ACCESSION AX623088
VERSION   AX623088.1 GI:28451029
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 129 11-JUL-2002;
        Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GTGGCGAAGG 19
|||||
Db 1 GTGGCGAATG 10

RESULT 31
AX624098
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 1139 from Patent WO02053774.
ACCESSION AX624098
VERSION   AX624098.1 GI:28452039
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 1139 11-JUL-2002;

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FEATURES
  source
    Henkel Kommanditgesellschaft auf Aktien (DE)
    Location/Qualifiers
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
Db 1 GTGGCGAATG 10

RESULT 32
AX624741
LOCUS AX624741 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1782 from Patent WO02053774.
ACCESSION AX624741
VERSION AX624741.1 GI:28452682
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1782 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    Location/Qualifiers
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
Db 2 CGATGTGGCG 11

RESULT 33
AX626676
LOCUS AX626676 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3717 from Patent WO02053774.
ACCESSION AX626676
VERSION AX626676.1 GI:28454714
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 3717 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    Location/Qualifiers
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
Db 1 GTGGCGAATG 10

RESULT 34
AX626754
LOCUS AX626754 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3795 from Patent WO02053774.
ACCESSION AX626754
VERSION AX626754.1 GI:28454792
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 3795 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    Location/Qualifiers
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
Db 11 GCGCAGTGGC 2

RESULT 35
AX628541
LOCUS AX628541 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5582 from Patent WO02053774.
ACCESSION AX628541
VERSION AX628541.1 GI:28456579
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5582 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    Location/Qualifiers
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
Db 2 GCGCTGTGGC 11

RESULT 36
AX629565

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LOCUS       AX629565                      11 bp    DNA          linear          PAT 21-FEB-2003
DEFINITION   Sequence 6606 from Patent WO02053774.
ACCESSION    AX629565
VERSION      AX629565.1  GI:28457603
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6606 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source          1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              6  CGCTGTGGCG 15
                |||||
Db              1  CGCTGTGGGG 10

RESULT 37
LOCUS       AX629817/c                    11 bp    DNA          linear          PAT 21-FEB-2003
DEFINITION   Sequence 6858 from Patent WO02053774.
ACCESSION    AX629817
VERSION      AX629817.1  GI:28457855
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6858 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source          1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              10 GTGGCGAAGG 19
                |||||
Db              11 GTGGAGAGG 2

RESULT 38
LOCUS       AX630364/c                    11 bp    DNA          linear          PAT 21-FEB-2003
DEFINITION   Sequence 7405 from Patent WO02053774.
ACCESSION    AX630364
VERSION      AX630364.1  GI:28458402
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7405 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source          1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              10 GTGGCGAAGG 19
                |||||
Db              11 GTGGCGAATG 10

RESULT 39
LOCUS       AX630509                      11 bp    DNA          linear          PAT 21-FEB-2003
DEFINITION   Sequence 7550 from Patent WO02053774.
ACCESSION    AX630509
VERSION      AX630509.1  GI:28458547
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7550 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source          1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              1  GGTGCGCGCTG 10
                |||||
Db              10 GGGCGCGCTG 1

RESULT 40
LOCUS       AX631519                      11 bp    DNA          linear          PAT 21-FEB-2003
DEFINITION   Sequence 8561 from Patent WO02053774.
ACCESSION    AX631519
VERSION      AX631519.1  GI:28459585
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 8561 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source          1..11
             /organism="Homo sapiens"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
    |||||
Db 1 GTGGCGAATG 10

RESULT 41
AX632162
LOCUS AX632162 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9204 from Patent WO02053774.
ACCESSION AX632162
VERSION AX632162.1 GI:28467777
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9204 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
      1..11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
    |||||
Db 2 CGATGTGGCG 11

RESULT 42
A71524/c
LOCUS A71524 12 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 83 from Patent WO9813521.
ACCESSION A71524
VERSION A71524.1 GI:4775136
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified
          sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fesce,R. and Consalez,G.
TITLE METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
          PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
JOURNAL Patent: WO 9813521-A 83 02-APR-1998;
          FESCE RICCARDO (IT)
FEATURES
source Location/Qualifiers
      1..12
      /organism="unidentified"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
    |||||
Db 12 GTGACGAAGG 3

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
    |||||
Db 1 GTGGCGAATG 10

RESULT 43
ARI172146
LOCUS ARI172146 12 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6303293.
ACCESSION ARI172146
VERSION ARI172146.1 GI:17911637
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
          Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Patterson,D.R., Puskas,J.A., Song,K. and Linnen,J.M.
TITLE Oligonucleotide reverse transcription primers for efficient
          detection of HIV-1 and HIV-2 and methods of use thereof
JOURNAL Patent: US 6303293-A 2 16-OCT-2001;
          Location/Qualifiers
FEATURES
source 1..12
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
    |||||
Db 1 CCCTGTGGCG 10

RESULT 44
AR678905/c
LOCUS AR678905 12 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 50 from patent US 6902894.
ACCESSION AR678905
VERSION AR678905.1 GI:67620099
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
          1 (bases 1 to 12)
REFERENCE 1 (bases 1 to 12)
AUTHORS Yang,M. and Woo,H.S.
TITLE Mutation detection on RNA polymerase beta subunit gene having
          rifampin resistance
JOURNAL Patent: US 6902894-A 50 07-JUN-2005;
          Genetel Pharmaceuticals Ltd.; Hong Kong;
          CNX;
FEATURES
source Location/Qualifiers
      1..12
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
    |||||
Db 11 GCGCTGGGC 2

RESULT 45
BD000788
LOCUS BD000788 12 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide reverse transcription primers for efficient
          detection of HIV-1 and HIV-2 and methods of use thereof.
ACCESSION BD000788
VERSION BD000788.1 GI:18623901
KEYWORDS JP 2000342274-A/2.
          synthetic construct
SOURCE synthetic constructs;
          other sequences; artificial sequences.
ORGANISM
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REFERENCE 1 (bases 1 to 12)
AUTHORS Patterson,D.R., Puscus,J.A., Son,K. and Lynen,J.M.
TITLE Oligonucleotide reverse transcription primers for efficient
JOURNAL detection of HIV-1 and HIV-2 and methods of use thereof
COMMENT Patent: JP 2000342274-A 2 12-DEC-2000;
OS ORTHO CLINICAL DIAGNOSTICS INC
PN JP 2000342274-A/2
PD 12-DEC-2000
PF 02-FEB-2000 JP 2000025419
PR 02-FEB-1999 US 60/118417
PI DAVID R PATTERSON, JOHN A. PUSCUS, KEMIN SON, JEFFREY M. LYNEN
PC C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, G01N33/569, PC
C12N15/00
CC
FH Key 1. .12 Location/Qualifiers
FT source /organism='Artificial Sequence'.
FEATURES
source
1. .12 Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CCCTGTGGCG 15
Db | | | | | | | |
1 CCCTGTGGCG 10
RESULT 46
BD083127
LOCUS Human matured/activated dendritic cell expression genes.
DEFINITION
ACCESSION BD083127
VERSION JP 2001327293-A 48 27-NOV-2001;
KEYWORDS JAPAN SCIENCE AND TECHNOLOGY CORP
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 150 27-NOV-2001;
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/48
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
NAGAI
PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
CC
FH Key 1. .10 Location/Qualifiers
FT source /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CTGTGGCG 15
Db | | | | | | | |
2 CTGTGGCG 9
RESULT 48
BD240116
LOCUS Preparation and use of superior vaccines.
DEFINITION
ACCESSION BD240116
VERSION JP 2002534056-A/1534.
KEYWORDS JAPAN SCIENCE AND TECHNOLOGY CORP
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1534 15-OCT-2002;
COMMENT GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1534
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992, 19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878, 19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000, 19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999, 19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042, 19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044, 19-JUN-1998 US 60/089844 PR

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19-JUN-1998 US 60/090800,19-JUN-1998 US 60/089833 PR
 19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
 19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
 19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
 08-DEC-1998 US 60/111715
 PI BRUCE L ROBERTS, SRINIVAS SHANKARA
 PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
 C12N1/19
 PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
 G01N37/00,
 PC C12N15/00, C12N5/00, C12N15/00
 CC Preparation and use of superior vaccines
 FH Key Location/Qualifiers
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 FT /organism='Homo sapiens (human)'.
 FT Location/Qualifiers
 1..10
 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

FEATURES

source

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAAG 18
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 DB 3 TGGCGAAG 10

RESULT 49

E54818
 LOCUS Human normal liver cell expression genes. 10 bp DNA linear PAT 27-AUG-2002
 DEFINITION
 E54818
 ACCESSION
 E54818.1 GI:22556301
 VERSION
 E54818.1 GI:22556301
 KEYWORDS
 JP 2001211883-A/170.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.

REFERENCE 1 (bases 1 to 10)
 Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
 Human normal liver cell expression genes

TITLE Patent: JP 2001211883-A 170 07-AUG-2001;

JOURNAL SCIENCE & TECH AGENCY

COMMENT OS Homo sapiens (human)

PN JP 2001211883-A/170

PD 07-AUG-2001

PF 31-JAN-2000 JP 2000023170

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI

PC C12N15/09, C07K16/18, C12P21/02, C12N15/00

CC YAMASHITA

FH Key Location/Qualifiers.

1..10
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 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

FEATURES

source

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGTG 12
 |||||
 DB 3 GCGCTGTG 10

RESULT 50

AX152803

LOCUS AX152803 10 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 718 from Patent WO0138577.
 AX152803
 ACCESSION
 AX152803.1 GI:14534454
 VERSION
 AX152803.1 GI:14534454
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.

REFERENCE

1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.

AUTHORS Human transcriptomes

TITLE Patent: WO 0138577-A 718 31-MAY-2001;

JOURNAL The Johns Hopkins University (US)

FEATURES Location/Qualifiers

1..10

/organism='Homo sapiens'

/mol_type='unassigned DNA'

/db_xref='taxon:9606'

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGTG 12
 |||||
 DB 3 GCGCTGTG 10

RESULT 51

AX301612
 LOCUS AX301612 10 bp DNA linear PAT 30-NOV-2001
 DEFINITION Sequence 326 from Patent WO0185941.
 AX301612
 ACCESSION
 AX301612.1 GI:17382695
 VERSION
 AX301612.1 GI:17382695
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.

REFERENCE 1 Versteeg,R. and Caron,H.N.

AUTHORS Myc targets

TITLE Patent: WO 0185941-A 326 15-NOV-2001;

JOURNAL Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)

COMMENT Location/Qualifiers

1..10

/organism='Homo sapiens'

/mol_type='unassigned DNA'

/db_xref='taxon:9606'

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGTG 12
 |||||
 DB 3 GCGCTGTG 10

RESULT 52

AX302590
 LOCUS AX302590 10 bp DNA linear PAT 30-NOV-2001
 DEFINITION Sequence 108 from Patent WO0175177.
 AX302590
 ACCESSION
 AX302590.1 GI:17383117
 VERSION
 AX302590.1 GI:17383117
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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REFERENCE
AUTHORS Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 0175177-A 108 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TCGCGCTG 10
Db 2 TCGCGCTG 9
RESULT 53
BD007778 10 bp DNA linear PAT 31-JAN-2002
LOCUS LPS activated human monocyte expressing genes.
DEFINITION BD007778
ACCESSION BD007778.1 GI:18636151
VERSION JP 2001069993-A/54.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Matsuhashima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 54 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/54
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
FH Key Location/Qualifiers
FT source 1. .10
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FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CTGTGGCG 15
Db 2 CTGTGGCG 9
RESULT 54
CS058186/c
LOCUS CS058186
DEFINITION Sequence 83 from Patent WO2005028671.
ACCESSION CS058186
VERSION CS058186.1 GI:62551138
KEYWORDS

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SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 83 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 42.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCTGTGGC 14
Db 8 GCTGTGGC 1
RESULT 55
AX623147/c
LOCUS AX623147
DEFINITION Sequence 188 from Patent WO02053774.
ACCESSION AX623147
VERSION AX623147.1 GI:28451088
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 188 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 42.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCTGTGGC 14
Db 8 GCTGTGGC 1
RESULT 56
AX628349/c
LOCUS AX628349
DEFINITION Sequence 5390 from Patent WO02053774.
ACCESSION AX628349
VERSION AX628349.1 GI:28456387
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin

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JOURNAL      Patent: WO 02053774-A 5390 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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              /db_xref="taxon:9606"

Query Match   42.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGGC 14
        |||||
Db       8 GCTGTGGC 1

RESULT 57
AX630568/c
LOCUS      AX630568 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7609 from Patent WO02053774.
ACCESSION  AX630568
VERSION     AX630568.1 GI:28458606
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7609 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source      Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   42.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGGC 14
        |||||
Db       8 GCTGTGGC 1

RESULT 58
BD269102
LOCUS      BD269102 11 bp DNA linear PAT 17-JUL-2003
DEFINITION Directed evolution of microorganisms.
ACCESSION  BD269102
VERSION     BD269102.1 GI:33078870
KEYWORDS    JP 2002543834-A/6.
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1 (bases 1 to 11)
            Schellenberger,V., Liu,A.D. and Selifonova,O.V.
REFERENCE   1
AUTHORS     Schellenberger,V., Liu,A.D. and Selifonova,O.V.
TITLE       Directed evolution of microorganisms
JOURNAL     Patent: JP 2002543834-A 6 24-DEC-2002;
            GENENCOR INTERNATIONAL INC
COMMENT     OS Artificial Sequence
            PN JP 2002543834-A/6
            PD 24-DEC-2002
            PF 15-MAY-2000 JP 2000618443
            PR 19-MAY-1999 US 09/314847
            PI VOLKER SCHELLENBERGER,AMY D LIU,OLGA V SELIFONOVA PC
            C12N15/09,C12N1/21,C12N15/01// (C12N1/21,C12R1:185),C12N15/00, PC
            C12N15/00
            CC pos102 mutD mutated gene

JOURNAL      Patent: WO 02053774-A 5390 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source      Location/Qualifiers
              1..11
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              /mol_type="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

Query Match   41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTCCGCGCTGTG 12
        |||||
Db       1 GTCCGCGCTGTG 11

RESULT 59
CQ833123
LOCUS      CQ833123 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 494 from Patent WO2004059002.
ACCESSION  CQ833123
VERSION     CQ833123.1 GI:50832730
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE       Method for determining the homeostasis of hairy skin
JOURNAL     Patent: WO 2004059002-A 494 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source      Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 TGTGGCGAAGG 19
        |||||
Db       1 TGTGGCGAAG 11

RESULT 60
CQ833801
LOCUS      CQ833801 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1172 from Patent WO2004059002.
ACCESSION  CQ833801
VERSION     CQ833801.1 GI:50833408
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE       Method for determining the homeostasis of hairy skin
JOURNAL     Patent: WO 2004059002-A 1172 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source      Location/Qualifiers
              1..11
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCTGTGGCG 15
Db 1 GGGCTGTGGAG 11

RESULT 61
CQ837135/c
LOCUS
DEFINITION
Sequence 2193 from Patent WO2004059001.
ACCESSION
CQ837135
VERSION
CQ837135.1 GI:50836669
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
AUTHORS
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
Method for determining markers of human facial skin
JOURNAL
Patent: WO 2004059001-A 2193 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCTGCTCT 11
Db 11 GGTCTGCTCT 11

RESULT 62
AR203918
LOCUS
DEFINITION
Sequence 8 from patent US 6365410.
ACCESSION
AR203918
VERSION
AR203918.1 GI:21500430
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Schellenberger,V., Liu,A.D. and Selifonova,O.V.
TITLE
Directed evolution of microorganisms
JOURNAL
Patent: US 6365410-A 8 02-APR-2002;
FEATURES
Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 41.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
Db 1 GTCCCGCTGTG 11

RESULT 63
AR471274/c
LOCUS
DEFINITION
Sequence 851 from Patent WO02053773.
ACCESSION
AR471274
VERSION
AR471274.1 GI:22206399
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
AUTHORS
Hofmann,K., Conradt,M. and Petersohn,D.

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AR487539
LOCUS
DEFINITION
Sequence 10 from patent US 6706503.
ACCESSION
AR487539
VERSION
AR487539.1 GI:47252783
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Schellenberger,V., Liu,A.D. and Selifonova,O.V.
TITLE
Directed evolution of microorganisms
JOURNAL
Patent: US 6706503-A 10 16-MAR-2004;
Genencor International, Inc.; Palo Alto, CA
FEATURES
Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 41.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
Db 1 GTCCCGCTGTG 11

RESULT 64
AX049397
LOCUS
DEFINITION
Sequence 8 from Patent WO0070037.
ACCESSION
AX049397
VERSION
AX049397.1 GI:12226137
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct
REFERENCE
1
AUTHORS
Schellenberger,V., Liu,A.D. and Selifonova,O.V.
TITLE
Directed evolution of microorganisms
JOURNAL
Patent: WO 0070037-A 8 23-NOV-2000;
GENENCOR INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
source
1..11
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="POS102 mutD mutated gene"

Query Match
Best Local Similarity 41.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
Db 1 GTCCCGCTGTG 11

RESULT 65
AX471274/c
LOCUS
DEFINITION
Sequence 851 from Patent WO02053773.
ACCESSION
AX471274
VERSION
AX471274.1 GI:22206399
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
AUTHORS
Hofmann,K., Conradt,M. and Petersohn,D.

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TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 851 11-JUL-2002;
HENKEL KGAA (DE)

FEATURES
source
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14
| | | | | | | |
Db 11 CTCGCTGGGGC 1

RESULT 66
AX471408/c
LOCUS AX471408 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 985 from Patent WO02053773.
ACCESSION AX471408
VERSION AX471408.1 GI:22206533
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 985 11-JUL-2002;
HENKEL KGAA (DE)

FEATURES
source
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGGAAG 18
| | | | | | | |
Db 11 CTGGGGGCTAAG 1

RESULT 67
AX471445
LOCUS AX471445 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1022 from Patent WO02053773.
ACCESSION AX471445
VERSION AX471445.1 GI:22206570
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1022 11-JUL-2002;
HENKEL KGAA (DE)

FEATURES
source
Location/Qualifiers
1. .11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGGAAG 18
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Db 1 CTGGGGGGAAG 11

RESULT 68
AX622989
LOCUS AX622989 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 30 from Patent WO02053774.
ACCESSION AX622989
VERSION AX622989.1 GI:28450930
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 30 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1. .11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14
| | | | | | | |
Db 1 CACGCAGTGGC 11

RESULT 69
AX624192/c
LOCUS AX624192 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1233 from Patent WO02053774.
ACCESSION AX624192
VERSION AX624192.1 GI:28452133
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1233 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1. .11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGGAAG 18
| | | | | | | |
Db 11 CTGGGGGCTAAG 1

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RESULT 70
AX626026
LOCUS AX626026 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3067 from Patent WO02053774.
ACCESSION AX626026
VERSION AX626026.1 GI:28454064
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3067 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 CTGTGGCGGAAG 18
|||||
Db 1 CTGGGGGGGAAG 11

RESULT 71
AX627479
LOCUS AX627479 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4520 from Patent WO02053774.
ACCESSION AX627479
VERSION AX627479.1 GI:28455517
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4520 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 CTGTGGCGGAAG 18
|||||
Db 1 CTGTGTCCAAG 11

RESULT 72
AX628487
LOCUS AX628487 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5528 from Patent WO02053774.
ACCESSION AX628487
VERSION AX628487.1 GI:28456525
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5528 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 CTGTGGCGGAAG 18
|||||
Db 1 CTGTGTCCAAG 11

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5528 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CGCGCTGTGGC 14
|||||
Db 11 CTCGCTGGGCG 1

RESULT 73
AX629205
LOCUS AX629205 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6246 from Patent WO02053774.
ACCESSION AX629205
VERSION AX629205.1 GI:28457243
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6246 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTGGCGCTGT 11
|||||
Db 11 GGTCCACCTGT 1

RESULT 74
AX630410
LOCUS AX630410 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7451 from Patent WO02053774.
ACCESSION AX630410
VERSION AX630410.1 GI:28458448
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7451 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTGGCGCTGT 11
|||||
Db 11 GGTCCACCTGT 1

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source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGCGCTGTGGC 14
Db 1 CAGCGAGTGGC 11

RESULT 75
AX631613/c
LOCUS
DEFINITION
Sequence 8655 from Patent WO02053774.
ACCESSION
AX631613
VERSION
AX631613.1 GI:28459689
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 8655 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAG 18
Db 11 CTGGGGCTAAG 1

RESULT 76
AX632853/c
LOCUS
DEFINITION
Sequence 9895 from Patent WO02053774.
ACCESSION
AX632853
VERSION
AX632853.1 GI:28468468
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 9895 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAG 19
Db 11 TGTGCCAAGG 1

RESULT 77
AR098894/c
LOCUS
DEFINITION
Sequence 30 from patent US 6077685.
ACCESSION
AR098894
VERSION
AR098894.1 GI:12808660
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE
Tumor suppressor merlin and antibodies thereof
JOURNAL
Patent: US 6077685-A 30 20-JUN-2000;
FEATURES
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1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 38.9%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16
Db 10 CTGTGGGGA 2

RESULT 78
AR098900/c
LOCUS
DEFINITION
Sequence 36 from patent US 6077685.
ACCESSION
AR098900
VERSION
AR098900.1 GI:12808666
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE
Tumor suppressor merlin and antibodies thereof
JOURNAL
Patent: US 6077685-A 36 20-JUN-2000;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 38.9%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16
Db 10 CTGTGGGGA 2

RESULT 79
AR167218
LOCUS
DEFINITION
Sequence 52 from patent US 6284466.
ACCESSION
AR167218
VERSION
AR167218.1 GI:16243729
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Benson,A.

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TITLE      Method of detecting genetic polymorphisms using over represented
JOURNAL    Patent: US 6284466-A 52 04-SEP-2001;
FEATURES   Location/Qualifiers
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             1..10
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  9  TGTGGCGAA 17
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Db   2  TCTGGCGAA 10

RESULT 80
LOCUS      BD083089
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION  BD083089
VERSION     BD083089.1 GI:22628699
KEYWORDS   JP 2001327293-A/10.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE       Human matured/activated dendritic cell expression genes
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
           PN JP 2001327293-A/10
           PD 27-NOV-2001
           PF 22-MAY-2000
           PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
             NAGAI
           PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
           CC
           FH Key Location/Qualifiers
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             /mol_type="genomic DNA"
             /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  11 TGGCGAAGG 19
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Db   2  TGGTGAAGG 10

RESULT 81
LOCUS      BD166770
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166770
VERSION     BD166770.1 GI:27872582
KEYWORDS   JP 2002209591-A/315.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Kaneko,S. and Yamaashita,T.
TITLE       Human liver disease-expressing genes
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP
            Patent: JP 2002209591-A 315 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP

Method of detecting genetic polymorphisms using over represented
sequences
Patent: US 6284466-A 52 04-SEP-2001;
Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  9  TGTGGCGAA 17
    |||||
Db   2  TCTGGCGAA 10

RESULT 80
LOCUS      BD083089
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION  BD083089
VERSION     BD083089.1 GI:22628699
KEYWORDS   JP 2001327293-A/10.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE       Human matured/activated dendritic cell expression genes
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
           PN JP 2001327293-A/10
           PD 27-NOV-2001
           PF 22-MAY-2000
           PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
             NAGAI
           PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
           CC
           FH Key Location/Qualifiers
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             /mol_type="genomic DNA"
             /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  11 TGGCGAAGG 19
    |||||
Db   2  TGGTGAAGG 10

RESULT 81
LOCUS      BD166770
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166770
VERSION     BD166770.1 GI:27872582
KEYWORDS   JP 2002209591-A/315.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Kaneko,S. and Yamaashita,T.
TITLE       Human liver disease-expressing genes
JOURNAL     JAPAN SCIENCE AND TECHNOLOGY CORP
            Patent: JP 2002209591-A 315 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP

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COMMENT      OS Homo sapiens (human)
           PN JP 2002209591-A/315
           PD 30-JUL-2002
           PF 19-JAN-2001 JP 2001012328
           PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO
             YAMASHITA
           PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
             C12P21/08,
           CC C12N15/00,
           CC Human liver disease-expressing genes
           FH Key Location/Qualifiers
           FT source
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             /organism="Homo sapiens (human)".
           FT Location/Qualifiers
             1..10
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GGTGCGGCT 9
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Db   2  GGACGGGCT 10

RESULT 82
LOCUS      BD166788
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166788
VERSION     BD166788.1 GI:27872600
KEYWORDS   JP 2002209591-A/333.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Kaneko,S. and Yamaashita,T.
TITLE       Human liver disease-expressing genes
JOURNAL     Patent: JP 2002209591-A 333 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
           PN JP 2002209591-A/333
           PD 30-JUL-2002
           PF 19-JAN-2001 JP 2001012328
           PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO
             YAMASHITA
           PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
             C12P21/08,
           CC C12N15/00,
           CC Human liver disease-expressing genes
           FH Key Location/Qualifiers
           FT source
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             /organism="Homo sapiens (human)".
           FT Location/Qualifiers
             1..10
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GGTGCGGCT 9
    |||||
Db   2  GGACGGGCT 10

RESULT 83
LOCUS      BD166960
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166960
VERSION     BD166960.1 GI:27872600
KEYWORDS   JP 2002209591-A/333.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Kaneko,S. and Yamaashita,T.
TITLE       Human liver disease-expressing genes
JOURNAL     Patent: JP 2002209591-A 333 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP

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LOCUS BD166960 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166960
VERSION BD166960.1 GI:27872772
KEYWORDS JP 2002209591-A/505.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 505 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/505
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10 /organism='Homo sapiens (human)'.
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred.No.57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTGCGGCT 9
DB 2 GGACGCGCT 10
RESULT 84
LOCUS BD166975 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166975
VERSION BD166975.1 GI:27872787
KEYWORDS JP 2002209591-A/520.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 520 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/520
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
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PC C12N15/00
CC Human liver disease-expressing genes
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Best Local Similarity 88.9%; Pred.No.57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTGCGGCT 9
DB 2 GGACGCGCT 10
RESULT 85
LOCUS BD167006 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167006
VERSION BD167006.1 GI:27872818
KEYWORDS JP 2002209591-A/551.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 551 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/551
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
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CC Human liver disease-expressing genes
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTGCGGCT 9
DB 2 GGACGCGCT 10
RESULT 86
LOCUS BD167029 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167029
VERSION BD167029.1 GI:27872841
KEYWORDS JP 2002209591-A/574.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 574 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/574
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12P21/08,
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CC Human liver disease-expressing genes
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Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTG 10

Db 2 GACGCGCTG 10

RESULT 87

BD167056 10 bp DNA linear PAT 17-JAN-2003
LOCUS Human liver disease-expressing genes.
DEFINITION BD167056
ACCESSION BD167056.1 GI:27872868
VERSION JP 2002209591-A/601.
KEYWORDS unclassified.
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 10)
Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
Human liver disease-expressing genes
Patent: JP 2002209591-A 601 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/601
PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
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PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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Location/Qualifiers
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Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGGCT 9

Db 2 GGACGCGCT 10

RESULT 88

BD167151 10 bp DNA linear PAT 17-JAN-2003
LOCUS Human liver disease-expressing genes.
DEFINITION BD167151
ACCESSION BD167151.1 GI:27872963
VERSION

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;

KEYWORDS JP 2002209591-A/696.

SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 696 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/696
PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI

YAMASHITA

PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
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CC Human liver disease-expressing genes
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Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

Db 2 TGGTGAAGG 10

LOCUS Human liver disease-expressing genes.
DEFINITION BD167184
ACCESSION BD167184.1 GI:27872996
VERSION JP 2002209591-A/729.
KEYWORDS unclassified.
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 729 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/729
PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI

YAMASHITA

PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

Db 2 TGGTGAAGG 10

LOCUS Human liver disease-expressing genes.
DEFINITION BD167184
ACCESSION BD167184.1 GI:27872996
VERSION JP 2002209591-A/729.
KEYWORDS unclassified.
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 729 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/729
PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI

YAMASHITA

PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12P21/08,
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CC Human liver disease-expressing genes
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Best Local Similarity 88.9%; Pred. No. 57;


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PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
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Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
Db 10 GCTGTGGCG 2

RESULT 93
BD240490
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240490
VERSION BD240490.1 GI:33050260
KEYWORDS JP 2002534056-A/1908.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1908 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1908
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
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19-JUN-1998 US 60/090000, 19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999, 19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042, 19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090044, 19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090080, 19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078, 19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
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PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
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Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
Db 10 GCTGTGGCG 2

RESULT 94
BD240685
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240685
VERSION BD240685.1 GI:33050455
KEYWORDS JP 2002534056-A/2103.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 2103 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/2103
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
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C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
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Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
Db 2 GCGCTGTGG 10
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RESULT 95
LOCUS      CQ889057
DEFINITION Sequence 3 from Patent WO2004062555.
ACCESSION  CQ889057
VERSION     CQ889057.1  GI:54304970
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Rappold-Hoerbrand,G. and Haecker,B.
TITLE       Use of natriuretic peptides for the treatment of stature disorders
            related to the shox gene
JOURNAL     Patent: WO 2004062555-A 3 29-JUL-2004;
            Rappold-Hoerbrand, Gudrun (DE)
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Best Local Similarity 88.9%;  Pred. No. 57;
Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      11  TGGCGAAGG 19
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Db       1  TGGGGAAGG 9

RESULT 96
LOCUS      E39471
DEFINITION Genes with human dendritic cell expression.
ACCESSION  E39471
VERSION     E39471.1  GI:18621562
KEYWORDS    JP 2000279181-A/4.
SOURCE      Homo sapiens (human)
ORGANISM    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE       Genes with human dendritic cell expression
JOURNAL     Patent: JP 2000279181-A 4 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/4
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
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Best Local Similarity 88.9%;  Pred. No. 57;
Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      11  TGGCGAAGG 19
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Db       1  TGGGGAAGG 9

RESULT 97
LOCUS      E39633
DEFINITION Genes with human dendritic cell expression.
ACCESSION  E39633
VERSION     E39633.1  GI:18621724
KEYWORDS    JP 2000279181-A/166.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE       Genes with human dendritic cell expression
JOURNAL     Patent: JP 2000279181-A 166 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/166
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
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Best Local Similarity 88.9%;  Pred. No. 57;
Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      11  TGGCGAAGG 19
        ||| |||||
Db       1  TGGGGAAGG 2

RESULT 98
LOCUS      E39676
DEFINITION Genes with human dendritic cell expression.
ACCESSION  E39676
VERSION     E39676.1  GI:18621767
KEYWORDS    JP 2000279181-A/209.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE       Genes with human dendritic cell expression
JOURNAL     Patent: JP 2000279181-A 209 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/209
            PD 10-OCT-2000
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Query Match      38.9%;  Score 7.4;  DB 1;  Length 10;
Best Local Similarity 88.9%;  Pred. No. 57;
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Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  7  GGTGTGGCG 15
Db   1  GGTGTGGCG 9

RESULT 99
E54650
LOCUS      E54650          10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION  E54650
VERSION    E54650.1 GI:22556133
KEYWORDS  JP 2001211883-A/2.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE     Human normal liver cell expression genes
JOURNAL   Patent: JP 2001211883-A 2 07-AUG-2001;
COMMENT   SCIENCE & TECH AGENCY
           OS Homo sapiens (human)
           PN JP 2001211883-A/2
           PD 07-AUG-2001
           PF 31-JAN-2000 JP 2000023170
           PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
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Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  11  TGGCGAAGG 19
Db   2  TGGTGAAGG 10

RESULT 101
I79734/c
LOCUS      I79734          10 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 30 from patent US 5707863.
ACCESSION  I79734
VERSION    I79734.1 GI:3208024
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE     Tumor suppressor gene merlin
JOURNAL   Patent: US 5707863-A 30 13-JAN-1998;
COMMENT   SCIENCE & TECH AGENCY
           OS Homo sapiens (human)
           PN JP 2001211883-A/2
           PD 07-AUG-2001
           PF 31-JAN-2000 JP 2000023170
           PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
           YAMASHITA
           PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
           CC

FEATURES
  source    Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  8  CTGTGGCGA 16
Db   10  CTGTGGGGA 2

RESULT 102
I79740/c
LOCUS      I79740          10 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 36 from patent US 5707863.
ACCESSION  I79740
VERSION    I79740.1 GI:3208030
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE     Tumor suppressor gene merlin
JOURNAL   Patent: US 5707863-A 36 13-JAN-1998;
COMMENT   SCIENCE & TECH AGENCY
           OS Homo sapiens (human)
           PN JP 2001211883-A/195
           PD 07-AUG-2001
           PF 31-JAN-2000 JP 2000023170
           PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
           YAMASHITA
           PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
           CC

FEATURES
  source    Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GGTGGCGCT 9
Db   2  GGACGCGCT 10

RESULT 100
E54843
LOCUS      E54843          10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION  E54843
VERSION    E54843.1 GI:22556326
KEYWORDS  JP 2001211883-A/195.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE     Human normal liver cell expression genes
JOURNAL   Patent: JP 2001211883-A 195 07-AUG-2001;

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Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGCA 16
|||||||
Db 10 CTGTGGCGCA 2

RESULT 103
AR261814/c
LOCUS
DEFINITION Sequence 240 from patent US 6322995.
ACCESSION AR261814
VERSION AR261814.1 GI:28072954
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Hohmann,H.-P., Humbelin,M., van Loon,A. and Schurter,W.
TITLE Riboflavin production
JOURNAL Patent: US 6322995-A 240 27-NOV-2001;
P. Hoffmann-La Roche AG; Basel;
EPX;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCGCTGTG 12
|||||||
Db 9 CGCGCTGGG 1

RESULT 104
AR477257/c
LOCUS
DEFINITION Sequence 9 from patent US 6696274.
ACCESSION AR477257
VERSION AR477257.1 GI:47234570
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Tchistiakova,L., Li,S., Pietrzynski,G. and Alakhov,V.
TITLE Ligand for enhancing oral and CNS delivery of biological agents
JOURNAL Patent: US 6696274-A 9 24-FEB-2004;
Supratek Pharma, Inc.;
WOX;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9
|||||||
Db 10 GGTCGCGCT 2

RESULT 105
AR533687/c
LOCUS
DEFINITION Sequence 12 from patent US 6733755.
ACCESSION AR533687

VERSION AR533687.1 GI:53923681
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Tchistiakova,L., Li,S., Pietrzynski,G. and Alakhov,V.
TITLE Ligand for vascular endothelial growth factor receptor
JOURNAL Patent: US 6733755-A 12 11-MAY-2004;
Supratek Pharma, Inc.;
WOX;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9
|||||||
Db 10 GGTCGCGCT 2

RESULT 106
AR630145
LOCUS
DEFINITION Sequence 199 from patent US 6838556.
ACCESSION AR630145
VERSION AR630145.1 GI:59762469
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.P.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 199 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTG 10
|||||||
Db 1 GCGCGCTG 9

RESULT 107
AR642556/c
LOCUS
DEFINITION Sequence 29 from patent US 6864052.
ACCESSION AR642556
VERSION AR642556.1 GI:62779710
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
TITLE Enhanced sequencing by hybridization using pools of probes
JOURNAL Patent: US 6864052-A 29 08-MAR-2005;
Callida Genomics, Inc.; Sunnyvale, CA
FEATURES
source
Location/Qualifiers
1..10


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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 38.9%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGCA 16
Db 10 CTGTGGCAA 2

RESULT 108
AR642557/c
LOCUS
DEFINITION
Sequence 30 from patent US 6864052.
Accession
Version
Keywords
Source
Organism
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Dmanac,R., Dmanac,S., Kita,D., Cooke,C. and Xu,C.
TITLE
Enhanced sequencing by hybridization using pools of probes
JOURNAL
Patent: US 6864052-A 30 08-MAR-2005;
Callida Genomics, Inc.; Sunnyvale, CA
FEATURES
source
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 38.9%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGCA 16
Db 9 CTGTGGCAA 1

RESULT 109
AR649447/c
LOCUS
DEFINITION
Sequence 92 from patent US 6875606.
Accession
Version
Keywords
Source
Organism
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Leonard,S. and Freedman,R.
TITLE
Human .alpha.-7 nicotinic receptor promoter
JOURNAL
Patent: US 6875606-A 92 05-APR-2005;
The United States of America as represented by the Department of
Veterans Affairs; Washington, DC
FEATURES
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 38.9%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGCA 16
Db 10 CTGTGGGAGA 2

RESULT 110
AX113023
LOCUS
DEFINITION
Sequence 70 from Patent WO0127267.
Accession
Version
Keywords
Source
Organism
Mus sp.
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS
Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
TITLE
Genes differentially expressed in tr1 cells and their use in the
manufacture of immunoregulatory compositions
JOURNAL
Patent: WO 0127267-A 70 19-APR-2001;
ISIS INNOVATION LIMITED (GB)
FEATURES
source
1..10
Location/Qualifiers
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"

Query Match
Best Local Similarity 38.9%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
Db 2 TGGTGAAGG 10

RESULT 111
AX152364
LOCUS
DEFINITION
Sequence 279 from Patent WO0138577.
Accession
Version
Keywords
Source
Organism
Homo sapiens (human)
Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1
AUTHORS
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE
Human transcriptomes
JOURNAL
Patent: WO 0138577-A 279 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.9%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGCCTGTGG 13
Db 2 GGCCTGTGG 10

RESULT 112
AX152365
LOCUS
DEFINITION
Sequence 280 from Patent WO0138577.
Accession
Version
Keywords
Source
Organism
Homo sapiens (human)
Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 280 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
| | | | |
Db 2 GGGCTGTGG 10

RESULT 113
AX152532/c
LOCUS AX152532 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 447 from Patent WO0138577.
ACCESSION AX152532
VERSION AX152532.1 GI:14534183
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 447 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
| | | | |
Db 9 CGCTGGGC 1

RESULT 114
AX152671/c
LOCUS AX152671 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 586 from Patent WO0138577.
ACCESSION AX152671
VERSION AX152671.1 GI:14534322
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 586 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
| | | | |
Db 9 CGCTGGGC 1

RESULT 115
AX152819/c
LOCUS AX152819 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 734 from Patent WO0138577.
ACCESSION AX152819
VERSION AX152819.1 GI:14534470
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 734 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
| | | | |
Db 10 CGCAGTGGC 2

RESULT 116
AX153110
LOCUS AX153110 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1025 from Patent WO0138577.
ACCESSION AX153110
VERSION AX153110.1 GI:14534761
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1025 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
| | | | |
Db 10 TGGAGAAGG 2

RESULT 117
AX153110
LOCUS AX153110 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1025 from Patent WO0138577.
ACCESSION AX153110
VERSION AX153110.1 GI:14534761
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1025 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
| | | | |
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Db      1 GCTGTCGG 9
||||| |||
RESULT 117
AX153149
LOCUS      AX153149          10 bp  DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 1064 from Patent WO0138577.
ACCESSION  AX153149
VERSION     AX153149.1  GI:14534800
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 1064 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
            source
              1..10
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  11 TGGCGAAGG 19
    ||| ||||
Db   2 TGGTGAAGG 10

RESULT 118
AX207895/c
LOCUS      AX207895          10 bp  DNA      linear      PAT 31-AUG-2001
DEFINITION Sequence 12 from Patent WO0157067.
ACCESSION  AX207895
VERSION     AX207895.1  GI:15422493
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Tchistiakova,L., Li,S., Pietrzynski,G. and Alakhov,V.
TITLE      Ligand for vascular endothelial growth factor receptor
JOURNAL    Patent: WO 0157067-A 12 09-AUG-2001;
            SUPRATEK PHARMA INC. (CA)
FEATURES   Location/Qualifiers
            source
              1..10
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="chemical synthesis"
Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GGTGCGCGCT 9
    ||| ||||
Db   10 GGTGCGCT 2

RESULT 119
AX301491/c
LOCUS      AX301491          10 bp  DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 205 from Patent WO0185941.
ACCESSION  AX301491
VERSION     AX301491.1  GI:17382574

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KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Versteeg,R. and Caron,H.N.
TITLE      Myc targets
JOURNAL    Patent: WO 0185941-A 205 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES   Location/Qualifiers
            source
              1..10
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GGTGCGCGCT 9
    ||| ||||
Db   10 GGTGCGCT 2

RESULT 120
AX328381/c
LOCUS      AX328381          10 bp  DNA      linear      PAT 07-JAN-2002
DEFINITION Sequence 9 from Patent WO0190139.
ACCESSION  AX328381
VERSION     AX328381.1  GI:18098355
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Tchistiakova,L., Li,S., Pietrzynski,G. and Alakhov,V.
TITLE      A ligand for enhancing oral and cns delivery of biological agents
JOURNAL    Patent: WO 0190139-A 9 29-NOV-2001;
            SUPRATEK PHARMA, INC. (CA)
FEATURES   Location/Qualifiers
            source
              1..10
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="nucleotide"
Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GGTGCGCGCT 9
    ||| ||||
Db   10 GGTGCGCT 2

RESULT 121
AX354798/c
LOCUS      AX354798          10 bp  DNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 1 from Patent WO0186293.
ACCESSION  AX354798
VERSION     AX354798.1  GI:18619529
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Popkov,M., Mandeville,R., Romar,O. and Alakhov,V.
TITLE      Designing and screening random libraries of compounds
JOURNAL    Patent: WO 0186293-A 1 15-NOV-2001;
            SUPRATEK PHARMA, INC. (CA) ; Biophage, Inc. (CA)
FEATURES   Location/Qualifiers

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source
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="nucleotides isolated by chemical synthesis and
biosynthesis using E. coli"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGGCGCT 9
||| |||||
Db 10 GGTGGCGCT 2

RESULT 122
AX958217/c
LOCUS AX958217 10 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 20 from Patent WO03046156.
ACCESSION AX958217
VERSION AX958217.1 GI:40785870
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE
1 Claude,P.P.
AUTHORS Novel bacterial biomasses, method for obtaining same and uses
TITLE thereof for bacterization of soils and crop residues
JOURNAL Patent: WO 03046156-A 20 05-JUN-2003;
Valbios (FR)

FEATURES
source
1. .10
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Azobacter"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCGCTGTG 12
||| |||||
Db 10 CGCGCTGGG 2

RESULT 123
BD007752
LOCUS BD007752 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007752
VERSION BD007752.1 GI:18636125
KEYWORDS JP 2001069993-A/28.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 28 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/28
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
A61P29/00,

source
1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
||| |||||
Db 10 GCTTTGGCG 2

RESULT 125
BD007925
LOCUS BD007925 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007925
VERSION BD007925.1 GI:18636298
KEYWORDS JP 2001069993-A/201.
SOURCE Homo sapiens (human)

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PC A61P31/00, C12P21/08, C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .10
/organism='Homo sapiens (human)'.
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source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
||| |||||
Db 2 TGGTGAAGG 10

RESULT 124
BD007843/c
LOCUS BD007843 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007843
VERSION BD007843.1 GI:18636216
KEYWORDS JP 2001069993-A/119.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 119 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/119
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00, C12P21/08, C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .10
/organism='Homo sapiens (human)'.
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source
1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
||| |||||
Db 10 GCTTTGGCG 2

RESULT 125
BD007925
LOCUS BD007925 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007925
VERSION BD007925.1 GI:18636298
KEYWORDS JP 2001069993-A/201.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Matsushina,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 201 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/201
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00.
PC A61P31/00.C12P21/08.C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FEATURES
source
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 38.8%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
|||||
Db 1 GCTGTGGCG 9

RESULT 126
AR002177/c
LOCUS AR002177 10 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 31 from patent US 5741490.
ACCESSION AR002177
VERSION AR002177.1 GI:3963731
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
Krawczynski,K.Z. and Yarbough,P.D.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 5741490-A 31 21-APR-1998;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
|||||
Db 7 TGGCGAA 1

RESULT 127
AR071782/c
LOCUS AR071782 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 11 from patent US 5912147.
ACCESSION AR071782
VERSION AR071782.1 GI:7222670
KEYWORDS

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SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 11 15-JUN-1999;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTCGCGC 8
|||||
Db 10 GTCGCGC 4

RESULT 128
AR092694
LOCUS AR092694 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 6 from patent US 5998193.
ACCESSION AR092694
VERSION AR092694.1 GI:10019446
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL Patent: US 5998193-A 6 07-DEC-1999;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
|||||
Db 4 CTGTGGC 10

RESULT 129
AR106678
LOCUS AR106678 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 6 from patent US 6107078.
ACCESSION AR106678
VERSION AR106678.1 GI:12821208
KEYWORDS
SOURCE Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL Patent: US 6107078-A 6 22-AUG-2000;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 CTTGTGC 14
Db      |||||
        4 CTTGTGC 10

RESULT 130
LOCUS   AR107802
DEFINITION Sequence 48 from patent US 6110667.
ACCESSION AR107802
VERSION   AR107802.1 GI:12823289
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
JOURNAL sequences based on K-tuple analysis
FEATURES Patent: US 6110667-A 48 29-AUG-2000;
          Location/Qualifiers
          1..10
          /organism="unknown"
          /mol_type="unassigned DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
Db      |||||
        4 GCTGTGG 10

RESULT 131
LOCUS   AR174035/c
DEFINITION Sequence 25 from patent US 6306624.
ACCESSION AR174035
VERSION   AR174035.1 GI:17914355
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 25 23-OCT-2001;
FEATURES Location/Qualifiers
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          /organism="unknown"
          /mol_type="unassigned DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCGAA 17
Db      |||||
        9 TGGCGAA 3

RESULT 132
LOCUS   BD065207
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065207
VERSION   BD065207.1 GI:22610810
KEYWORDS JP 2001509017-A/143.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

QY      8 CTTGTGC 14
Db      |||||
        4 CTTGTGC 10

RESULT 130
LOCUS   AR107802
DEFINITION Sequence 48 from patent US 6110667.
ACCESSION AR107802
VERSION   AR107802.1 GI:12823289
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
JOURNAL sequences based on K-tuple analysis
FEATURES Patent: US 6110667-A 48 29-AUG-2000;
          Location/Qualifiers
          1..10
          /organism="unknown"
          /mol_type="unassigned DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
Db      |||||
        4 GCTGTGG 10

RESULT 131
LOCUS   AR174035/c
DEFINITION Sequence 25 from patent US 6306624.
ACCESSION AR174035
VERSION   AR174035.1 GI:17914355
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 25 23-OCT-2001;
FEATURES Location/Qualifiers
          1..10
          /organism="unknown"
          /mol_type="unassigned DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCGAA 17
Db      |||||
        9 TGGCGAA 3

RESULT 132
LOCUS   BD065207
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065207
VERSION   BD065207.1 GI:22610810
KEYWORDS JP 2001509017-A/143.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

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Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 10)
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
Characterization of the yeast transcriptome
Patent: JP 2001509017-A 143 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/143
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES
source
1..10
/organism='Saccharomyces cerevisiae'
/mol_type='genomic DNA'
/db_xref='taxon:4932'

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CGCTGTG 12
Db      |||||
        4 CGCTGTG 10

RESULT 133
LOCUS   BD161475/c
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161475
VERSION   BD161475.1 GI:27867233
KEYWORDS JP 2002186482-A/297.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 297 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
          PN JP 2002186482-A/297
          PD 02-JUL-2002
          PF 19-DEC-2000 JP 2000385816
          PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
          C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
          activated Th1 and Th2 cell expression genes FH Key
          Location/Qualifiers
          FT source 1..10
          FT /organism='Homo sapiens (human)'.
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source
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
Db      |||||
        7 GCTGTGG 1

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RESULT 134
BD166636/c
LOCUS
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166636
VERSION BD166636.1 GI:27872448
KEYWORDS JP 2002209591-A/181.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 181 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/181
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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source
1..10
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GCGCTGT 11
Db 7 GCGCTGT 1
RESULT 135
BD167128/c
LOCUS
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167128
VERSION BD167128.1 GI:27872940
KEYWORDS JP 2002209591-A/673.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 673 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/673
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GCGCTGT 11
Db 7 GCGCTGT 1
RESULT 136
BD225345/c
LOCUS
DEFINITION Compositions and methods for the identification of lung tumor cells.
ACCESSION BD225345
VERSION BD225345.1 GI:33035115
KEYWORDS JP 2002509707-A/27.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE Compositions and methods for the identification of lung tumor cells
JOURNAL Patent: JP 2002509707-A 27 02-APR-2002;
GENZYME CORP
COMMENT OS Artificial Sequence
PN JP 2002509707-A/27
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541180
PR 31-MAR-1998 US 60/080037
PI GARY A BEAUDRY, STEPHEN L MADDEN, ARTHUR H BRTELSEN PC
C12N15/09,A01K67/027,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
G01N33/566//
PC A61K45/00,A61P9/00,A61P35/00,C12N15/00,C12N5/00 CC
Compositions and methods for the identification of lung tumor cells
FH Key Location/Qualifiers
FT source 1..10
/organism='Artificial Sequence'.
FEATURES
source
1..10
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CTGTGGC 14
Db 9 CTGTGGC 3
RESULT 137
BD238881
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238881
VERSION BD238881.1 GI:33048651
KEYWORDS JP 2002534056-A/299.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominiidae; Homo.
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/299
PD 2002-07-01
PF 2002-07-01
PI
PC
CC
FH
FT

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REFERENCE
AUTHORS      1 (bases 1 to 10)
TITLE        Roberts,B.L. and Shankara,S.
JOURNAL      Preparation and use of superior vaccines
              Patent: JP 2002534056-A 299 15-OCT-2002;
COMMENT      GENZYME CORP
OS           Homo sapiens (human)
PN           JP 2002534056-A/299
PD           15-OCT-2002
PF           18-JUN-1999 JP 2000554749
PR           19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI          BRUCE L ROBERTS, SRINIVAS SHANKARA
PC          C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
              G01N37/00,
              G01N33/53,G01N33/53,G01N33/53,G01N33/566, PC
PC          C12N15/00,C12N5/00,C12N15/00
CC          Preparation and use of superior vaccines
CH          Preparation and use of superior vaccines
FH          Key Location/Qualifiers
FT          source 1..10
              /organism='Homo sapiens (human)'.
              Location/Qualifiers
              1..10
              /organism='Homo sapiens'
              /mol_type='genomic DNA'
              /db_xref='taxon:9606'

FEATURES
source
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 CGCTGTG 12
            |||||
Db           1 CGCTGTG 7

RESULT 138
LOCUS       BD239109/c
DEFINITION Preparation and use of superior vaccines.
ACCESSION   BD239109
VERSION     BD239109.1 GI:33048879
KEYWORDS    JP 2002534056-A/527.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Roberts,B.L. and Shankara,S.
TITLE       Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 527 15-OCT-2002;
COMMENT     GENZYME CORP
OS          Homo sapiens (human)
PN          JP 2002534056-A/527
PD          15-OCT-2002
PF          18-JUN-1999 JP 2000554749
PR          19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
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AUTHORS      1 (bases 1 to 10)
TITLE        Roberts,B.L. and Shankara,S.
JOURNAL      Preparation and use of superior vaccines
              Patent: JP 2002534056-A 299 15-OCT-2002;
COMMENT      GENZYME CORP
OS           Homo sapiens (human)
PN           JP 2002534056-A/299
PD           15-OCT-2002
PF           18-JUN-1999 JP 2000554749
PR           19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
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08-DEC-1998 US 60/111715
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PC          C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
              G01N37/00,
              G01N33/53,G01N33/53,G01N33/53,G01N33/566, PC
PC          C12N15/00,C12N5/00,C12N15/00
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CH          Preparation and use of superior vaccines
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Query Match 36.8%; Score 7; DB 1; Length 10;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 CTGTGGC 14
            |||||
Db           9 CTGTGGC 3

RESULT 139
LOCUS       BD240437/c
DEFINITION Preparation and use of superior vaccines.
ACCESSION   BD240437
VERSION     BD240437.1 GI:33050207
KEYWORDS    JP 2002534056-A/1855.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Roberts,B.L. and Shankara,S.
TITLE       Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 1855 15-OCT-2002;
COMMENT     GENZYME CORP
OS          Homo sapiens (human)
PN          JP 2002534056-A/1855
PD          15-OCT-2002
PF          18-JUN-1999 JP 2000554749
PR          19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
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Db 9 GCTGTGG 3

RESULT 140
BD240601
LOCUS BD240601 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240601
VERSION BD240601.1 GI:33050371
KEYWORDS JP 2002534056-A/2019.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 2019 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/2019
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
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19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
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19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
|||||
Db 9 GCTGTGG 3

RESULT 141
BD249594
LOCUS BD249594 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Pi-ta gene imparting disease resistance to plants.
ACCESSION BD249594
VERSION BD249594.1 GI:33059364
KEYWORDS JP 2002525033-A/9.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 10)
AUTHORS Valent,B.S. and Bryan,G.T.
TITLE Pi-ta gene imparting disease resistance to plants
JOURNAL Patent: JP 2002525033-A 9 13-AUG-2002;
EI DU PONT DE NEMOURS AND CO
COMMENT OS Artificial Sequence
PN JP 2002525033-A/9
PD 13-AUG-2002
PF 03-AUG-1999 JP 2000563786
PR 04-AUG-1998 US 60/095229,21-JUN-1999 US 09/336946 PI
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC
Description of Artificial Sequence:Synthetic oligonucleotide FH
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FT source 1..10
/organism='Artificial Sequence'.

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGT 11
|||||
Db 7 GCGCTGT 1

RESULT 142
BD251793
LOCUS BD251793 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Endo-selection in orthogenesis.
ACCESSION BD251793
VERSION BD251793.1 GI:33061563
KEYWORDS JP 2002537836-A/3.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 10)
AUTHORS Short,J.M. and Frey,G.J.
TITLE Endo-selection in orthogenesis
JOURNAL Patent: JP 2002537836-A 3 12-NOV-2002;
DIVERSA CORP
COMMENT OS Artificial Sequence
PN JP 2002537836-A/3
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603365

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PR 09-MAR-1999 US 09/267118,26-MAR-1999 US 09/276860 PR
14-JUN-1999 US 09/332835
PI JAY M. SHORT,GERHARD JOHANN FREY
PC C12N15/09,C12N9/96,C12N15/00
CC BspG I restriction site
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10
Db |||||
1 CGCGCTG 7

RESULT 143
E54722/c
LOCUS E54722 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION E54722
VERSION E54722.1 GI:22556205
KEYWORDS JP 2001211883-A/74.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima K., Hashimoto, S., Kaneko, S. and Yamaehita, T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 74 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/74
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
YAMASHITA
PC C12N15/09, C07K16/18, C12P21/02, C12N15/00
CC C12N15/09, C07K16/18, C12P21/02, C12N15/00
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCG 15
Db |||||
7 TGTGGCG 1

RESULT 144
E64716/c
LOCUS E64716 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for distinguishing rice variety.
ACCESSION E64716
VERSION E64716.1 GI:18623011
KEYWORDS JP 2000287691-A/2.
SOURCE unidentified
ORGANISM unidentified

PR 09-MAR-1999 US 09/267118,26-MAR-1999 US 09/276860 PR
14-JUN-1999 US 09/332835
PI JAY M. SHORT,GERHARD JOHANN FREY
PC C12N15/09,C12N9/96,C12N15/00
CC BspG I restriction site
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10
Db |||||
1 CGCGCTG 7

RESULT 143
E54722/c
LOCUS E54722 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION E54722
VERSION E54722.1 GI:22556205
KEYWORDS JP 2001211883-A/74.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima K., Hashimoto, S., Kaneko, S. and Yamaehita, T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 74 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/74
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
YAMASHITA
PC C12N15/09, C07K16/18, C12P21/02, C12N15/00
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QY 9 TGTGGCG 15
Db |||||
7 TGTGGCG 1

RESULT 144
E64716/c
LOCUS E64716 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for distinguishing rice variety.
ACCESSION E64716
VERSION E64716.1 GI:18623011
KEYWORDS JP 2000287691-A/2.
SOURCE unidentified
ORGANISM unidentified

unclassified.
1 (bases 1 to 10)
Otsubo,K., Nakamura,S., Teshima,H., Okatome,H. and Kawasaki,S.
Method for distinguishing rice variety
Patent: JP 2000287691-A 2 17-OCT-2000;
NATL FOOD RES INST,KENICHI OTSUBO,HIDECHIKA TESHIMA,HIROSHI OKATOME
OS Oryza sativa L. (rice)
PN JP 2000287691-A/2
PD 17-OCT-2000
PF 09-APR-1999 JP 1999102709
PR KENICHI OTSUBO,SUMIKO NAKAMURA,HIDECHIKA TESHIMA, PI HIROSHI
OKATOME.
PI SHINJI KAWASAKI
PC C12N15/09,C12Q1/68,G01N33/10,C12N15/00
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Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
Db |||||
7 GCTGTGG 1

RESULT 145
AR202187/c
LOCUS AR202187 10 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6 from patent US 6361974.
ACCESSION AR202187
VERSION AR202187.1 GI:20256726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Short,J.M., Djavakhishvili,T.David. and Frey,G.Johann.
TITLE Exonuclease-mediated nucleic acid reassembly in directed evolution
JOURNAL Patent: US 6361974-A 6 26-MAR-2002;
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10
Db |||||
1 CGCGCTG 7

RESULT 146
AR254267/c
LOCUS AR254267 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 13 from patent US 6479731.
ACCESSION AR254267
VERSION AR254267.1 GI:27303040
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)

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AUTHORS Valent, B.S. and Bryan, G.T.
 TITLE Pi-ta gene conferring fungal disease resistance to plants
 JOURNAL Patent: US 6479731-A 13 12-NOV-2002;
 E. I. du Pont de Nemours and Company; Wilmington, DE

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Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGT 11
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 Db 7 GCGCTGT 1

RESULT 147
 AR303347/c
 LOCUS AR303347 10 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 72 from patent US 6544736.
 ACCESSION AR303347
 VERSION AR303347.1 GI:31692123
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Shimamoto, A., Furuichi, Y., Shibata, Y., Funaki, H., Ohara, E. and Watahiki, M.
 TITLE Method for synthesizing cDNA from mRNA sample
 JOURNAL Patent: US 6544736-A 72 08-APR-2003;
 Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo; JPX;

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 /mol_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
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 Db 10 GCTGTGG 4

RESULT 148
 AR303679
 LOCUS AR303679 10 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 404 from patent US 6544736.
 ACCESSION AR303679
 VERSION AR303679.1 GI:31692455
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Shimamoto, A., Furuichi, Y., Shibata, Y., Funaki, H., Ohara, E. and Watahiki, M.
 TITLE Method for synthesizing cDNA from mRNA sample
 JOURNAL Patent: US 6544736-A 404 08-APR-2003;
 Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo; JPX;

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 /mol_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12
 | | | | |
 Db 4 CGCTGTG 10

RESULT 149
 AR306871/c
 LOCUS AR306871 10 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 23 from patent US 6551476.
 ACCESSION AR306871
 VERSION AR306871.1 GI:31697271
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Scherba, E.S.
 TITLE Noble-metal coated inert anode for aluminum production
 JOURNAL Patent: US 6551476-A 23 22-APR-2003;
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 source /organism="unknown"
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
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 Db 7 GCTGTGG 1

RESULT 150
 AR351634
 LOCUS AR351634 10 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 92 from patent US 6588746.
 ACCESSION AR351634
 VERSION AR351634.1 GI:33753430
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Dobrindt, D. and Fischer, U.
 TITLE Device for generating an offset of transported flexible sheet material
 JOURNAL Patent: US 6588746-A 92 08-JUL-2003;
 NexPress Solutions LLC; Rochester, NY; DEX;

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QY 12 GCGGAAG 18
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 Db 4 GCGGAAG 10

RESULT 151
 AR351635
 LOCUS AR351635 10 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 93 from patent US 6588746.
 ACCESSION AR351635

Db 3 GGTCCG 9

RESULT 156

AR410161

LOCUS AR410161 10 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 6 from patent US 6635449.

ACCESSION AR410161

VERSION AR410161.1 GI:40161386

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Short, J.M.

TITLE Exonuclease-mediated nucleic acid reassembly in directed evolution

JOURNAL Patent: US 6635449-A 6 21-OCT-2003;

Diversa Corporation; San Diego, CA

FEATURES

source

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Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10

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Db 1 CGCGCTG 7

RESULT 157

AR477264

LOCUS AR477264 10 bp DNA linear PAT 14-MAY-2004

DEFINITION Sequence 5 from patent US 6696275.

ACCESSION AR477264

VERSION AR477264.1 GI:47234597

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Short, J.M. and Frey, G.J.

TITLE End selection in directed evolution

JOURNAL Patent: US 6696275-A 5 24-FEB-2004;

Diversa Corporation; San Diego, CA

FEATURES

source

1. .10

/organism="unknown"

/mol_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10

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Db 1 CGCGCTG 7

RESULT 158

AR489166

LOCUS AR489166 10 bp DNA linear PAT 15-MAY-2004

DEFINITION Sequence 6 from patent US 6709841.

ACCESSION AR489166

VERSION AR489166.1 GI:47256094

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Short, J.M. and Frey, G.J.

TITLE End selection in directed evolution

JOURNAL Patent: US 6696275-A 5 24-FEB-2004;

Diversa Corporation; San Diego, CA

FEATURES

source

1. .10

/organism="unknown"

/mol_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10

|||||

Db 1 CGCGCTG 7

Short, J.M.

Exonuclease-mediated gene assembly in directed evolution

Patent: US 6709841-A 6 23-MAR-2004;

Diversa Corporation; San Diego, CA

FEATURES

source

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/organism="unknown"

/mol_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10

|||||

Db 1 CGCGCTG 7

RESULT 159

AR490750

LOCUS AR490750 10 bp DNA linear PAT 15-MAY-2004

DEFINITION Sequence 10 from patent US 6713279.

ACCESSION AR490750

VERSION AR490750.1 GI:47258162

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Short, J.M.

TITLE Non-stochastic generation of genetic vaccines and enzymes

JOURNAL Patent: US 6713279-A 10 30-MAR-2004;

Diversa Corporation; San Diego, CA

FEATURES

source

1. .10

/organism="unknown"

/mol_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10

|||||

Db 1 CGCGCTG 7

RESULT 160

AR561751

LOCUS AR561751 10 bp DNA linear PAT 08-OCT-2004

DEFINITION Sequence 15 from patent US 6759195.

ACCESSION AR561751

VERSION AR561751.1 GI:53975402

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Bentley, W.E. and Gill, R.

TITLE Method of differential display of prokaryotic messenger RNA by RT-PCR

JOURNAL Patent: US 6759195-A 15 06-JUL-2004;

University of Maryland Biotechnology Institute; Baltimore, MD

FEATURES

source

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/organism="unknown"

/mol_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17

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Db          |||||
4 TGGCGAA 10

RESULT 161
LOCUS      AR568611          10 bp      DNA      linear      PAT 14-DEC-2004
DEFINITION Sequence 6 from patent US 6740506.
ACCESSION  AR568611
VERSION     AR568611.1  GI:56568059
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Short,J.M. and Frey,G.J.
TITLE     End selection in directed evolution
JOURNAL   Patent: US 6740506-A 6 25-MAY-2004;
          Diversa Corporation; San Diego, CA
FEATURES   Location/Qualifiers
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
        |||||
        1 CGCGCTG 7

RESULT 162
LOCUS      AR630146/c          10 bp      DNA      linear      PAT 14-FEB-2005
DEFINITION Sequence 200 from patent US 6838556.
ACCESSION  AR630146
VERSION     AR630146.1  GI:59762471
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
          Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
          Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE     Promoters for regulated gene expression
JOURNAL   Patent: US 6838556-A 200 04-JAN-2005;
          Genelabs Technologies, Inc.; Redwood City, CA
FEATURES   Location/Qualifiers
            source
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                /organism="unknown"
                /mol_type="genomic DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
        |||||
        1 CGCGCTG 7

RESULT 163
LOCUS      AR641621/c          10 bp      DNA      linear      PAT 20-APR-2005
DEFINITION Sequence 25 from patent US 6861238.
ACCESSION  AR641621
VERSION     AR641621.1  GI:62777326
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
TITLE     Enhanced sequencing by hybridization using pools of probes
JOURNAL   Patent: US 6864052-A 32 08-MAR-2005;
          Callida Genomics, Inc.; Sunnyvale, CA
FEATURES   Location/Qualifiers
            source
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
        |||||
        8 CGCGCTG 2

RESULT 164
LOCUS      AR642558/c          10 bp      DNA      linear      PAT 20-APR-2005
DEFINITION Sequence 31 from patent US 6864052.
ACCESSION  AR642558
VERSION     AR642558.1  GI:62779712
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
TITLE     Enhanced sequencing by hybridization using pools of probes
JOURNAL   Patent: US 6864052-A 31 08-MAR-2005;
          Callida Genomics, Inc.; Sunnyvale, CA
FEATURES   Location/Qualifiers
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                /mol_type="genomic DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGCG 14
        |||||
        8 CTGTGCG 2

RESULT 165
LOCUS      AR642559/c          10 bp      DNA      linear      PAT 20-APR-2005
DEFINITION Sequence 32 from patent US 6864052.
ACCESSION  AR642559
VERSION     AR642559.1  GI:62779713
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
TITLE     Enhanced sequencing by hybridization using pools of probes
JOURNAL   Patent: US 6864052-A 32 08-MAR-2005;
          Callida Genomics, Inc.; Sunnyvale, CA
FEATURES   Location/Qualifiers
            source
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                /mol_type="genomic DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGCG 14
        |||||
        8 CTGTGCG 2
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Qy      8 CTGTGGC 14
Db      |||||
        7 CTGTGGC 1

RESULT 166
AX152609
LOCUS      AX152609      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 524 from Patent WO0138577.
ACCESSION  AX152609
VERSION     AX152609.1 GI:14534260
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE       Human transcriptomes
JOURNAL     Patent: WO 0138577-A 524 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES    Location/Qualifiers
            source
              1..10
                /organism="Homo sapiens"
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CTGTGGC 14
Db      |||||
        4 CTGTGGC 10

RESULT 167
AX666643
LOCUS      AX666643      10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 92 from Patent WO0242459.
ACCESSION  AX666643
VERSION     AX666643.1 GI:29291111
KEYWORDS
SOURCE      synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL     Patent: WO 0242459-A 92 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES    Location/Qualifiers
            source
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
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                /note="example target DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 GGCGAAG 18
Db      |||||
        4 GGCGAAG 10

RESULT 170
AX668204
LOCUS      AX668204      10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 1653 from Patent WO0242459.
ACCESSION  AX668204
VERSION     AX668204.1 GI:29291483
KEYWORDS
SOURCE      synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.

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Qy      8 CTGTGGC 14
Db      |||||
        7 CTGTGGC 1

RESULT 166
AX152609
LOCUS      AX152609      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 524 from Patent WO0138577.
ACCESSION  AX152609
VERSION     AX152609.1 GI:14534260
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE       Human transcriptomes
JOURNAL     Patent: WO 0138577-A 524 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES    Location/Qualifiers
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                /organism="Homo sapiens"
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CTGTGGC 14
Db      |||||
        4 CTGTGGC 10

RESULT 167
AX666643
LOCUS      AX666643      10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 92 from Patent WO0242459.
ACCESSION  AX666643
VERSION     AX666643.1 GI:29291111
KEYWORDS
SOURCE      synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL     Patent: WO 0242459-A 92 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES    Location/Qualifiers
            source
              1..10
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="example target DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 GGCGAAG 18
Db      |||||
        4 GGCGAAG 10

RESULT 170
AX668204
LOCUS      AX668204      10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 1653 from Patent WO0242459.
ACCESSION  AX668204
VERSION     AX668204.1 GI:29291483
KEYWORDS
SOURCE      synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.

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TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers

JOURNAL Patent: WO 0242459-A 1653 30-MAY-2002;
Sangamo Biosciences Inc. (US)

FEATURES
source

1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7
|||||
Db 3 GGTCGCG 9

RESULT 171

AX668205
LOCUS AX668205 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1654 from Patent WO0242459.
ACCESSION AX668205
VERSION AX668205.1 GI:29291484

KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Liu,Q.

AUTHORS Position dependent recognition of gnn nucleotide triplets by zinc fingers

TITLE

JOURNAL Patent: WO 0242459-A 1654 30-MAY-2002;
Sangamo Biosciences Inc. (US)

FEATURES

1. .10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="example target DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7
|||||
Db 3 GGTCGCG 9

RESULT 172

AX668218
LOCUS AX668218 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1667 from Patent WO0242459.
ACCESSION AX668218

VERSION AX668218.1 GI:29291497

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Liu,Q.

AUTHORS Position dependent recognition of gnn nucleotide triplets by zinc fingers

TITLE

JOURNAL Patent: WO 0242459-A 1667 30-MAY-2002;
Sangamo Biosciences Inc. (US)

FEATURES

1. .10
Location/Qualifiers
/organism="synthetic construct"
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/note="example target DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7
|||||
Db 3 GGTCGCG 9

RESULT 173

AX753482/c
LOCUS AX753482 10 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 27 from Patent EP1310556.
ACCESSION AX753482

VERSION AX753482.1 GI:32166242

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.

AUTHORS Composition and methods for the identification of lung tumor cells

TITLE

JOURNAL Patent: EP 1310556-A 27 14-MAY-2003;

GENZYME CORPORATION (US)

FEATURES

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Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGCG 14
|||||
Db 9 CTGTGCG 3

Search completed: May 9, 2006, 15:46:51
Job time : 0.001 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 15:48:19 ; Search time 0.001 Seconds
(without alignments)
22.382 Million cell updates/sec

Title: US-09-904-968A-19-COPY
Perfect score: 19
Sequence: 1 ggtcgcgtgtggaagg 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 57 seqs, 589 residues

Total number of hits satisfying chosen parameters: 114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 57 summaries

Database : isdb19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10.4	54.7	14	1	US-09-874-601-115
2	10.4	54.7	14	1	Sequence 115, App
3	9.8	51.6	14	1	Patent No. 5427929
4	9	47.4	10	1	Sequence 33, Appl
5	9	47.4	10	1	Sequence 18, Appl
6	9	47.4	10	1	Sequence 18, Appl
7	9	47.4	10	1	Sequence 18, Appl
8	9	47.4	10	1	Sequence 18, Appl
9	9	47.4	10	1	Sequence 18, Appl
10	9	47.4	10	1	Sequence 18, Appl
11	9	47.4	10	1	Sequence 18, Appl
12	9	47.4	10	1	Sequence 11, Appl
13	8.4	44.2	11	1	Sequence 305, App
14	8.4	44.2	12	1	Sequence 2, Appl
15	8.4	44.2	12	1	Sequence 50, Appl
16	7.8	41.1	11	1	Sequence 8, Appl
17	7.8	41.1	11	1	Sequence 10, Appl
18	7.4	38.9	10	1	Sequence 30, Appl
19	7.4	38.9	10	1	Sequence 36, Appl
20	7.4	38.9	10	1	Sequence 259, App
21	7.4	38.9	10	1	Sequence 260, App
22	7.4	38.9	10	1	Sequence 259, App
23	7.4	38.9	10	1	Sequence 260, App
24	7.4	38.9	10	1	Sequence 30, Appl
25	7.4	38.9	10	1	Sequence 36, Appl
26	7.4	38.9	10	1	Sequence 36, Appl
27	7.4	38.9	10	1	Sequence 52, Appl
28	7.4	38.9	10	1	Sequence 241, App
29	7.4	38.9	10	1	Sequence 9, Appl
30	7.4	38.9	10	1	Sequence 12, Appl
31	7.4	38.9	10	1	Sequence 199, App
32	7.4	38.9	10	1	Sequence 29, Appl
33	7.4	38.9	10	1	Sequence 30, Appl
					Sequence 92, Appl

C 34	7	36.8	10	1	US-08-259-148A-31	Sequence 31, Appl
C 35	7	36.8	10	1	US-07-876-941A-47	Sequence 47, Appl
C 36	7	36.8	10	1	US-08-734-973-11	Sequence 11, Appl
C 37	7	36.8	10	1	US-08-265-484B-6	Sequence 6, Appl
C 38	7	36.8	10	1	US-08-724-466B-25	Sequence 25, Appl
C 39	7	36.8	10	1	US-08-765-257A-6	Sequence 6, Appl
C 40	7	36.8	10	1	US-08-522-384-48	Sequence 48, Appl
C 41	7	36.8	10	1	US-08-882-164D-25	Sequence 25, Appl
C 42	7	36.8	10	1	US-09-535-754-6	Sequence 6, Appl
C 43	7	36.8	10	1	US-09-336-946B-13	Sequence 13, Appl
C 44	7	36.8	10	1	US-09-508-753B-72	Sequence 72, Appl
C 45	7	36.8	10	1	US-09-508-753B-404	Sequence 404, App
C 46	7	36.8	10	1	US-10-042-111-23	Sequence 23, Appl
C 47	7	36.8	10	1	US-10-108-077-6	Sequence 6, Appl
C 48	7	36.8	10	1	US-09-867-262-5	Sequence 5, Appl
C 49	7	36.8	10	1	US-10-087-426-6	Sequence 6, Appl
C 50	7	36.8	10	1	US-09-498-557-10	Sequence 10, Appl
C 51	7	36.8	10	1	US-09-885-551A-6	Sequence 6, Appl
C 52	7	36.8	10	1	US-09-534-366A-15	Sequence 15, Appl
C 53	7	36.8	10	1	US-09-875-453B-200	Sequence 200, App
C 54	7	36.8	10	1	US-09-668-482-25	Sequence 25, Appl
C 55	7	36.8	10	1	US-09-479-608A-31	Sequence 31, Appl
C 56	7	36.8	10	1	US-09-479-608A-32	Sequence 32, Appl
C 57	7	36.8	10	1	US-10-029-221C-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-874-601-115
; Sequence 115, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-115

Query Match 54.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.8;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGGAAG 19
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Db 1 CUGUGGAGAAG 12

RESULT 2
5427929-4
; Patent No. 5427929
; APPLICANT: RICHARDS, RODNEY M.; JONES, THEODORE; SNITMAN, DAVID

;L.;BROWN, GREGORY S.
; TITLE OF INVENTION: METHOD FOR REDUCING CARRYOVER CONTAMINATION
; IN AN AMPLIFICATION PROCEDURE
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/57,192
; FILING DATE: 3-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 686,478
; FILING DATE: 19-APR-1991
; APPLICATION NUMBER: 517,631
; FILING DATE: 01-MAY-1990
; SEQ ID NO:4:
; LENGTH: 14
5427929-4

Query Match 54.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 2.8;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCGAAG 18
||| ||| ||| |||
Db 1 GCTGTGGCGAAG 12

RESULT 3
US-09-647-344A-33
; Sequence 33, Application US/09647344A
; Patent No. 6586180
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.PCT.US
; CURRENT APPLICATION NUMBER: US/09/647,344A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 33
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-09-647-344A-33

Query Match 51.6%; Score 9.8; DB 1; Length 14;
Best Local Similarity 69.2%; Pred. No. 3.9;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGCGCTGTGGC 14
|: |||: |||
Db 2 GUGGCGUGGGGC 14

RESULT 4
US-08-826-246-18/c
; Sequence 18, Application US/08826246
; Patent No. 6048709
; GENERAL INFORMATION:
; APPLICANT: Faib, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,246
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/799,910
; FILING DATE: 13-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,787
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-078-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-826-246-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
||||| |||
Db 10 GTGGCGAAG 2

RESULT 5
US-08-944-495-18/c
; Sequence 18, Application US/08944495
; Patent No. 6087477
; GENERAL INFORMATION:
; APPLICANT: Faib, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,495
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/799,910
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-067-999

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; US-08-944-495-18

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```

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 10 GTGGCGAAG 18
Db 10 GTGGCGAAG 2

```

RESULT 6

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; US-09-126-640-18/c
; Sequence 18, Application US/09126640A
; Patent No. 6099823
; GENERAL INFORMATION:
; APPLICANT: FALB, Dean A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; FILE REFERENCE: 7853-126

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; CURRENT APPLICATION NUMBER: US/09/126,640A
; CURRENT FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 08/870,434
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 08/799,910
; EARLIER FILING DATE: 1997-02-13
; EARLIER APPLICATION NUMBER: 60/011,787
; EARLIER FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-126-640-18

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```

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 10 GTGGCGAAG 18
Db 10 GTGGCGAAG 2

```

RESULT 7

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; US-08-925-588-18/c
; Sequence 18, Application US/08925588
; Patent No. 6221628
; GENERAL INFORMATION:

```

```

; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; THE TREATMENT AND DIAGNOSIS OF
; CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY

```

```

; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,588
; FILING DATE: 08-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/799,910
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-067-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
; US-08-925-588-18

```

```

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 10 GTGGCGAAG 18
Db 10 GTGGCGAAG 2

```

RESULT 8

```

; US-09-288-292A-18/c
; Sequence 18, Application US/09288292A
; Patent No. 6359194
; GENERAL INFORMATION:

```

```

; APPLICANT: Dean A. Falb
; APPLICANT: Katherine Galvin
; APPLICANT: Michael Donovan
; APPLICANT: Dennis Huszar
; APPLICANT: Michael A. Gimbrone, Jr.
; TITLE OF INVENTION: Compositions and Methods for the Treatment and Diagnosis of
; TITLE OF INVENTION: Cardiovascular Disease
; FILE REFERENCE: 7853-140-999
; CURRENT APPLICATION NUMBER: US/09/288,292A
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 08/870,434
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/799,910
; PRIOR FILING DATE: 1997-02-13
; PRIOR APPLICATION NUMBER: 60/011,787
; PRIOR FILING DATE: 1996-02-16
; PRIOR APPLICATION NUMBER: 08/485,573
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/386,844
; PRIOR FILING DATE: 1995-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-288-292A-18

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Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
|||||
Db 10 GTGGCGAAG 2

RESULT 9

US-09-372-044-18/c
; Sequence 18, Application US/09372044A
; Patent No. 6492126
; GENERAL INFORMATION:
; APPLICANT: Dean FALB et al.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease
; FILE REFERENCE: 7853-152
; CURRENT APPLICATION NUMBER: US/09/372,044A
; CURRENT FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-044-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
|||||
Db 10 GTGGCGAAG 2

RESULT 10

US-08-825-486-18/c
; Sequence 18, Application US/08825486
; Patent No. 6534641
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,486
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/799,910
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-077-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090

; TELERAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-825-486-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
|||||
Db 10 GTGGCGAAG 2

RESULT 11

US-08-826-248-18/c
; Sequence 18, Application US/08826248
; Patent No. 6759210
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,248
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/799,910
; FILING DATE: 13-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,787
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-079-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-826-248-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
|||||
Db 10 GTGGCGAAG 2

RESULT 12
US-09-706-228-11/c
; Sequence 11, Application US/09706228
; Patent No. 6803215
; GENERAL INFORMATION:
; APPLICANT: Shaw, Pang-Chui
; APPLICANT: Wang, Jun
; APPLICANT: But, Paul Pui-Hay
; APPLICANT: Ha, Wai-Yan
; APPLICANT: Yau, Forrest C.F.
; TITLE OF INVENTION: The Chinese University of Hong Kong
; TITLE OF INVENTION: Sequence Characterization Amplified Region (SCAR) Test
; Patent No. 6803215
; TITLE OF INVENTION: for the Authentication of Traditional Chinese Medicinal
; FILE REFERENCE: 016285-001500US
; CURRENT APPLICATION NUMBER: US/09/706,228
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer OPC-20
US-09-706-228-11

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
|||||
Db 10 GTGGCGAAG 2

RESULT 13
US-09-249-155A-305
; Sequence 305, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-305

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCGA 16
|||||

Db 1 GCTGTGGCCA 10

RESULT 14
US-09-494-102A-2
; Sequence 2, Application US/09494102A
; Patent No. 6303293
; GENERAL INFORMATION:
; APPLICANT: Patterson, David
; APPLICANT: Puskas, John
; APPLICANT: Song, Keming
; APPLICANT: Linmen, KemingJeffrey
; TITLE OF INVENTION: OLIGONUCLEOTIDE REVERSE TRANSCRIPTION PRIMERS FOR EFFICIENT DE
; FILE REFERENCE: 2094/1E284-US1
; CURRENT APPLICATION NUMBER: US/09/494,102A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/118,417
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: Oligonucleotide primer
US-09-494-102A-2

Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCTGTGGCG 15
|||||
Db 1 CCCTGTGGCG 10

RESULT 15
US-09-949-041A-50/c
; Sequence 50, Application US/09949041A
; Patent No. 6902894
; GENERAL INFORMATION:
; APPLICANT: Yang, Meng
; APPLICANT: Woo, Hok
; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Ri
; FILE REFERENCE: fp4637
; CURRENT APPLICATION NUMBER: US/09/949,041A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-949-041A-50

Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
|||||
Db 11 GCGCTGGGCG 2

RESULT 16
US-09-314-847A-8
; Sequence 8, Application US/09314847A

```

; Patent No. 6365410
; GENERAL INFORMATION:
; APPLICANT: Schellenberger, Volker
; APPLICANT: Liu, Amy D.
; APPLICANT: Selifonova, Olga V.
; TITLE OF INVENTION: Directed Evolution of Microorganisms
; FILE REFERENCE: GC560
; CURRENT APPLICATION NUMBER: US/09/314,847A
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pos102 mutD mutated gene
US-09-314-847A-8

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTCCGCGCTGTG 12
Db      1 GTCCGCGCTGTG 11

RESULT 17
US-10-037-677A-10
; Sequence 10, Application US/10037677A
; Patent No. 6706503
; GENERAL INFORMATION:
; APPLICANT: Schellenberger, Volker
; APPLICANT: Liu, Amy D.
; APPLICANT: Selifonova, Olga V.
; TITLE OF INVENTION: Directed Evolution of Microorganisms
; FILE REFERENCE: GC560-D1
; CURRENT APPLICATION NUMBER: US/10/037,677A
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 09/314,847
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pos102 mutD mutated gene
US-10-037-677A-10

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTCCGCGCTGTG 12
Db      1 GTCCGCGCTGTG 11

RESULT 18
US-08-171-718-30/c
; Sequence 30, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-171-718-30

Query Match          38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CTGTGGCGGA 16
Db      10 CTGTGGCGGA 2

RESULT 19
US-08-171-718-36/c
; Sequence 36, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718

```

;
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-171-718-36

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16
Db 10 CTGTGGCCA 2

RESULT 20
US-08-388-353-259/c
; Sequence 259, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-260

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
Db 9 GTGGCTAAG 1

RESULT 22
US-08-488-551B-259/c
; Sequence 259, Application US/08488551B

;
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-259

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
Db 10 GTGGCTAAG 2

RESULT 21
US-08-388-353-260/c
; Sequence 260, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-260

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
Db 9 GTGGCTAAG 1

RESULT 22
US-08-488-551B-259/c
; Sequence 259, Application US/08488551B

```
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-260

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
Db 9 GTGGCTAAG 1

RESULT 24
US-08-478-087-30/c
; Sequence 30, Application US/08478087
; Patent No. 6077685
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,087
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,718
```


;/ FILING DATE: 22-DEC-1993
;/ APPLICATION NUMBER: US 08/108,808
;/ FILING DATE: 19-AUG-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/022,034
;/ FILING DATE: 25-FEB-1993
;/ PRIOR APPLICATION DATA: US 08/026,063
;/ APPLICATION NUMBER: US 08/026,063
;/ FILING DATE: 04-MAR-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Brown, Anne
;/ REGISTRATION NUMBER: 36,463
;/ REFERENCE/DOCKET NUMBER: 0609.3850003
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (202) 371-2600
;/ TELEFAX: (202) 371-2540
;/ INFORMATION FOR SEQ ID NO: 30:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 10 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-478-087-30

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16
DB 10 CTGTGGCGA 2

RESULT 25
US-08-478-087-36/c
;/ Sequence 36, Application US/08478087
;/ Patent No. 6077685
;/ GENERAL INFORMATION:
;/ APPLICANT: Trofatter, James A.
;/ APPLICANT: MacCollin, Mia M.
;/ APPLICANT: Guehlla, James F.
;/ TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
;/ TITLE OF INVENTION: Thereof
;/ NUMBER OF SEQUENCES: 120
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;/ STREET: 1100 New York Avenue, N.W., Suite 600
;/ CITY: Washington
;/ STATE: D.C.
;/ COUNTRY: USA
;/ ZIP: 20005-3934
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent In Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/478,087
;/ FILING DATE: 07-JUN-1995
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/171,718
;/ FILING DATE: 22-DEC-1993
;/ APPLICATION NUMBER: US 08/108,808
;/ FILING DATE: 19-AUG-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/022,034
;/ FILING DATE: 25-FEB-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/026,063
;/ FILING DATE: 04-MAR-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Brown, Anne

;/ REGISTRATION NUMBER: 36,463
;/ REFERENCE/DOCKET NUMBER: 0609.3850003
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (202) 371-2600
;/ TELEFAX: (202) 371-2540
;/ INFORMATION FOR SEQ ID NO: 36:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 10 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-478-087-36

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16
DB 10 CTGTGGCGA 2

RESULT 26
US-09-398-499-52
;/ Sequence 52, Application US/09398499
;/ Patent No. 6284466
;/ GENERAL INFORMATION:
;/ APPLICANT: Benson, Andrew K.
;/ TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
;/ FILE REFERENCE: UNL 2963
;/ CURRENT APPLICATION NUMBER: US/09/398,499
;/ CURRENT FILING DATE: 1999-09-17
;/ PRIOR APPLICATION NUMBER: 60/101,011
;/ PRIOR FILING DATE: 1998-09-18
;/ NUMBER OF SEQ ID NOS: 58
;/ SOFTWARE: Patent In Ver. 2.1
;/ SEQ ID NO 52
;/ LENGTH: 10
;/ TYPE: DNA
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Description of Artificial Sequence:Primer
;/ US-09-398-499-52

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAA 17
DB 2 TGTGGCGAA 10

RESULT 27
US-08-899-241-240/c
;/ Sequence 240, Application US/08899241A
;/ Patent No. 6322995
;/ GENERAL INFORMATION:
;/ APPLICANT: Hohmann, Hans-Peter
;/ APPLICANT: Huembelin, Markus
;/ APPLICANT: van Loon, Adolphus
;/ APPLICANT: Schurter, Walter
;/ TITLE OF INVENTION: Improved Riboflavin Production
;/ FILE REFERENCE: Improved Riboflavin Prod
;/ CURRENT APPLICATION NUMBER: US/08/899,241A
;/ CURRENT FILING DATE: 1997-07-23
;/ EARLIER APPLICATION NUMBER: 9611905.4
;/ EARLIER FILING DATE: 1996-07-24
;/ NUMBER OF SEQ ID NOS: 252
;/ SOFTWARE: Patent In Ver. 2.0
;/ SEQ ID NO 240
;/ LENGTH: 10
;/ TYPE: DNA

```

RESULT 31
US-09-479-608A-29/c
; Sequence 29, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-29

Query Match          38.9%;   Score 7.4;   DB 1;   Length 10;
Best Local Similarity 88.9%;   Pred. No. 22;

```

```
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 16
   |||||
Db 10 CTGTGGCAA 2

RESULT 32
US-09-479-608A-30/c
; Sequence 30, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-30

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 16
   |||||
Db 9 CTGTGGCAA 1

RESULT 33
US-08-956-518A-92/c
; Sequence 92, Application US/08956518A
; Patent No. 6875606
; GENERAL INFORMATION:
; APPLICANT: Leonard, Sherry
; APPLICANT: Freedman, Robert
; TITLE OF INVENTION: ALPHA-7 NICOTINIC RECEPTOR
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,518A
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-03042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-705-8410
```

```
; TELEFAX: 415-397-8338
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-956-518A-92

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 16
   |||||
Db 10 CTGTGGGAGA 2

RESULT 34
US-08-259-148A-31/c
; Sequence 31, Application US/08259148A
; Patent No. 5741490
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R.
; APPLICANT: Bradley, Daniel W.
; APPLICANT: Two, Jr-Shin
; APPLICANT: Purdy, Michael A.
; APPLICANT: Tam, Albert W.
; APPLICANT: Krawczynski, Krzysztof Z.
; APPLICANT: Yarbough, Patrice D.
; TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,148A
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 822,335
; FILING DATE: 17-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,888
; FILING DATE: 05-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 420,921
; FILING DATE: 13-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 367,486
; FILING DATE: 16-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 336,672
; FILING DATE: 11-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 208,997
; FILING DATE: 17-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0093.20
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
US-08-259-148A-31

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
|||
Db 7 TGGCGAA 1

RESULT 35
US-07-876-941A-47/c
Sequence 47, Application US/07876941A
Patent No. 5885768
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Tam, Albert W.
APPLICANT: Mitchell, Carl
TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
Antibodies
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 4600-0093.33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
US-07-876-941A-47

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
|||
Db 7 TGGCGAA 1

RESULT 36
US-08-734-973-11/c
Sequence 11, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-11

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGCGGC 8
 Db 10 GTGCGGC 4

RESULT 37

US-08-265-484B-6
 ; Sequence 6, Application US/08265484B
 ; Patent No. 5998193
 ; GENERAL INFORMATION:
 ; APPLICANT: Keese, Paul
 ; APPLICANT: Stapper, Marianne
 ; APPLICANT: Perriman, Rhonda
 ; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
 ; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
 ; TITLE OF INVENTION: Ribozymes and Compositions Thereof
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/265,484B
 ; FILING DATE: 24-JUN-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 45284
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0525
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Other Nucleic Acid
 ; US-08-265-484B-6

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 71.4%; Pred. No. 27;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
 Db 4 CUGUGGC 10

RESULT 38

US-08-724-466B-25/c
 ; Sequence 25, Application US/08724466B
 ; Patent No. 6063606
 ; GENERAL INFORMATION:
 ; APPLICANT: Petkovich, P. Martin, White, Jay A.,
 ; APPLICANT: Beckett, Barbara R., Jones, Glenville
 ; TITLE OF INVENTION: Retinoid Metabolizing Protein
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Casels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; ZIP: M5L 1A9
 ; COUNTRY: Canada

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,466B
 ; FILING DATE: October 1, 1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/667,546
 ; FILING DATE: June 21, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 50767/00004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-724-466B-25

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
 Db 9 TGGCGAA 3

RESULT 39

US-08-765-257A-6
 ; Sequence 6, Application US/08765257A
 ; Patent No. 6107078
 ; GENERAL INFORMATION:
 ; APPLICANT: Keese, Paul
 ; APPLICANT: Stapper, Marianne
 ; APPLICANT: Perriman, Rhonda
 ; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,
 ; TITLE OF INVENTION: Stems And Loops, tRNA Embedded Ribozymes
 ; TITLE OF INVENTION: and Compositions Thereof
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH, 1.44Mb
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/765,257A
 ; FILING DATE: June 24, 1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 45284
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 977 9550
 ; TELEFAX: 212 977 9809
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-765-257A-6

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
|:|:|
Db 4 CUGUGGC 10

RESULT 40
US-08-522-384-48
; Sequence 48, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-48

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
|:|:|
Db 4 GCTGTGG 10

RESULT 41
US-08-164D-25/c
; Sequence 25, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996

; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-25

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
|:|:|
Db 9 TGGCGAA 3

RESULT 42
US-09-535-754-6
; Sequence 6, Application US/09535754
; Patent No. 6361974
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHSHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/09/535,754
; CURRENT FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspGI restriction site
US-09-535-754-6

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10
|:|:|
Db 1 CGCGCTG 7

RESULT 43
US-09-336-946B-13/c
; Sequence 13, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A P1-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229

; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-336-946B-13

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGT 11
|||||
Db 7 GCGCTGT 1

RESULT 44
US-09-508-753B-72/c
; Sequence 72, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: AKIRA SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: YUKO SHIBATA
; APPLICANT: HIROKO FUNAKI
; APPLICANT: EIJI OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-72

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
|||||
Db 10 GCTGTGG 4

RESULT 45
US-09-508-753B-404
; Sequence 404, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: AKIRA SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: YUKO SHIBATA
; APPLICANT: HIROKO FUNAKI
; APPLICANT: EIJI OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472

; SEQ ID NO 404
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-404

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12
|||||
Db 4 CGCTGTG 10

RESULT 46
US-10-042-111-23/c
; Sequence 23, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-23

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
|||||
Db 7 GCTGTGG 1

RESULT 47
US-10-108-077-6
; Sequence 6, Application US/10108077
; Patent No. 6635449
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTI
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/108,077
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence

```
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-108-077-6

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
DB      1 CGCGCTG 7

RESULT 48
US-09-867-262-5
; Sequence 5, Application US/09867262
; Patent No. 6696275
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: FRET, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-087-426-6

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
DB      1 CGCGCTG 7

RESULT 50
US-09-498-557-10
; Sequence 10, Application US/09498557
; Patent No. 6713279
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES AND ENZYMES
; FILE REFERENCE: DIVER1460-12
; CURRENT APPLICATION NUMBER: US/09/498,557
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 09/332,835
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-498-557-10

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
DB      1 CGCGCTG 7

RESULT 49
US-10-087-426-6
; Sequence 6, Application US/10087426
; Patent No. 6709841
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-23
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
```


Qy 4 CGCGCTG 10
 |||||
 Db 1 CGCGCTG 7

RESULT 51

US-09-885-551A-6
 ; Sequence 6, Application US/09885551A
 ; Patent No. 6740506
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: SHORT, Jay
 ; APPLICANT: DZAVAKHISHVILI, Tsothe
 ; APPLICANT: FREY, Gerhard
 ; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
 ; FILE REFERENCE: DIVER1460-14
 ; CURRENT APPLICATION NUMBER: US/09/885,551A
 ; CURRENT FILING DATE: 2001-06-19
 ; PRIOR APPLICATION NUMBER: US/09/535,754
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 09/522,289
 ; PRIOR FILING DATE: 2000-03-09
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: BspG I restriction site
 US-09-885-551A-6

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGCGCTG 10
 |||||
 Db 1 CGCGCTG 7

RESULT 52

US-09-534-366A-15
 ; Sequence 15, Application US/09534366A
 ; Patent No. 6759195
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentley, William E.
 ; APPLICANT: Gill, Ryan T.
 ; TITLE OF INVENTION: Method of Differential Display of Prokaryotic Messenger
 ; FILE REFERENCE: Bentley et al., Method of . . .
 ; CURRENT APPLICATION NUMBER: US/09/534,366A
 ; CURRENT FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: PROV 60/126,038
 ; PRIOR FILING DATE: 1999-03-25
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthesized
 US-09-534-366A-15

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGGCGAA 17
 |||||

Db 4 TGGCGAA 10

RESULT 53

US-09-875-453B-200/c
 ; Sequence 200, Application US/09875453B
 ; Patent No. 6838556
 ; GENERAL INFORMATION:
 ; APPLICANT: Kim, Jungsoh P.
 ; APPLICANT: Starr, Douglas B.
 ; APPLICANT: Tam, Albert W.
 ; APPLICANT: Laurance, Megan E.
 ; APPLICANT: Michelotti, Emil F.
 ; APPLICANT: Velligan, Mark D.
 ; APPLICANT: Latour, Derek R.
 ; APPLICANT: Thomas, Rita L.
 ; APPLICANT: Kongpachith, Ana
 ; APPLICANT: Sheppard, Liana T.
 ; APPLICANT: Lim, Moon Young
 ; APPLICANT: Bruice, Thomas W.
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
 ; FILE REFERENCE: 54600-8135-US00
 ; CURRENT APPLICATION NUMBER: US/09/875,453B
 ; CURRENT FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: US 60/209,549
 ; PRIOR FILING DATE: 2000-06-06
 ; NUMBER OF SEQ ID NOS: 246
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 200
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: mutated sequence
 US-09-875-453B-200

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGCGCTG 10
 |||||
 Db 8 CGCGCTG 2

RESULT 54

US-09-668-482-25/c
 ; Sequence 25, Application US/09668482
 ; Patent No. 6861238
 ; GENERAL INFORMATION:
 ; APPLICANT: Petkovich, P. Martin, White, Jay A.;
 ; APPLICANT: Beckett, Barbara R., Jones, Glenville
 ; TITLE OF INVENTION: Retinoid Metabolizing Protein
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5L 1A9
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/668,482
 ; FILING DATE: 25-Sep-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,164
 ; FILING DATE: June 25, 1997
 ; APPLICATION NUMBER: 08/667,546

```
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 25
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25
US-09-668-482-25

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
Db 9 TGGCGAA 3

RESULT 55
US-09-479-608A-31/c
; Sequence 31, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-31

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
Db 8 CTGTGGC 2

RESULT 56
US-09-479-608A-32/c
; Sequence 32, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-32

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
Db 8 CTGTGGC 2

RESULT 57
US-10-029-221C-5
; Sequence 5, Application US/10029221C
; Patent No. 6939689
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; APPLICANT: DJAVAKHISHVILI, TSOTNE D.
; APPLICANT: FREY, GERHARD J.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-21
; CURRENT APPLICATION NUMBER: US/10/029,221C
; CURRENT FILING DATE: 2003-01-10
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; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-029-221C-5

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10
Db 1 CGCGCTG 7

Search completed: May 9, 2006, 15:48:19
Job time : 0.001 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 15:49:45 ; Search time 0.001 Seconds
(without alignments)
167.086 Million cell updates/sec

Title: US-09-904-968A-19-COPY
Perfect score: 19
Sequence: 1 ggtcgcgtgtgccaagg 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 414 seqs, 4397 residues

Total number of hits satisfying chosen parameters: 828

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 414 summaries

Database : ngsl9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1	Human PKD1 gene mu
2	11	57.9	13	1	Oligonucleotide SE
3	11	57.9	13	1	Oligonucleotide SE
4	10.4	54.7	14	1	Amplification prob
5	10.4	54.7	14	1	Rod opsin hairpin
6	10	52.6	12	1	MODY 3 diabetes-as
7	10	52.6	13	1	Oligonucleotide SE
8	10	52.6	13	1	Oligonucleotide SE
9	9.8	51.6	13	1	Oligonucleotide SE
10	9.8	51.6	13	1	Oligonucleotide SE
11	9.8	51.6	13	1	Oligonucleotide SE
12	9.8	51.6	13	1	Oligonucleotide SE
13	9.8	51.6	13	1	Oligonucleotide SE
14	9.8	51.6	13	1	Oligonucleotide SE
15	9.8	51.6	13	1	Oligonucleotide SE
16	9.8	51.6	13	1	Oligonucleotide SE
17	9.8	51.6	14	1	HSV RNA fragment 1
18	9.4	49.5	12	1	Oligonucleotide pr
19	9.4	49.5	12	1	Oligonucleotide pr
20	9.4	49.5	12	1	Oligonucleotide pr
21	9.4	49.5	12	1	PCR primer used in
22	9.4	49.5	12	1	Bacterial strain i
23	9.4	49.5	12	1	Wilding bacterial
24	9.4	49.5	12	1	Primer used in bac
25	9.4	49.5	13	1	Oligonucleotide SE
26	9.4	49.5	13	1	Oligonucleotide SE
27	9.4	49.5	13	1	Oligonucleotide SE
28	9.4	49.5	13	1	Oligonucleotide SE
29	9.4	49.5	13	1	Oligonucleotide SE
30	9.4	49.5	13	1	Oligonucleotide SE
31	9.4	49.5	13	1	Oligonucleotide SE
32	9.4	49.5	13	1	Oligonucleotide SE
33	9.4	49.5	13	1	Oligonucleotide SE

34	9.4	49.5	13	1	ABH19540	Oligonucleotide SE
35	9.4	49.5	13	1	ABH19543	Oligonucleotide SE
36	9.4	49.5	13	1	ABP16163	Oligonucleotide SE
37	9.4	49.5	13	1	ABH19542	Oligonucleotide SE
38	9.4	49.5	13	1	ABF04974	Oligonucleotide SE
39	9.4	49.5	13	1	ABF03145	Oligonucleotide SE
40	9.4	49.5	13	1	ABF16162	Oligonucleotide SE
41	9.4	49.5	13	1	ABF16245	Oligonucleotide SE
42	9.4	49.5	13	1	ABC76993	Oligonucleotide SE
43	9.4	49.5	13	1	ABC76992	Oligonucleotide SE
44	9.4	49.5	13	1	ABC86974	Oligonucleotide SE
45	9.4	49.5	13	1	ABH19541	Oligonucleotide SE
46	9.4	49.5	13	1	ABF03963	Oligonucleotide SE
47	9.4	49.5	13	1	ABH65140	Oligonucleotide SE
48	9.4	49.5	13	1	ABH32687	Oligonucleotide SE
49	9.4	49.5	13	1	ADZ85140	MODY 3 diabetes-as
50	9	47.4	10	1	AAV94476	Human FcHd540 gene
51	9	47.4	10	1	AAV34958	Synthetic Agaricus
52	9	47.4	10	1	AAZ58826	Human MUC11 gene a
53	9	47.4	10	1	AAZ50718	Reverse primer for
54	9	47.4	10	1	ABL60664	Panax species geno
55	9	47.4	11	1	ABV69628	Human skin EST 741
56	9	47.4	12	1	AB104019	Oligonucleotide pr
57	8.8	46.3	12	1	AAV65455	Primer pBS800-23J
58	8.8	46.3	12	1	AB159311	Oligonucleotide pr
59	8.8	46.3	12	1	AB124865	Oligonucleotide pr
60	8.8	46.3	12	1	ABH89194	Oligonucleotide pr
61	8.8	46.3	12	1	ABX10162	Human TIGR/Myocili
62	8.8	46.3	12	1	ADW86997	Protein labelling
63	8.4	44.2	10	1	AAZ77822	Human dendritic ce
64	8.4	44.2	10	1	AAZ77845	Human dendritic ce
65	8.4	44.2	10	1	AAZ84021	Metastatic breast
66	8.4	44.2	10	1	AAZ85539	Metastatic breast
67	8.4	44.2	10	1	AAZ84999	Metastatic breast
68	8.4	44.2	10	1	AAZ85922	Metastatic breast
69	8.4	44.2	10	1	AAZ81487	Metastatic breast
70	8.4	44.2	10	1	AAZ84108	Metastatic breast
71	8.4	44.2	10	1	AAH64063	Human ubiquitously
72	8.4	44.2	10	1	AAF42948	Yeast NORF gene SA
73	8.4	44.2	10	1	AAF41527	Yeast NORF gene SA
74	8.4	44.2	10	1	ABL88334	Human CHRN gene p
75	8.4	44.2	10	1	ABN87962	Human CSR preferre
76	8.4	44.2	10	1	ABV78444	Human Th1 cell pre
77	8.4	44.2	10	1	AAZ97347	Human CRYBB1 gene
78	8.4	44.2	10	1	ABL45886	Human EDG6 gene al
79	8.4	44.2	10	1	AB199149	Human CDS2 ASO PC
80	8.4	44.2	10	1	AAZ52054	Human CES2 gene po
81	8.4	44.2	10	1	ACA94569	DNA tag from human
82	8.4	44.2	10	1	ADK13021	Human glioma endot
83	8.4	44.2	11	1	AAZ20067	DNA primer for HLA
84	8.4	44.2	11	1	AAZ18995	Murine MRL SAGE ta
85	8.4	44.2	11	1	ABQ86261	Human skin stress/
86	8.4	44.2	11	1	ABQ87168	Human skin stress/
87	8.4	44.2	11	1	ABV65931	Human skin EST 371
88	8.4	44.2	11	1	ABV69764	Human skin EST 755
89	8.4	44.2	11	1	ABV70774	Human skin EST 855
90	8.4	44.2	11	1	ABV69072	Human skin EST 685
91	8.4	44.2	11	1	ABV69619	Human skin EST 740
92	8.4	44.2	11	1	ABV71417	Human skin EST 920
93	8.4	44.2	11	1	ABV63353	Human skin EST 113
94	8.4	44.2	11	1	ABV66009	Human skin EST 379
95	8.4	44.2	11	1	ABV67796	Human skin EST 558
96	8.4	44.2	11	1	ABV68820	Human skin EST 660
97	8.4	44.2	11	1	ABV63996	Human skin EST 178
98	8.4	44.2	11	1	ABV62343	Human hair-bearing
99	8.4	44.2	11	1	ADQ35656	Human hair-bearing
100	8.4	44.2	11	1	ADQ36012	Human hair-bearing
101	8.4	44.2	11	1	ADQ35381	Human hair-bearing
102	8.4	44.2	11	1	ADQ32141	Human facial skin-
103	8.4	44.2	11	1	ADQ34986	Human facial skin-
104	8.4	44.2	11	1	ADQ35029	Human facial skin-
105	8.4	44.2	11	1	ADQ34095	Human facial skin-
106	8.4	44.2	12	1	AAV65451	Primer pBS800-23E

107	8.4	44.2	12	1	AAV65548	Forward primer 18	c 180	7.4	38.9	10	1	AAZ79074	Human dendritic ce
108	8.4	44.2	12	1	AAV65547	Forward primer 17	181	7.4	38.9	10	1	AAZ79675	Human dendritic ce
109	8.4	44.2	12	1	AAV65546	Forward primer 16	182	7.4	38.9	10	1	AAZ79480	Human dendritic ce
110	8.4	44.2	12	1	AAA74607	HIV-specific rever	c 183	7.4	38.9	10	1	AAZ78781	Metastatic breast
111	8.4	44.2	12	1	AB123621	Oligonucleotide pr	c 184	7.4	38.9	10	1	AAZ82348	Metastatic breast
112	8.4	44.2	12	1	AB112916	Oligonucleotide pr	c 185	7.4	38.9	10	1	AAZ81963	Metastatic breast
c 113	8.4	44.2	12	1	AB106621	Oligonucleotide pr	c 186	7.4	38.9	10	1	AAZ85441	Metastatic breast
c 114	8.4	44.2	12	1	AB164116	Oligonucleotide pr	187	7.4	38.9	10	1	AAZ83525	Metastatic breast
c 115	8.4	44.2	12	1	ABH90350	Oligonucleotide pr	188	7.4	38.9	10	1	AAZ82033	Metastatic breast
116	8.4	44.2	12	1	ABH95969	Oligonucleotide pr	189	7.4	38.9	10	1	AAZ84603	Metastatic breast
117	8.4	44.2	12	1	ABH73785	Oligonucleotide pr	c 190	7.4	38.9	10	1	AAZ81044	Metastatic breast
118	8.4	44.2	12	1	ABH90189	Oligonucleotide pr	c 191	7.4	38.9	10	1	AAZ81349	Metastatic breast
119	8.4	44.2	12	1	ABH72007	Oligonucleotide pr	c 192	7.4	38.9	10	1	AAZ82759	Metastatic breast
120	8.4	44.2	12	1	AB125686	Oligonucleotide pr	c 193	7.4	38.9	10	1	AAZ81572	Metastatic breast
121	8.4	44.2	12	1	AB126828	Oligonucleotide pr	c 194	7.4	38.9	10	1	AAZ81415	Metastatic breast
c 122	8.4	44.2	12	1	ABH90031	Oligonucleotide pr	c 195	7.4	38.9	10	1	AAZ82829	Metastatic breast
c 123	8.4	44.2	12	1	AB129748	Oligonucleotide pr	c 196	7.4	38.9	10	1	AAZ84942	Metastatic breast
124	8.4	44.2	12	1	AB112040	Oligonucleotide pr	c 197	7.4	38.9	10	1	AAZ80867	Metastatic breast
125	8.4	44.2	12	1	AB117107	Oligonucleotide pr	198	7.4	38.9	10	1	AAZ74122	Human monocyte and
126	8.4	44.2	12	1	AB150801	Oligonucleotide pr	199	7.4	38.9	10	1	AAZ73917	Human dendritic ce
127	8.4	44.2	12	1	ABH95967	Oligonucleotide pr	c 200	7.4	38.9	10	1	AAZ74079	Human dendritic ce
c 128	8.4	44.2	12	1	ADH90353	Oligonucleotide pr	201	7.4	38.9	10	1	AAZ56244	Human macrophage g
c 129	8.4	44.2	12	1	ADC33639	M. tuberculosis PC	202	7.4	38.9	10	1	AAZ56333	Human macrophage g
c 130	8.4	44.2	12	1	AD245204	Parallel stranded	203	7.4	38.9	10	1	AAZ56136	Human monocyte gen
c 131	8	42.1	10	1	AAZ79106	Human dendritic ce	204	7.4	38.9	10	1	AAZ14154	E. coli K-12 lead
132	8	42.1	10	1	AAZ81742	Metastatic breast	c 205	7.4	38.9	10	1	AAZ73645	Probe #14 for sequ
c 133	8	42.1	10	1	AAZ85240	Metastatic breast	c 206	7.4	38.9	10	1	AAZ73646	Probe #15 for sequ
c 134	8	42.1	10	1	AAZ85260	Metastatic breast	207	7.4	38.9	10	1	AAZ170450	Oligonucleotide us
135	8	42.1	10	1	AAZ84921	Metastatic breast	208	7.4	38.9	10	1	AAH19999	Mouse Treg immunor
136	8	42.1	10	1	AAZ84042	Metastatic breast	209	7.4	38.9	10	1	AAI67372	Human FKBP8 gene p
137	8	42.1	10	1	AAZ79746	Human colon prefer	c 210	7.4	38.9	10	1	AAZ09210	Oligonucleotide ON
138	8	42.1	10	1	AAH63878	Human ubiquitously	c 211	7.4	38.9	10	1	AAH63607	Human ubiquitously
139	8	42.1	10	1	AAH32681	LPS activated huma	c 212	7.4	38.9	10	1	AAH63746	Human ubiquitously
140	8	42.1	10	1	ABA06193	Human normal hepat	213	7.4	38.9	10	1	AAH64224	Human ubiquitously
141	8	42.1	10	1	ABA83148	Claudin 2 ovarian	214	7.4	38.9	10	1	AAH63440	Human ubiquitously
142	8	42.1	10	1	AAF433250	Yeast NORF gene SA	215	7.4	38.9	10	1	AAH63439	Human ubiquitously
143	8	42.1	10	1	ABL42674	Human maturation/a	216	7.4	38.9	10	1	AAH64185	Human ubiquitously
144	8	42.1	10	1	ABX42776	Human maturation/a	c 217	7.4	38.9	10	1	AAH63894	Human ubiquitously
145	8	42.1	10	1	ABK96054	Human LiFE gene po	c 218	7.4	38.9	10	1	AAZ20721	Primer #13 used to
146	8	42.1	10	1	AAI48073	Human CSF3 gene al	c 219	7.4	38.9	10	1	AAH32655	LPS activated huma
147	8	42.1	10	1	ABK23699	Transcript tag DNA	220	7.4	38.9	10	1	AAH32828	LPS activated huma
148	8	42.1	10	1	ACA94662	DNA tag from human	c 221	7.4	38.9	10	1	AAH32746	Human phospholipid
149	8	42.1	10	1	ACA94515	DNA tag from human	c 222	7.4	38.9	10	1	ABA81653	Human normal hepat
150	8	42.1	10	1	ADS76513	Breast cancer dete	223	7.4	38.9	10	1	ABA06025	Human normal hepat
151	8	42.1	10	1	ADS78031	Breast cancer dete	224	7.4	38.9	10	1	ABA06218	Human normal hepat
152	8	42.1	10	1	ADU176514	Breast cancer dete	225	7.4	38.9	10	1	AAZ91471	Human CHR5 gene,
c 153	8	42.1	10	1	ADU19803	Hypoxia-related tu	c 226	7.4	38.9	10	1	AAF36041	Yeast NORF gene SA
c 154	8	42.1	11	1	ABV69823	Human skin EST 760	c 227	7.4	38.9	10	1	AAF43354	Yeast NORF gene SA
c 155	8	42.1	11	1	ABV62402	Human skin EST 188	c 228	7.4	38.9	10	1	AAF39191	Yeast NORF gene SA
c 156	8	42.1	11	1	ABV67604	Human skin EST 539	c 229	7.4	38.9	10	1	AAF34571	Yeast NORF gene SA
c 157	7.8	41.1	11	1	AAZ85261	mutD promoter sequ	230	7.4	38.9	10	1	AAF35628	Yeast NORF gene SA
158	7.8	41.1	11	1	ABQ87267	Human skin stress/	231	7.4	38.9	10	1	AAF37416	Yeast NORF gene SA
c 159	7.8	41.1	11	1	ABQ87096	Human skin stress/	c 232	7.4	38.9	10	1	AAF36771	Yeast NORF gene SA
c 160	7.8	41.1	11	1	ABQ87230	Human skin stress/	c 233	7.4	38.9	10	1	AAF37531	Yeast NORF gene SA
c 161	7.8	41.1	11	1	ABV68460	Human skin EST 624	c 234	7.4	38.9	10	1	AAF43175	Yeast NORF gene SA
c 162	7.8	41.1	11	1	ABV69665	Human skin EST 745	c 235	7.4	38.9	10	1	AAF43253	Yeast NORF gene SA
c 163	7.8	41.1	11	1	ABV65281	Human skin EST 306	236	7.4	38.9	10	1	AAF43167	Yeast NORF gene SA
c 164	7.8	41.1	11	1	ABV67742	Human skin EST 552	237	7.4	38.9	10	1	AAZ19671	Primer-extension o
c 165	7.8	41.1	11	1	ABV70868	Human skin EST 865	c 238	7.4	38.9	10	1	ABL01179	Human AKR1B1 gene
c 166	7.8	41.1	11	1	ABV63447	Human skin EST 123	c 239	7.4	38.9	10	1	AAZ98835	Colony stimulating
c 167	7.8	41.1	11	1	ABV72108	Human skin EST 989	c 240	7.4	38.9	10	1	ABL42636	Human maturation/a
c 168	7.8	41.1	11	1	ABV66734	Human skin EST 452	c 241	7.4	38.9	10	1	AAZ25385	Human primer #2 to
169	7.8	41.1	11	1	ABV62244	Human skin EST 30.	242	7.4	38.9	10	1	ABN81464	Human HTATIP PCR p
170	7.8	41.1	11	1	ADQ36355	Human hair-bearing	243	7.4	38.9	10	1	ABK96027	Human LiFE gene po
171	7.8	41.1	11	1	ADQ35677	Human hair-bearing	244	7.4	38.9	10	1	AAZ48067	Human CSF3 gene al
c 172	7.8	41.1	11	1	ADQ34103	Human facial skin-	c 245	7.4	38.9	10	1	AAZ48068	Human CSF3 gene al
173	7.8	41.1	11	1	ADT79188	Oligonucleotide #1	c 246	7.4	38.9	10	1	AAZ27409	Oligo #2, to const
c 174	7.8	41.1	11	1	ADZ24827	Human SNP detectio	c 247	7.4	38.9	10	1	ABL39499	Human ETEB primer-
c 175	7.4	38.9	10	1	AAQ71089	Merlin exon 7 spli	248	7.4	38.9	10	1	ABT05346	Human NAGA-alpha g
c 176	7.4	38.9	10	1	AAQ71095	Merlin exon 10 spli	c 249	7.4	38.9	10	1	ABT05344	Human NAGA-alpha g
c 177	7.4	38.9	10	1	AAQ96664	HIV-1 NL4-3 nef ge	c 250	7.4	38.9	10	1	AAZ99201	UDP glycosyltransf
c 178	7.4	38.9	10	1	AAQ96663	HIV-1 NL4-3 nef ge	c 251	7.4	38.9	10	1	ABV84886	Human thymosin bet
179	7.4	38.9	10	1	AAZ18633	p53 serial analysi	252	7.4	38.9	10	1	ABV84695	Chronic hepatitis

253	7.4	38.9	10	1	ABV84505	Human apolipoprote	326	7	36.8	10	1	AAZ82560	Metastatic breast
254	7.4	38.9	10	1	ABV84523	Human HCC underexp	C 327	7	36.8	10	1	AAZ82992	Metastatic breast
255	7.4	38.9	10	1	ABV84710	Human apolipoprote	328	7	36.8	10	1	AAZ99863	Prokaryote RT-PCR
256	7.4	38.9	10	1	ABV84764	Chronic hepatitis	C 329	7	36.8	10	1	AAZ73648	Probe #17 for sequ
257	7.4	38.9	10	1	ABV84791	Human apolipoprote	C 330	7	36.8	10	1	AAA73647	Probe #16 for sequ
258	7.4	38.9	10	1	ABV84741	Chronic hepatitis	C 331	7	36.8	10	1	AAA70761	PCR primer #7 for
259	7.4	38.9	10	1	ABV84919	Human apolipoprote	C 332	7	36.8	10	1	AAZ04437	Human DAXX DNA pri
260	7.4	38.9	10	1	ABV84967	Human thymosin bet	333	7	36.8	10	1	AAH63684	Human ubiquitously
C 261	7.4	38.9	10	1	ABK23578	Transcript tag DNA	334	7	36.8	10	1	AAZ57302	Human CHRN2 allele
C 262	7.4	38.9	10	1	ABA96213	Half-site oligonuc	335	7	36.8	10	1	AAZ31259	GC-rich template c
263	7.4	38.9	10	1	AAZ19821	Oligonucleotide #1	C 336	7	36.8	10	1	AAZ41713	Anti-PEP gene cons
264	7.4	38.9	10	1	ABA93366	Human ACAA1 gene p	C 337	7	36.8	10	1	ABA06097	Human normal hepat
C 265	7.4	38.9	10	1	AAZ19954	Primer-extension o	C 338	7	36.8	10	1	AAZ36769	Yeast NORF gene SA
C 266	7.4	38.9	10	1	ABL45924	Human EDG6 gene al	339	7	36.8	10	1	AAZ37041	Yeast NORF gene SA
C 267	7.4	38.9	10	1	ABK81557	Human CASP5 gene a	340	7	36.8	10	1	AAZ33704	Yeast NORF gene SA
C 268	7.4	38.9	10	1	ABK96167	Human CYP1A2 allel	C 341	7	36.8	10	1	AAZ36509	Yeast NORF gene SA
C 269	7.4	38.9	10	1	AAZ94665	Human PLTP gene al	C 342	7	36.8	10	1	AAZ43548	Yeast NORF gene SA
C 270	7.4	38.9	10	1	ADZ25031	Human AANAT gene p	343	7	36.8	10	1	AAZ33404	Yeast NORF gene SA
271	7.4	38.9	10	1	ABK30052	Vancomycin-resista	C 344	7	36.8	10	1	AAZ40064	Yeast NORF gene SA
272	7.4	38.9	10	1	ABL36392	Human lysosomal ac	345	7	36.8	10	1	AAZ40212	Yeast NORF gene SA
273	7.4	38.9	10	1	AAZ48136	Human neuropeptide	C 346	7	36.8	10	1	AAZ34364	Yeast NORF gene SA
C 274	7.4	38.9	10	1	AAZ95939	Human CALM1 gene a	347	7	36.8	10	1	AAZ36295	Yeast NORF gene SA
C 275	7.4	38.9	10	1	AAZ96001	Human CALM1 gene a	C 348	7	36.8	10	1	AAZ42137	Yeast NORF gene SA
276	7.4	38.9	10	1	ABK81811	Human CHRM5 gene p	C 349	7	36.8	10	1	AAZ37397	Yeast NORF gene SA
277	7.4	38.9	10	1	ACA94410	DNA tag from human	350	7	36.8	10	1	AAZ43249	Yeast NORF gene SA
C 278	7.4	38.9	10	1	ACA94519	DNA tag from human	351	7	36.8	10	1	AAZ40108	Yeast NORF gene SA
C 279	7.4	38.9	10	1	ACA94580	DNA tag from human	352	7	36.8	10	1	AAZ43351	Yeast NORF gene SA
C 280	7.4	38.9	10	1	ADZ15526	Biological molecu	C 353	7	36.8	10	1	AAZ33705	Yeast NORF gene SA
C 281	7.4	38.9	10	1	ADZ19154	Azotobacter bacter	C 354	7	36.8	10	1	AAZ41416	Yeast NORF gene SA
C 282	7.4	38.9	10	1	ADG55513	UCP2 primer extens	355	7	36.8	10	1	AAZ41494	Yeast NORF gene SA
C 283	7.4	38.9	10	1	ADN89094	Hyperlipidemia tre	356	7	36.8	10	1	AAZ37535	Yeast NORF gene SA
284	7.4	38.9	10	1	ADN89098	Hyperlipidemia tre	357	7	36.8	10	1	AAZ33686	Yeast NORF gene SA
C 285	7.4	38.9	10	1	ADQ82166	Human Short statur	358	7	36.8	10	1	AAZ36000	Yeast NORF gene SA
C 286	7.4	38.9	10	1	ADR27907	Human VE-statin ex	C 359	7	36.8	10	1	AAZ42020	Yeast NORF gene SA
C 287	7.4	38.9	10	1	ADR27977	Murine VE-statin i	C 360	7	36.8	10	1	AAZ95850	Human NPY1R gene a
C 288	7.4	38.9	10	1	ADR88561	Alpha 7 nicotinic	C 361	7	36.8	10	1	AAZ26712	Primer #8 used to
C 289	7.4	38.9	10	1	ADS76954	Breast cancer dete	362	7	36.8	10	1	AAZ26712	Human GPR31 gene p
C 290	7.4	38.9	10	1	ADS77992	Breast cancer dete	363	7	36.8	10	1	ABZ98814	Colony stimulating
C 291	7.4	38.9	10	1	ADS77023	Breast cancer dete	364	7	36.8	10	1	ABZ71544	Zinc finger protei
C 292	7.4	38.9	10	1	ADS76564	Breast cancer dete	365	7	36.8	10	1	ABZ71291	Zinc finger protei
C 293	7.4	38.9	10	1	ADS76953	Breast cancer dete	366	7	36.8	10	1	ABZ71292	Zinc finger protei
C 294	7.4	38.9	10	1	ADS77055	Breast cancer dete	367	7	36.8	10	1	ABZ71662	Zinc finger protei
C 295	7.4	38.9	10	1	ADS78162	Breast cancer dete	368	7	36.8	10	1	ABZ71661	Zinc finger protei
C 296	7.4	38.9	10	1	ADS76565	Breast cancer dete	369	7	36.8	10	1	ABZ71661	Zinc finger protei
C 297	7.4	38.9	10	1	ADS77023	Breast cancer dete	370	7	36.8	10	1	ABZ98858	Human CFL1 primer
C 298	7.4	38.9	10	1	ADU19102	Hypoxia-related tu	371	7	36.8	10	1	ABZ98858	Human CFL1 primer
C 299	7.4	38.9	10	1	ADU18946	Hypoxia-related tu	C 372	7	36.8	10	1	ABZ98858	Human CFL1 primer
300	7.4	38.9	10	1	ADU18864	Hypoxia-related tu	C 373	7	36.8	10	1	ABZ98858	Human CFL1 primer
301	7.4	38.9	10	1	ADZ24419	Human SNP detectio	C 374	7	36.8	10	1	ABZ98858	Human CFL1 primer
302	7.4	38.9	10	1	ADZ24430	Human SNP detectio	C 375	7	36.8	10	1	ABZ98858	Human CFL1 primer
303	7.4	38.9	10	1	AEA37223	MoMLV derived vect	C 376	7	36.8	10	1	ABZ98858	Human CFL1 primer
304	7.4	38.9	10	1	AAZ29313	5'-primer for mamm	C 377	7	36.8	10	1	ABZ98858	Human CFL1 primer
C 305	7.4	38.9	10	1	AAZ29313	Degenerate RT-PCR	C 378	7	36.8	10	1	ABZ98858	Human CFL1 primer
C 306	7.4	38.9	10	1	AAZ12230	Differential displ	C 379	7	36.8	10	1	ABZ98858	Human CFL1 primer
C 307	7.4	38.9	10	1	AAZ34959	Synthetic Agaricus	C 380	7	36.8	10	1	AAZ95992	Vancomycin-resista
308	7.4	38.9	10	1	AAZ50187	Yeast tag for addi	C 381	7	36.8	10	1	ADH22188	Human CALM1 gene a
C 309	7.4	38.9	10	1	AAZ35966	Primer used in RAP	382	7	36.8	10	1	ACC41737	Primer extension D
C 310	7.4	38.9	10	1	AAZ77467	US5912147 primer 1	C 383	7	36.8	10	1	ABZ14391	Zinc finger protei
C 311	7.4	38.9	10	1	AAZ28347	Lung cancer indica	384	7	36.8	10	1	ADZ62122	Nucleic acid PCR a
C 312	7.4	38.9	10	1	AAZ61441	Primer SP4A5 for g	385	7	36.8	10	1	ADA63307	Zinc finger target
313	7.4	38.9	10	1	AAZ79591	Human dendritic ce	386	7	36.8	10	1	ADA63696	Zinc finger target
314	7.4	38.9	10	1	AAZ77871	Human dendritic ce	387	7	36.8	10	1	ADA63683	Zinc finger target
C 315	7.4	38.9	10	1	AAZ79427	Human dendritic ce	388	7	36.8	10	1	ADA62121	Zinc finger target
C 316	7.4	38.9	10	1	AAZ78099	Human dendritic ce	389	7	36.8	10	1	ADA63682	Zinc finger target
317	7.4	38.9	10	1	AAZ82030	Metastatic breast	390	7	36.8	10	1	ADZ81067	LINE retro-positio
C 318	7.4	38.9	10	1	AAZ83360	Metastatic breast	C 391	7	36.8	10	1	ADZ81067	Opineurin promore
C 319	7.4	38.9	10	1	AAZ84570	Metastatic breast	392	7	36.8	10	1	ADZ81067	Synthetic zinc fin
320	7.4	38.9	10	1	AAZ82784	Metastatic breast	393	7	36.8	10	1	ADZ81067	Synthetic zinc fin
C 321	7.4	38.9	10	1	AAZ84917	Metastatic breast	394	7	36.8	10	1	ADZ81067	Synthetic zinc fin
C 322	7.4	38.9	10	1	AAZ86247	Metastatic breast	395	7	36.8	10	1	ADZ81067	Synthetic zinc fin
323	7.4	38.9	10	1	AAZ81792	Metastatic breast	396	7	36.8	10	1	ADZ81067	Synthetic zinc fin
324	7.4	38.9	10	1	AAZ81334	Metastatic breast	397	7	36.8	10	1	ADZ81067	Synthetic zinc fin
325	7.4	38.9	10	1	AAZ85903	Metastatic breast	C 398	7	36.8	10	1	ADZ81067	Extendable oligo E

399 7 36.8 10 1 ADI13679 Extracellular tumor
 C 400 7 36.8 10 1 ADL70389 Enhancer sequence
 C 401 7 36.8 10 1 ADR36844 West Nile virus de
 C 402 7 36.8 10 1 ADR36844 Loquat crown-gall
 C 403 7 36.8 10 1 ADR27959 Murine VE-statin e
 C 404 7 36.8 10 1 ADU18248 Hypoxia-related tu
 C 405 7 36.8 10 1 ADU19824 Hypoxia-related tu
 C 406 7 36.8 10 1 ADU18636 Hypoxia-related tu
 C 407 7 36.8 10 1 ADU18717 Hypoxia-related tu
 C 408 7 36.8 10 1 ADU66846 zP450RAI gene isol
 C 409 7 36.8 10 1 ADV90786 Degenerate primer,
 C 410 7 36.8 10 1 ADY62603 Zebrafish p45ORAI
 C 411 7 36.8 10 1 ADY95141 Oligonucleotide re
 C 412 7 36.8 10 1 ADY95142 Oligonucleotide re
 C 413 7 36.8 10 1 ADY95147 Oligonucleotide re
 C 414 7 36.8 10 1 ADY95148 Oligonucleotide re

ALIGNMENTS

RESULT 1
 AAD30245
 ID AAD30245 standard; DNA; 19 BP.
 XX
 AC AAD30245;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human PKD1 gene mutation detecting nested PCR primer, 1F1.
 XX
 KW Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;
 KW acquired cystic disease; transgenic animal; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200206529-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US022035.
 XX
 PR 13-JUL-2000; 2000US-0218261P.
 PR 13-APR-2001; 2001US-0283691P.
 XX
 PA (UYOO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Germino GG, Watnick TJ, Phakdeekitcharoen B;
 XX
 PS WPI; 2002-179805/23.
 XX
 CC Novel primer for diagnosing polycystic kidney disease-associated
 PT disorder, comprises regions having sequence that selectively hybridizes
 PT to polycystic kidney disease gene sequence.
 XX
 PS Claim 6; Page 100; 192pp; English.
 XX
 CC The present invention relates to compositions and methods useful for the
 CC identification and detection of polycystic kidney disease (PKD1) gene
 CC mutations. The invention also relates to primers comprising a 5' region
 CC having a sequence that selectively hybridizes to a PKD1 gene sequence and
 CC optionally, to a PKD1 homologue sequence and an adjacent 3' region having
 CC a sequence that selectively hybridizes to a PKD1 gene sequence and not to
 CC a PKD1 homologue sequence. Primer pairs of the invention are useful for
 CC detecting the presence or absence of a mutation in a PKD1 polynucleotide
 CC in a sample, for identifying a subject at risk for a PKD1-associated
 CC disorder such as autosomal dominant polycystic kidney disease (ADPKD) or
 CC acquired cystic disease and for diagnosing a PKD1-associated disorder in
 CC a subject. They are useful for selectively amplifying a region of a PKD1
 CC gene. PKD1 DNA fragments are useful detecting the presence of a mutant
 CC PKD1 polynucleotide in a sample, as a probe for an amplification
 CC reaction, in hybridisation or amplification assays of biological samples
 CC to detect abnormalities of PKD1 expression and for engineering transgenic

CC animals. The present sequence is a PCR primer used to detect mutation in
 CC human PKD1 gene
 XX
 SQ Sequence 19 BP; 2 A; 4 C; 10 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0;
 QY 1 GGTGCGCTGTGGCGAAGG 19
 Db 1 GGTGCGCTGTGGCGAAGG 19
 |||||
 RESULT 2
 ABF16246
 ID ABF16246 standard; DNA; 13 BP.
 XX
 AC ABF16246;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 116243 for detecting SNP TSC0029111.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 PS WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 116243; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 1 Other;
 Query Match 57.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0;
 QY 9 TGTGCGAAGG 19
 Db 2 TGTGCGAAGG 12
 |||||

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RESULT 3
ABF16247/c
ID ABF16247 standard; DNA; 13 BP.
XX
AC ABF16247;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 116244 for detecting SNP TSC0029111.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
PS Claim 1; SEQ ID NO 116244; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI99989
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 1 Other;
XX
Query Match 57.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 9 TGTGGCGAAGG 19
DB 12 TGTGGCGAAGG 2
XX
RESULT 4
AAQ15000
ID AAQ15000 standard; DNA; 14 BP.
XX
AC AAQ15000;
XX
DT 17-FEB-1992 (first entry)
XX
DE Amplification probe AP2 with single base mismatch to target sequence.
XX
KW ligase chain reaction; LCR; carryover contamination; ss.
XX

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OS Synthetic.
XX
PN WO9117270-A.
XX
PD 14-NOV-1991.
XX
PF 01-MAY-1990; 90US-00517631.
XX
PR 01-MAY-1990; 90US-00517631.
PR 19-APR-1991; 91US-00686478.
XX
PA (AMGE-) AMGEN.
XX
PI Richards RM, Jones T, Snitman DL;
XX
DR WPI; 1991-353789/48.
XX
Redn. of amplification prod. contamination - in amplification procedure
and kits for use in polymerase or ligase chain reaction procedures.
XX
Example 1 and 2; Fig 11B; 134pp; English.
XX
Restriction enzyme modification sites are introduced into amplification
sequence AS1 (see AAQ14998) during LCR using amplification probes AP1,
AP2 and AP3 (see AAQ14999 and AAQ15001 for the other two APs).
XX
Amplification sequence AS1 contains the corresponding preferred pseudo
restriction sites
XX
SQ Sequence 14 BP; 3 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
XX
Query Match 54.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 7 GCTGTGGCGAAG 18
DB 1 GCTGTGGCGAAG 12
XX
RESULT 5
ABZ72886
ID ABZ72886 standard; RNA; 14 BP.
XX
AC ABZ72886;
XX
DT 09-APR-2003 (first entry)
XX
DE Rod opsin hairpin ribozyme oligonucleotide.
XX
Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
WO200288320-A2.
XX
07-NOV-2002.
XX
01-MAY-2002; 2002WO-US013679.
XX
01-MAY-2001; 2001US-00847601.
XX
(UYFL ) UNIV FLORIDA.
XX
Lewin AS, Shaw LC, Grant MB;
XX
WPI; 2003-111880/10.
XX
A recombinant adeno-associated virus-vectored ribozyme composition,
useful for treating a disease or dysfunction of the mammalian eye e.g.

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PT	retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.
XX	
XX	
PS	Example 5; Page 62; 115pp; English.
XX	
CC	The present invention describes a recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, comprising the amino acid sequence of rod opsin, INOS, RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a vector comprising a polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal degeneration. (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (I) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. ABZ72763 to ABZ72953 represent sequences used in the exemplification of the present invention
CC	
XX	
SQ	Sequence 14 BP; 5 A; 1 C; 6 G; 0 T; 2 U; 0 Other;
Query Match	54.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity	75.0%; Pred. No. 24;
Matches	9; Conservative 2; Mismatches 1; Indels 0; Gaps 0
Qy	8 CTGTGCGAAGG 19
	: : : :
Db	1 CUGUGGAAGAAG 12
RESULT 6	
ADZ85151/c	
ID	ADZ85151 standard; DNA; 12 BP.
XX	
AC	ADZ85151;
XX	
DT	28-JUL-2005 (first entry)
XX	
DE	MODY 3 diabetes-associated probe, SEQ ID 27.
XX	
KW	Analyte detection; microarray; probe; ss; diabetes..
XX	
OS	Unidentified.
XX	
PN	US2005112677-A1.
XX	
PD	26-MAY-2005.
XX	
Pf	22-NOV-2004; 2004US-00994626.
XX	
PR	22-NOV-2003; 2003KR-00083356.
XX	
PA	(SHIM/) SHIM J.
XX	
F1	Shim J;
DR	WPI; 2005-403357/41.
XX	


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XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
  Query Match      52.6%; Score 10; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 33;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
   |||||
Db 13 TGTGGCGAAG 4

RESULT 8
ABC20756
ID ABC20756 standard; DNA; 13 BP.
XX
AC ABC20756;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 20773 for detecting SNP TSC0004222.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 20773; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
  Query Match      52.6%; Score 10; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 33;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
   |||||
Db 13 TGTGGCGAAG 4

RESULT 9
ABC23004
ID ABC23004 standard; DNA; 13 BP.
XX
AC ABC23004;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 23021 for detecting SNP TSC0004520.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 23021; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 1 C; 8 G; 4 T; 0 U; 0 Other;
  Query Match      51.6%; Score 9.8; DB 1; Length 13;
  Best Local Similarity 84.6%; Pred. No. 37;
  Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGCGCTGTGG 13
   |||||
Db 1 GGTGCGCTGTGG 13

RESULT 10

```

RESULT 10

XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 88990; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 51.6%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 37;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TCAGCGCTGTGCG 15
 Db ||||| |||||
 13 TCAGCGCTGTGCG 1
 RESULT 13
 ABC23005/c
 ID ABC23005 standard; DNA; 13 BP.
 XX
 AC ABC23005;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 23022 for detecting SNP TSC0004520.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 23022; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 4 A; 8 C; 1 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 51.6%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 37;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GGTGCGCTGTGCG 13
 Db ||||| |||||
 13 GGTGCGCTGTGCG 1
 RESULT 14
 ABC88956
 ID ABC88956 standard; DNA; 13 BP.
 XX
 AC ABC88956;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 88973 for detecting SNP TSC0022356.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 88973; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 0 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 51.6%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 37;

```

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCG 15
   ||||| |||||
Db 1 TCGCGTGTGTGGC 13

RESULT 15
ABC88972
ID ABC88972 standard; DNA; 13 BP.
XX
AC ABC88972;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 88989 for detecting SNP TSC0022356.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 88989 for detecting SNP TSC0022356.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPITG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 88989; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABR00010-ABR82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCG 15
   ||||| |||||
Db 1 TCGCGCGTGTGGC 13

RESULT 16
ABF17106
ID ABF17106 standard; DNA; 13 BP.
XX
AC ABF17106;
XX

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```

DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 117103 for detecting SNP TSC0029306.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPITG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 117103; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABR00010-ABR82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTGGCGAAGG 19
   ||||| |||||
Db 1 GTTGTGGTGAAGG 13

RESULT 17
AAZ23797
ID AAZ23797 standard; RNA; 14 BP.
XX
AC AAZ23797;
XX
DT 14-JAN-2000 (first entry)
XX
DE HSV RNA fragment 15.
XX
KW Antisense; DNA library; identification; multiple cloning site; MCS;
KW inhibition; ss.
XX
OS Herpes simplex virus unknown type.
XX
PN WO9950457-A1.
XX
PD 07-OCT-1999.
XX

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PF 28-MAR-1999; 99WO-US006742.
XX
PR 28-MAR-1998; 98US-0079792P.
PR 06-NOV-1998; 98US-0107504P.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Ruffner DE, Pierce ML, Chen Z;
XX
XX WPI; 1999-610866/52.
XX
XX Production of antisense libraries, used for identifying antisense agents
PT and for identifying target sites for antisense-mediated inhibition of a
PT selected gene.
XX
XX Example 4; Page 60; 63pp; English.
XX
XX This invention describes a novel method for generating an antisense
CC library targeted to a selected RNA transcript. The methods can be used
CC for identifying antisense agents and for identifying target sites for
CC antisense-mediated inhibition of a selected gene. The use of a direct
CC library for target site selection significantly simplifies the screening
CC process, since only very small libraries need be prepared and assayed.
CC AA223783-Z23798 represent RNA fragments derived from the Herpes simplex
CC virus genome which are used to illustrate the method of the invention
XX
XX Sequence 14 BP; 0 A; 4 C; 8 G; 0 T; 2 U; 0 Other;
SQ
    Query Match      51.6%; Score 9.8; DB 1; Length 14;
    Best Local Similarity 69.2%; Pred. NO. 34;
    Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGCGCTGTGGC 14
Db 2 GUGGCGCUGGGC 14

RESULT 18
ABH84869/c
ID ABH84869 standard; DNA; 12 BP.
XX
AC ABH84869;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 284862 for detecting SNP TSC0012030.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 284862; 29pp + Sequence Listing; German.
XX

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CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 8 C; 3 G; 0 T; 0 U; 0 Other;
SQ
    Query Match      49.5%; Score 9.4; DB 1; Length 12;
    Best Local Similarity 90.9%; Pred. NO. 49;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGCG 15
Db 11 GCGCGTGGCG 1

RESULT 19
ABH90694/c
ID ABH90694 standard; DNA; 12 BP.
XX
AC ABH90694;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 290687 for detecting SNP TSC0014474.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 290687; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX

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```

SQ  Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

Query Match      49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
Db  12 TGTGGCGAAGG 2

RESULT 20
ABI50257/c
ID  ABI50257 standard; DNA; 12 BP.
AC
XX
XX  ABI50257;
XX
XX  22-FEB-2002 (first entry)
XX
XX  Oligonucleotide primer SEQ ID NO 350230 for detecting SNP TSC0008276.
DE
XX  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX  Homo sapiens.
OS
XX  WO200177384-A2.
PN
XX  18-OCT-2001.
PD
XX
XX  06-APR-2001; 2001WO-IB000713.
PF
XX
XX  07-APR-2000; 2000DE-01019173.
PR
XX  (EPIG-) EPIGENOMICS AG.
PA
XX  Olek A, Piepenbrock C, Berlin K;
PI
XX  WPI; 2001-657177/75.
DR
XX
XX  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
XX  Claim 1; SEQ ID NO 350230; 29pp + Sequence Listing; German.
PS
XX  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match      49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
Db  12 TGTGGCGAAGG 2

RESULT 21
ADF57536
ADF57536 standard; DNA; 12 BP.
ADF57536;
12-FEB-2004 (first entry)
PCR primer used in method for detecting bacterial DNA in food, SEQ ID 37.
Food; bacterial; bacterium; Single Strain Counting-PCR; SSC-PCR; PCR;
primer; ss.
Unidentified.
JP2003250541-A.
09-SEP-2003.
27-FEB-2002; 2002JP-00052215.
27-FEB-2002; 2002JP-00052215.
(SAOL ) SANYO ELECTRIC CO LTD.
WPI; 2003-883774/82.
Foodstuff testing method involves amplifying DNA fragment of bacteria
extracted from foodstuff, by single strain counting polymerase chain
reaction method.
Claim 6; SEQ ID NO 37; 27pp; Japanese.
The present invention relates to a foodstuff testing method. The method
comprises extracting bacterial DNA fragment from foodstuff, amplifying
the DNA fragment by Single Strain Counting-PCR (SSC-PCR) method. The
amplified linear fragment is analyzed and the recycling method of
foodstuff is determined based on the analysis result. The present primer
was used to illustrate the method of the invention.
Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match      49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3 TCGCGCTGTGG 13
Db  1 TCGCGCTTGG 11

RESULT 22
ADG28788
ID  ADG28788 standard; DNA; 12 BP.
XX
XX  ADG28788;
XX
XX  26-FEB-2004 (first entry)
XX
XX  Bacterial strain identification-related PCR primer G44.
DE  Bacterial strain identification-related PCR primer G44.
XX  Escherichia coli; Bacillus; Shigella; bacterial strain identification;
KW  PCR; primer; ss.
XX  Bacteria.
OS
XX  JP2003169686-A.
PN
XX  17-JUN-2003.
PD
XX
XX  19-DEC-2001; 2001JP-00386731.
PF
XX
XX  25-SEP-2001; 2001JP-00292674.
PR
XX  (SAOL ) SANYO ELECTRIC CO LTD.
PA

```

XX WPI; 2003-783166/74.
 XX
 PT Identifying bacteria by amplifying DNA of bacteria by PCR,
 PT electrophoresing amplified DNA, obtaining electrophoretic image and
 PT identifying if bacteria is predetermined strain of *Escherichia coli* by
 PT DNA-fragment length.
 XX
 PS Example 1; SEQ ID NO 37; 114pp; Japanese.
 XX
 CC The invention relates to a novel method for identifying bacteria by
 CC amplifying DNA of the bacteria by PCR using a primer of specific
 CC sequence, electrophoresing the amplified DNA, obtaining an
 CC electrophoretic image and identifying whether the bacteria is a
 CC predetermined strain of *Escherichia coli*, *Bacillus* or *Shigella* by the
 CC appearance and position of DNA-fragment length within the electrophoretic
 CC image. The method of the invention may be useful for specifically
 CC identifying bacteria. The current sequence is that of the bacterial
 CC strain identification-related PCR primer of the invention.
 XX
 SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 49.5%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 49;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TCGCGCTGTGG 13
 Db 1 TCGCGCTTGG 11
 RESULT 23
 ADR05232
 ID ADR05232 standard; DNA; 12 BP.
 XX
 AC ADR05232;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Wilting bacterial-disease resistance carnation PCR primer, SEQ ID 2.
 XX
 KW Wilting bacterial-disease resistance; carnation; primer; PCR; ss.
 XX
 OS Unidentified.
 XX
 PN JP2004222532-A.
 XX
 PD 12-AUG-2004.
 XX
 PF 20-JAN-2003; 2003JP-00011119.
 XX
 PR 20-JAN-2003; 2003JP-00011119.
 XX
 PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 XX
 DR WPI; 2004-585595/57.
 XX
 XX Novel oligonucleotide useful for identifying wilting bacterial-disease
 PT resistance carnation and for selecting wilting bacterial-disease
 PT resistance carnation.
 XX
 PS Claim 1; SEQ ID NO 2; 14pp; Japanese.
 XX
 CC The invention relates to a novel oligonucleotide for selecting a wilting
 CC bacterial-disease resistance carnation. The oligonucleotide for selecting
 CC a wilting bacterial-disease resistance carnation is selected from
 CC ADR05232, ADR05233, ADR05234, ADR05235 or ADR05237. The
 CC oligonucleotide is useful for identifying a wilting bacterial-disease
 CC resistance carnation, which involves extracting DNA from the carnation,
 CC using it as a template, performing amplification of the DNA by PCR using
 CC one or a combination of the oligonucleotides, and carrying out
 CC electrophoresis analysis of the obtained amplified product. This
 CC polynucleotide sequence represents a wilting bacterial-disease resistance

CC carnation primer oligo of the invention.
 XX
 SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 49.5%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 49;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TCGCGCTGTGG 13
 Db 1 TCGCGCTTGG 11
 RESULT 24
 ADZ39909
 ID ADZ39909 standard; DNA; 12 BP.
 XX
 AC ADZ39909;
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE Primer used in bacteria detection #8.
 XX
 KW bacteria; primer; ss.
 XX
 OS Unidentified.
 XX
 PN JP2003265198-A.
 XX
 PD 24-SEP-2003.
 XX
 PF 19-MAR-2002; 2002JP-00075994.
 XX
 PR 19-MAR-2002; 2002JP-00075994.
 XX
 PA (SAOL) SANYO ELECTRIC CO LTD.
 XX
 DR WPI; 2004-084978/09.
 XX
 DE Identifying bacteria involves amplifying DNA fragment of bacteria by PCR
 PT using twelve kinds of primers specific sequence, subjecting amplified DNA
 PT to electrophoresis and identifying bacteria based on electrophoresis
 PT result.
 XX
 PS Claim 1; SEQ ID NO 8; 18pp; Japanese.
 XX
 CC The present invention relates to identifying bacteria by amplifying DNA
 CC fragments from bacteria by PCR using twelve kinds of primers, is new. The
 CC method and the associated apparatus are useful for identifying bacteria
 CC such as food poisoning bacteria. The detection and identification of
 CC bacteria is performed easily in short time. The present sequence
 CC represents a primer of the invention.
 XX
 SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 49.5%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 49;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TCGCGCTGTGG 13
 Db 1 TCGCGCTTGG 11
 RESULT 25
 ABH32686
 ID ABH32686 standard; DNA; 13 BP.
 XX
 AC ABH32686;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 232663 for detecting SNP TSC0056734.

```

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 232663; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 1 C; 8 G; 1 T; 0 U; 0 Other;
XX
Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 2 TGGGGCGAAGG 12
||| |||||
|| |||||

RESULT 26
ABC86975/c
ID ABC86975 standard; DNA; 13 BP.
XX
AC ABC86975;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 86992 for detecting SNP TSC0021858.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PS Claim 1; SEQ ID NO 63161; 29pp + Sequence Listing; German.

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PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 86992; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 11 TGTGGCGAAGG 1
||||| |||||

RESULT 27
ABC63144
ID ABC63144 standard; DNA; 13 BP.
XX
AC ABC63144;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 63161 for detecting SNP TSC0016688.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 63161; 29pp + Sequence Listing; German.

```


XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
 SQ Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
 |||||
 Db 2 TTGTGGCGAAGG 12

RESULT 28
 ABH65141/C
 ID ABH65141 standard; DNA; 13 BP.
 AC ABH65141;
 XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 265118 for detecting SNP TSC0064243.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 265118; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 2 A; 6 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
 |||||
 Db 12 TTGTGGCGAAGG 2

RESULT 29
 ABC53131/C
 ID ABC53131 standard; DNA; 13 BP.
 AC ABC53131;
 XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 53148 for detecting SNP TSC0014679.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 53148; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 1 Other;
 Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
 |||||
 Db 12 TTGTGGCGAAGG 2

RESULT 30

XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 53147; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 1 Other;
 SQ
 Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 TGTGGCGAAGG 19
 Db 2 TGTGGCGAAGG 12
 |||||
 RESULT 33
 ABF04975/C
 ID ABF04975 standard; DNA; 13 BP.
 XX
 XX ABF04975;
 AC
 XX 21-FEB-2002 (first entry)
 DT
 XX Oligonucleotide SEQ ID NO 104972 for detecting SNP TSC0026284.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 104972; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 TGTGGCGAAGG 19
 Db 13 TGTGGCGAAGG 3
 |||||
 RESULT 34
 ABH19540
 ID ABH19540 standard; DNA; 13 BP.
 XX
 XX ABH19540;
 AC
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide SEQ ID NO 219517 for detecting SNP TSC0053391.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 219517; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;

```

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 2 TGTGGCGAAGG 12

RESULT 35
ABH19543/c
ID ABH19543 standard; DNA; 13 BP.
XX AC ABH19543;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 219520 for detecting SNP TSC0053391.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPTG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 219520; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 6 C; 3 T; 0 G; 0 U; 0 Other;
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 6 C; 3 T; 0 G; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TGTGGAGAAGG 2

RESULT 36
ABF16163/c
ID ABF16163 standard; DNA; 13 BP.
XX AC ABF16163;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 219519 for detecting SNP TSC0053391.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPTG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 219520; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 6 C; 3 T; 0 G; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TGTGGAGAAGG 2

RESULT 37
ABH19542
ID ABH19542 standard; DNA; 13 BP.
XX AC ABH19542;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 219519 for detecting SNP TSC0053391.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.

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DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 116160 for detecting SNP TSC0029108.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPTG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 116160; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 8 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TGTGGCGAAGG 2

RESULT 37
ABH19542
ID ABH19542 standard; DNA; 13 BP.
XX AC ABH19542;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 219519 for detecting SNP TSC0053391.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.

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XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 219519; 29pp + Sequence Listing; German.
XX PS
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 49.5%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 46;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 9 TGTGGCGAAGG 19
XX Db 2 TGTGGAGAAGG 12
XX
XX RESULT 38
XX ABF04974
XX ID ABF04974 standard; DNA; 13 BP.
XX AC ABF04974;
XX XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 104971 for detecting SNP TSC0026284.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 219519; 29pp + Sequence Listing; German.
XX PS
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 49.5%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 46;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 9 TGTGGCGAAGG 19
XX Db 2 TGTGGAGAAGG 12
XX
XX RESULT 38
XX ABF04974
XX ID ABF04974 standard; DNA; 13 BP.
XX AC ABF04974;
XX XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 104971 for detecting SNP TSC0026284.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 219519; 29pp + Sequence Listing; German.
XX PS
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 49.5%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 46;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 9 TGTGGCGAAGG 19
XX Db 2 TGTGGAGAAGG 12
XX
XX RESULT 38
XX ABF04974
XX ID ABF04974 standard; DNA; 13 BP.
XX AC ABF04974;
XX XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 63162 for detecting SNP TSC0016688.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 63162; 29pp + Sequence Listing; German.
XX PS
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 49.5%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 46;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 9 TGTGGCGAAGG 19
XX Db 1 TGTGGAGAAGG 11
XX
XX RESULT 39
XX ABC63145/c
XX ID ABC63145 standard; DNA; 13 BP.
XX AC ABC63145;
XX XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 63162 for detecting SNP TSC0016688.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 63162; 29pp + Sequence Listing; German.
XX PS
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

```

methylation status.

Claim 1; SEQ ID NO 104971; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19

Db 1 TGTGGAGAAGG 11

RESULT 39

ABC63145/c

ID ABC63145 standard; DNA; 13 BP.

AC ABC63145;

DT 21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 63162 for detecting SNP TSC0016688.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 63162; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence

```

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match      49.5%; Score 9.4; DB 1; Length 13;
  Best Local Similarity 90.9%; Pred. No. 46;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
   |||||
Db 12 TTGTGGCGAAG 2

RESULT 40
ID ABF16162
XX ABF16162 standard; DNA; 13 BP.
AC ABF16162;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 116159 for detecting SNP TSC0029108.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 116159; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 1 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match      49.5%; Score 9.4; DB 1; Length 13;
  Best Local Similarity 90.9%; Pred. No. 46;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
   |||||
Db 2 TTGTGGCGGAG 12

RESULT 41
ID ABF16245/c
XX ABF16245 standard; DNA; 13 BP.
AC ABF16245;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 116242 for detecting SNP TSC0029111.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 116242; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;

  Query Match      49.5%; Score 9.4; DB 1; Length 13;
  Best Local Similarity 90.9%; Pred. No. 46;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
   |||||
Db 12 TTGTGGTGAAG 2

RESULT 42
ID ABC76993/c
XX ABC76993 standard; DNA; 13 BP.
AC ABC76993;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 77010 for detecting SNP TSC0019655.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 77010; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 1 Other;
 SQ Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTCCGCGCTGTG 12
 Db ||||| |||||
 12 GTCCGCGTTGTG 2
 RESULT 43
 ABC76992
 ID ABC76992 standard; DNA; 13 BP.
 XX ABC76992;
 AC 21-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 77009 for detecting SNP TSC0019655.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 86991; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 77009; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 1 A; 2 C; 5 G; 4 T; 0 U; 1 Other;
 SQ Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTCCGCGCTGTG 12
 Db ||||| |||||
 2 GTCCGCGTTGTG 12
 RESULT 44
 ABC86974
 ID ABC86974 standard; DNA; 13 BP.
 XX ABC86974;
 AC 21-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 86991 for detecting SNP TSC0021858.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 86991; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
 |||||
 Db 3 TGTGGCGAAGG 13

RESULT 45
 ABH19541/c
 ID ABH19541 standard; DNA; 13 BP.
 XX
 AC ABH19541;
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 219518 for detecting SNP TSC0053391.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPITG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 219518; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
 |||||
 Db 12 TGTGGCGAAGG 2

RESULT 46
 ABF03963/c
 ID ABF03963 standard; DNA; 13 BP.
 XX
 AC ABF03963;
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 103960 for detecting SNP TSC0025999.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPITG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 103960; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 5 A; 5 C; 2 G; 0 T; 0 U; 1 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGCTGT 11
 |||||
 Db 13 GGTGCGCTGT 3

RESULT 47
 ABH65140
 ID ABH65140 standard; DNA; 13 BP.


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PT oxide layer having thickness that may vary to wavelength of excitation
PS light used.
XX
XX Example 1; SEQ ID NO 16; 20pp; English.
XX The present invention relates to a novel substrate having an oxide layer,
CC which is useful in optically detecting a target material. The thickness
CC of the oxide layer may vary to the wavelength of excitation. The light used.
CC Also claimed is a method for detecting a target material, comprising
CC immobilizing a probe material on a substrate, reacting the immobilized
CC probe material and the target material, illuminating a reaction product
CC with excitation light, and measuring light emitted from the reaction
CC product by the excitation light. In an example from the invention, on
CC microarrays were fabricated by forming fused silica (SiO2) layers on
CC silicon wafers, followed by linkage with a coupling agent and
CC immobilization of oligonucleotide probes. The microarrays were then
CC incubated with labeled oligonucleotides and exposed to excitation light,
CC and light emitted from the target oligonucleotides was measured, to
CC evaluate the intensity of detected signals with respect to the thickness
CC of the SiO2 layers. ADZ85128-ADZ85203, MODY 3 diabetes-associated probes
CC used with the target sequence of human glyceraldehyde-3-phosphate
CC dehydrogenase (GAPDH), were used to show that when a target
CC oligonucleotide is detected using a microarray including a substrate with
CC an oxide layer a good signal is obtained compared to that with no oxide
CC layers.
XX
SQ Sequence 13 BP; 0 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
      Query Match      49.5%; Score 9.4; DB 1; Length 13;
      Best Local Similarity 90.9%; Pred. No. 46;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCQCGCTGTGG 13
Db 3 TCQCGCTGTGG 13
      || |||||

RESULT 50
AAT94476/c
ID AAT94476 standard; DNA; 10 BP.
XX
AC AAT94476;
XX
XX 03-MAR-1998 (first entry)
XX
DE Human Fchd540 gene reverse PCR primer.
XX
KW Fchd540 gene; differential expression; endothelial cell; human;
KW shear stress; cardiovascular disease; atherosclerosis; ischaemia;
KW reperfusion; hypertension; restenosis; arterial inflammation; therapy;
KW diagnosis; drug screening; marker; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9730065-A1.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US002291.
XX
XX 16-FEB-1996; 96US-0011787P.
XX
XX 13-FEB-1997; 97US-00799910.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Falb DA;
XX
XX WPI; 1997-424966/39.
XX
XX New genes differentially expressed in cardiovascular disease - used for
PT diagnosis, drug screening and treatment of cardiovascular disease, e.g.
PT atherosclerosis, restenosis, hypertension, etc.

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XX Example 6.1.3; Page 120; 163pp; English.
XX This oligonucleotide comprises a reverse primer specific to the novel
CC human fchd540 gene (see AAT94468) that is up-regulated in endothelial
CC cells subjected to shear stress. It was used with primer for-T11XC in a
CC differential display paradigm used to detect genes that are
CC differentially expressed in endothelial cells under fluid shear stress.
CC Shear stress is thought to be responsible for the prevalence of
CC atherosclerotic lesions in areas of unusual circulatory flow. The novel
CC fchd540 gene can be used in the diagnosis and treatment of cardiovascular
CC disease
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
      Query Match      47.4%; Score 9; DB 1; Length 10;
      Best Local Similarity 100.0%; Pred. No. 74;
      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
Db 10 GTGGCGAAG 2
      |||||

RESULT 51
AAV34958/c
ID AAV34958 standard; DNA; 10 BP.
XX
AC AAV34958;
XX
XX 13-OCT-1998 (first entry)
XX
DE Synthetic Agaricus bisporus RAPD primer.
XX
KW Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.
XX
OS Synthetic.
XX
XX WO9821975-A1.
XX
XX 28-MAY-1998.
XX
XX 19-NOV-1996; 96WO-US018686.
XX
XX 19-NOV-1996; 96WO-US018686.
XX
XX (AMYC-) AMYCEL INC.
XX
XX Loftus MG, Lodder SC, Legg EJ;
XX WPI; 1998-312054/27.
XX
XX New strains of Agaricus bisporus with improved cap whiteness - compared
PT with the U1 strain but retaining other desirable features of this strain.
XX
XX Disclosure; Page 10; 26pp; English.
XX
XX The sequence is that of an RAPD (random amplified DNA) primer which was
CC used in the isolation of an Agaricus bisporus mushroom strain which has
CC whiter caps, less scaling than known strains, particularly for mushrooms
CC produced in the first break, so it is more valuable (suitable for
CC marketing fresh rather than canning). It also retains the desirable
CC characteristics (good cap shape and shelf life, thick stem and veil) of
CC the U1 strain
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
      Query Match      47.4%; Score 9; DB 1; Length 10;
      Best Local Similarity 100.0%; Pred. No. 74;
      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
      |||||

```

```

Db      10 GTGGCGAAG 2

RESULT 52
AAZ58826/c
ID      AAZ58826 standard; DNA; 10 BP.
XX
XX
AC      AAZ58826;
XX
XX      25-APR-2000 (first entry)
XX
XX      Human MUC11 gene amplifying primer.
XX
XX      Mucin; MUC11; MUC12; human; chromosome 7q22; epithelial inflammation;
KW      Crohn's disease; ulcerative colitis; asthma; chronic bronchitis;
KW      colorectal cancer; cystic fibrosis; inflammatory bowel disease;
KW      breast cancer; PCR primer; ss.
XX
XX      Homo sapiens.
XX
XX      WO200004142-A1.
XX
XX      27-JAN-2000.
XX
XX      16-JUL-1999; 99WO-AU000579.
XX
XX      16-JUL-1998; 98AU-00004708.
XX
XX      (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA      (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
XX
XX      Williams SJ, Antalis TM, McGuckin MA, Gotley DC;
XX      WPI; 2000-182416/16.
XX
XX      Novel MUC nucleic acid corresponding to mucin gene, useful for treating
PT      associated disease conditions e.g. colorectal, breast cancer, cystic
PT      fibrosis and inflammatory bowel disease.
XX
XX      Example 5; Page 38; 103pp; English.
XX
XX      The invention provides mucin genes (MUC11 and MUC12) located on human
CC      chromosome 7q22. The mucin genes or its portion is used in detecting
CC      polymorphism, mutation, deletion, truncation and expansion in the gene or
CC      its gene transcript. Pharmaceutical compositions and gene therapy
CC      constructs comprising the mucin genes are used for treating disease
CC      conditions associated with aberrant Mucin expression, altered properties
CC      of mucus or epithelial inflammatory processes involving Mucins like
CC      Crohn's disease, ulcerative colitis, asthma, chronic bronchitis and
CC      colorectal cancer, cystic fibrosis, inflammatory bowel disease and breast
CC      cancer. The mucin genes and the polypeptides are used for determining
CC      these diseases or their predisposition. The MUC11 and MUC12 polypeptides
CC      are used for preparing antagonist and antibodies. The present sequence
CC      represents a primer for amplifying the human MUC11 gene
XX
XX      Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match      47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GTGGCGAAG 18
        |||||
Db      10 GTGGCGAAG 2

RESULT 53
AAZ50718/c
ID      AAZ50718 standard; DNA; 10 BP.
XX
XX
AC      AAZ50718;
XX
XX      31-MAY-2000 (first entry)
XX

```

```

XX      Reverse primer for differential display analysis of fchd540 gene.
XX
XX      PCR primer; fingerprint gene; human; cardiovascular disease;
KW      oncogenic disorder; diabetic retinopathy; fibroproliferative disorder;
KW      arteriosclerosis; TGF-beta signalling pathway; pancreatic cancer;
KW      angiogenesis; TGF; Transforming growth factor; inflammation; fibrosis;
KW      tumour growth; vascularisation; cytostatic; antidiabetic;
KW      ophthalmological; ss.
XX
XX      Homo sapiens.
XX
XX      WO200006206-A1.
XX
XX      10-FEB-2000.
XX
XX      30-JUL-1999; 99WO-US017394.
XX
XX      30-JUL-1998; 98US-00126640.
XX      (WILL-) MILLENNIUM PHARM INC.
XX      Falb DA;
XX
XX      WPI; 2000-205414/18.
XX
XX      Identifying substances for ameliorating symptoms of fibroproliferative
PT      diseases or oncogenic related disorders.
XX
XX      Example; Page 126; 214pp; English.
XX
XX      The patent discloses methods for the treatment and diagnosis of
CC      cardiovascular diseases by novel human genes (fingerprint genes) which
CC      are differentially expressed in different cardiovascular disease states.
CC      Compositions which can modify TGF-beta signalling pathway are identified
CC      by screening. These are used therapeutically to treat fibroproliferative
CC      and oncogenic disorders, especially TGF (Transforming growth factor) -
CC      beta related disorders, including diabetic retinopathy, inflammation,
CC      arteriosclerosis, pancreatic cancer, angiogenesis, fibrosis, tumour
CC      growth and vascularisation. The present sequence is the reverse PCR
CC      primer used to study the differential display of fingerprint gene,
CC      fchd540. Differential display was performed on endothelial cells
CC      subjected to laminar shear stress compared with static control. fchd540
CC      was detected as up-regulated under shear stress
XX
XX      Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match      47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GTGGCGAAG 18
        |||||
Db      10 GTGGCGAAG 2

RESULT 54
ABL60664/c
ID      ABL60664 standard; DNA; 10 BP.
XX
XX
AC      ABL60664;
XX
XX      27-AUG-2002 (first entry)
XX
XX      Panax species genomic DNA RAPD analysis primer OPC-20.
XX      Herbal; polymorphism; medicine; SCAR; rapid amplified polymorphic DNA;
KW      plant; RAPD; primer; ss.
XX
XX      Panax sp.
XX
XX      WO200236805-A2.
XX

```

PD 10-MAY-2002.
 XX
 PF 17-OCT-2001; 2001WO-US032602.
 XX
 PR 03-NOV-2000; 2000US-00706228.
 XX
 PA (UYCH-) UNIV CHINESE HONG KONG.
 XX
 PI Shaw P, Wang J, But PP, Ha W, Yau FCF;
 XX
 XX WPI; 2002-471504/50.
 DR
 PT Determining if an herbal material is of a *Mirabilis jalapa* or a *Panax*
 PT species, e.g. *P. ginseng*, or *P. quinquefolius*, comprises amplifying a
 PT polymorphic region of an extracted nucleic acid sequence using several
 PT primers.
 XX
 XX Example 3; Page 19; 50pp; English.
 PS
 CC The invention relates to determining whether a given herbal material is
 CC that of *Panax ginseng*, *P. quinquefolius*, *P. notoginseng* (Burk), *P.*
 CC *japonicus* major, *P. japonicus*, *P. trifolius*, *Mirabilis jalapa* L. or *P.*
 CC *cinosa* Roxb. The method involves amplifying a polymorphic region of the
 CC extracted nucleic acid using at least 2 different oligonucleotide primers
 CC that flank the polymorphic region. The method is useful for identifying
 CC ingredients in traditional Chinese medicines, and distinguishing them
 CC from common adulterants or ersatz ingredients, and for identifying an
 CC unknown sample as one of several possible known species, each
 CC characterized by the presence of a SCAR (sequence characterised amplified
 CC regions) absent from the others. The present sequence represents a primer
 CC for amplifying *Pinax* species genomic DNA, used for identification of
 CC polymorphic regions by RAPD (rapid amplified polymorphic DNA)
 CC fingerprinting
 XX
 XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 47.4%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 GTGGCGAAG 18
 Db 10 GTGGCGAAG 2
 |||||
 RESULT 55
 ABV69628
 ID ABV69628 standard; cDNA; 11 BP.
 XX
 AC ABV69628;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 7414.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antisborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-BP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX

DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 232; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 0 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 47.4%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GCGCTGTGG 13
 Db 3 GCGCTGTGG 11
 |||||
 RESULT 56
 ABI04019/c
 ID ABI04019 standard; DNA; 12 BP.
 XX
 AC ABI04019;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 303992 for detecting SNP TSC0020735.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB0000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 303992; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 47.4%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAA 17
 |||||
 DB 10 TGTGGCGAA 2

RESULT 57

AAV65455/c

ID AAV65455 standard; DNA; 12 BP.

AC AAV65455;

XX 08-DEC-1998 (first entry)

DT Primer pBS800-23J used in the course of the invention.

DE Nucleic acid determination; hybridisation; probe; mismatch; SBH;

KW sequencing by hybridisation; PCR primer; ss.

XX Synthetic.

OS JP10243785-A.

PN 14-SEP-1998.

PD 03-MAR-1997; 97JP-00047821.

PF 03-MAR-1997; 97JP-00047821.

PR (BUNS-) BUNSHI BIOHOTOINICS KENKYUSHO KK.

XX WPI; 1998-549781/47.

XX Determination of nucleic acid base sequence - is sensitive and rapid
 PT without mismatch in hybridisation as in sequencing by hybridisation
 PT method.

XX Example; Page 9; 20pp; Japanese.

XX Sequences shown in AAV65401 to AAV65580 represent PCR primers used in the
 CC course of the invention which provides a method for determining a single
 CC stranded nucleic acid base sequence. The method comprises separation of
 CC 4k oligonucleotide probe as a primer from all combinations of k base
 CC sequences and hybridising the probe and the nucleic acid to be tested.
 CC The probe is elongated to make a primer using the nucleic acid to be
 CC tested as a template and the elongated primer is determined. The base
 CC sequence of the nucleic acid is determined based on the elongated amount.
 CC The method allows sensitive and rapid determination of nucleic acid base
 CC sequence without mismatch in hybridisation as in sequencing by
 CC hybridisation (SBH) method

XX Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 46.3%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CGCTGTGGCGAA 17
 |||||
 DB 12 CGCTGTGGCGAA 1

RESULT 58

ABI59311/c

ID ABI59311 standard; DNA; 12 BP.

XX ABI59311;

XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 359284 for detecting SNP TSC0008283.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 359284; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 46.3%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGTGTGGCG 15
 |||||
 DB 12 CGCGTGTGGCG 1

RESULT 59

ABI24865/c

ID ABI24865 standard; DNA; 12 BP.

XX ABI24865;

XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 324838 for detecting SNP TSC003252.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 PD 18-OCT-2001.
 XX
 XX PF 06-APR-2001; 2001WO-IB0000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX PS Claim 1; SEQ ID NO 324838; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABR00010-ABR2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 46.3%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 GCTGTGGCGAAG 18
 Db | ||||| ||
 12 GATGTGGCGGAG 1
 RESULT 60
 ABH89194
 ID ABH89194 standard; DNA; 12 BP.
 AC
 AC ABH89194;
 XX
 XX DT 22-FEB-2002 (first entry)
 XX
 XX DE Oligonucleotide primer SEQ ID NO 289187 for detecting SNP TSC0013829.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 PD 18-OCT-2001.
 XX
 XX PF 06-APR-2001; 2001WO-IB0000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX PS Claim 1; SEQ ID NO 289187; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABR00010-ABR2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 12 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 46.3%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 GCGTGTGGCGGA 16
 Db | ||||| ||
 1 GGGTGTGGCGGA 12
 RESULT 61
 ABX10162
 ID ABX10162 standard; cDNA; 12 BP.
 XX
 AC ABX10162;
 XX
 XX DT 27-JAN-2003 (first entry)
 XX
 XX DE Human TIGR/Myocilin variant cDNA deletion 3' flank #5.
 KW Human; ss; TIGR; MYOC; Myocilin; Glaucoma; blindness;
 KW trabecular meshwork inducible glucocorticoid responsive protein;
 KW retinal degenerative disease; RDD; retinitis pigmentosa;
 KW macular degeneration; Usher syndrome; cardiovascular disease;
 KW congenital heart disease; myocardial ischaemia; stroke;
 KW acute endocarditis; hypertensive heart disease; arrhythmia;
 KW arteriosclerotic heart disease.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200282969-A2.
 XX
 XX PD 24-OCT-2002.
 XX
 XX PF 11-DEC-2001; 2001WO-US048622.
 XX
 XX PR 05-APR-2001; 2001US-0281442P.
 XX PR 23-JUL-2001; 2001US-0306899P.
 XX
 XX PA (KONG/) KONG T H.
 XX
 XX PI Kong TH;
 XX
 XX DR WPI; 2003-058597/05.
 XX
 XX PT Determining the presence or the risk of having glaucoma, retinal
 PT degenerative or cardiovascular diseases in a subject, comprises

PT generating transcriptional or translational profiles based on myocilin
 XX nucleic acids and proteins.

PS Disclosure; Fig 4c; 55pp; English.

XX The invention relates to determining whether a subject has or is at risk
 CC of developing glaucoma, retinal degenerative disease, or a cardiovascular
 CC disease, comprising generating a transcriptional or translational profile
 CC (i.e. 'fingerprint') in the subject or in a sample obtained from the
 CC subject, based on the expression of the different myocilin (MYOC, also
 CC known as trabecular meshwork inducible glucocorticoid responsive protein,
 CC TIGR) mRNA species or polypeptide forms, where a difference in the
 CC profile relative to that in a normal subject indicates that the subject
 CC has or is at risk of developing the above-mentioned diseases. Also
 CC included are: (1) a method for establishing MYOC genetic population
 CC profile in a population of individuals having glaucoma, retinal
 CC degenerative disease, or a cardiovascular disease; (2) a method for
 CC pharmacogenomically selecting a therapy to administer to an individual
 CC having glaucoma, retinal degenerative disease, or a cardiovascular
 CC disease, comprising determining MYOC genetic profile of an individual
 CC comparing the individual's MYOC genetic profile to MYOC genetic
 CC population profile, to select a therapy for administration to the
 CC individual; and a kit for determining whether a subject has or is likely
 CC to develop glaucoma, retinal degenerative disease, or a cardiovascular
 CC disease, comprising a probe or primer which hybridizes to the MYOC
 CC nucleic acid, or an antibody or peptide probe capable of specifically
 CC binding to the novel MYOC polypeptide(s), and instructions for use. The
 CC method is useful for the prognosis and/or diagnosis of glaucoma, retinal
 CC degenerative diseases (RDD) or cardiovascular diseases (e.g. blindness,
 CC retinitis pigmentosa, macular degeneration, Usher syndrome, congenital
 CC heart disease, myocardial ischaemia, stroke, acute endocarditis,
 CC hypertensive heart disease, arrhythmia and arteriosclerotic heart
 CC disease), and in screening assays for the identification of therapeutics
 CC and the evaluation of their effectiveness for treating the above-
 CC mentioned diseases in a subject. The present sequence represents the 3'
 CC flanking sequence surrounding the deletion present in a MYOC cDNA variant
 XX

SQ Sequence 12 BP; 0 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 46.3%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGCC 14
 Db 1 TCGCGCTGTGCC 12

RESULT 62
 ADW86997
 ID ADW86997 standard; DNA; 12 BP.

XX AC ADW86997;

XX DT 07-APR-2005 (first entry)

XX DE Protein labelling method sequence #199.

XX KW DNA purification; protein engineering; diagnosis; ss.

XX OS Unidentified.

XX PN WO2004113530-A1.

XX PD 29-DEC-2004.

XX PF 18-JUN-2004; 2004WO-JP008953.

XX PR 18-JUN-2003; 2003JP-00173634.

XX PA (MITU) MITSUBISHI CHEM CORP.

XX PI Naka D, Nakano H, Shiratori M, Kobayashi T, Suzuki K;

PI Hashimoto H, Sasaki T;

XX WPI; 2005-075248/08.

XX Novel polynucleotide having ability to increase labeling efficiency of
 PT labeling compound, useful for synthesizing labeled protein in presence of
 PT labeling compound.

PS Disclosure; Fig 20; 140pp; Japanese.

XX The invention relates to a polynucleotide (I) for synthesizing labeled
 CC protein and having ability to increase labeling efficiency of labeling
 CC compound, where protein is produced by adding labeling compound to 3',
 CC terminal of sequence encoding target protein of gene template, where
 CC labeling compound has label portion and acceptor portion having compound
 CC capable of binding to C-terminus of label portion and translating gene
 CC template in presence of labeled compound. (I) is useful for producing a
 CC labeling protein, which involves preparing a gene template by adding (I)
 CC to the 3'-terminal of base sequence encoding the target protein,
 CC translating the gene template in the presence of the labeling protein,
 CC containing acceptor portion and label portion, and obtaining protein
 CC synthesized in the translation system. The base sequence encoding the
 CC target protein either contains the termination codon or does not contain
 CC the termination codon. The labeling compound is added after the
 CC initiation of the translation. The labeled protein (LPI) is useful in a
 CC performance-analysis of a protein, which involves contacting the test
 CC substance with (LPI), and analyzing the interaction between the protein
 CC and the test substance. (I) has the ability to increase labeling
 CC efficiency of a labeling compound and thus effectively produces labeled
 CC protein. This sequence corresponds to a sequence used in the method of
 CC the invention.

SQ Sequence 12 BP; 2 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 46.3%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTGGCGAAG 18
 Db 1 GCGGCGCGGAAG 12

RESULT 63

AAZ77822/c

ID AAZ77822 standard; DNA; 10 BP.

XX AC AAZ77822;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:250.

XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN WO9965924-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013800.

XX PR 19-JUN-1998; 98US-0089833P.

XX PR 19-JUN-1998; 98US-0089844P.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089878P.

XX PR 19-JUN-1998; 98US-0089991P.

XX PR 19-JUN-1998; 98US-0089992P.

XX PR 19-JUN-1998; 98US-0089993P.

PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090003P.
 PR 19-JUN-1998; 98US-00900036P.
 PR 19-JUN-1998; 98US-00900039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX
 (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 DR
 XX
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 PT
 XX Claim 1; Page 71; 130pp; English.
 PS
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing and
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTGGCGCTG 10
 Db |||||||
 10 GGGCGCGCTG 1
 RESULT 64
 AAZ77845
 ID AAZ77845 standard; DNA; 10 BP.
 XX
 AC AAZ77845;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:273.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965924-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-008991P.
 PR 19-JUN-1998; 98US-008992P.
 PR 19-JUN-1998; 98US-008993P.
 PR 19-JUN-1998; 98US-008994P.
 PR 19-JUN-1998; 98US-008997P.
 PR 19-JUN-1998; 98US-008999P.
 PR 19-JUN-1998; 98US-009000P.
 PR 19-JUN-1998; 98US-009003P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX
 (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 DR
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 PT
 XX Claim 1; Page 72; 130pp; English.
 PS
 XX

CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGGG 15
 Db 1 CGCTGTGGGG 10

RESULT 65

AAZ84021
 ID AAZ84021 standard; DNA; 10 BP.

AC AAZ84021;

XX 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #3255.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX (GENZ) GENZYME CORP.

PA

PA (ROBE/) ROBERTS B L.

XX (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

PT Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and

PT treatment of cancer.

XX Claim 1; Page 146; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ8677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of

CC e.g. therapeutic genes (also ribozymes or antisense sequences),

CC particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in

CC vaccines; for diagnosing breast cancer and for raising specific

CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic

CC agents. Host cells that produce the polypeptides can be used to expand

CC and isolate populations of educated, antigen-specific immune effector

CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive

CC immunotherapy

XX SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19

Db 1 GTGGCGAAGG 10

RESULT 66

AAZ85539/c

ID AAZ85539 standard; DNA; 10 BP.

XX AC AAZ85539;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #4773.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

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XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 186; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
Db |||||
10 GCGCTGAGGC 1

RESULT 67
AAZ84999/c
ID AAZ84999 standard; DNA; 10 BP.
XX
XX AAZ84999;
AC
XX
DT 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #4233.
DE
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
OS
XX WO9965928-A2.
PN
XX
XX 23-DEC-1999.
PD
XX
XX 18-JUN-1999; 99WO-US013647.
PF
XX
XX 19-JUN-1998; 98US-0089853P.
PR
XX 19-JUN-1998; 98US-008997P.
PR
XX 19-JUN-1998; 98US-0090039P.
PR

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PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 171; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGGCTG 10
Db |||||
10 GGGCGGCTG 1

RESULT 68
AAZ85922
ID AAZ85922 standard; DNA; 10 BP.
XX
XX AAZ85922;
AC
XX
DT 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #5156.
DE
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
OS
XX WO9965928-A2.
PN
XX
XX 23-DEC-1999.
PD
XX
XX 18-JUN-1999; 99WO-US013647.
PF
XX 19-JUN-1998; 98US-0089853P.
PR
XX 19-JUN-1998; 98US-008997P.
PR
XX 19-JUN-1998; 98US-0090039P.
PR

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XX 18-JUN-1999; 99WO-US013647.
PF 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
PI WPI; 2000-106079/09.
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX Claim 1; Page 148; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
SQ Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGCGCTG 10
Db ||| |||||
10 GGTGCGCGCTG 1

RESULT 71
AAH64063/c
ID AAH64063 standard; cDNA; 10 BP.
XX AAH64063;
AC AAH64063;
XX 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 903.
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
OS WO200138577-A2.
PN
XX
```

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PD 31-MAY-2001.
XX 21-NOV-2000; 2000WO-US01922.
XX 24-NOV-1999; 99US-00448480.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX Claim 13; Page 59; 94pp; English.
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
SQ Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGCGCTG 10
Db ||| |||||
10 GGTGCGCGCTG 1

RESULT 72
AAH42948
ID AAH42948 standard; DNA; 10 BP.
XX AAH42948;
AC AAH42948;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11087.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
```

PS Example; Page 346; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

SQ Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGTGTG 12
||| |||||
Db 1 TCGTGTGTG 10

RESULT 73
AAF41527
ID AAF41527 standard; DNA; 10 BP.
XX AAF41527;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8266.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
PT Example; Page 295; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

SQ Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGCGGAA 17
||| |||||
Db 1 CTGTGCGTGA 10

RESULT 74
ABL88334/c
ID ABL88334 standard; DNA; 10 BP.
XX ABL88334;
XX 20-MAY-2002 (first entry)
XX Human CHRNE gene polymorphism detection primer, SEQ ID NO:68.
XX Human; cholinergic receptor nicotinic epsilon polypeptide; CHRNE;
KW chromosome 17p13-12; acetylcholine receptor; ACHR;
KW neuromuscular junction; skeletal muscle; postnatal development;
KW congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype;
KW genetic variant; single nucleotide polymorphism; SNP; gene therapy;
KW drug screening; primer extension; primer; ss.
XX Homo sapiens.
XX WO200198316-A2.
XX 27-DEC-2001.
XX 20-JUN-2001; 2001WO-US019835.
XX 20-JUN-2000; 2000US-0212870P.
XX (GENA-) GENAISSANCE PHARM INC.

PI Amaro E, Bieglecki KM, Kliem SE, Koshy B, Tanguay DA;
 XX WPI; 2002-130787/17.
 XX
 XX Novel genetic variants of cholinergic receptor, nicotinic, epsilon
 PT polypeptide gene useful in studying expression and function of the
 PT protein, and for screening drugs to treat diseases e.g. congenital
 PT myasthenic syndrome.
 XX
 XX Claim 19; Page 15; 104pp; English.
 XX
 CC The invention relates to a method for haplotyping the cholinergic
 CC receptor, nicotinic, epsilon polypeptide (CHRNE) gene (ABL88268) of an
 CC individual, and also describes 17 novel polymorphic sites within the
 CC human CHRNE gene. The CHRNE gene is located on chromosome 17p13-12 and
 CC contains 12 exons which encode a 493 amino acid protein (ABB49112). The
 CC CHRNE protein is one of the 5 subunits of mammalian acetylcholine
 CC receptors (AChRs) found at neuromuscular junctions in juveniles and
 CC adults, and is essential for the normal postnatal development of skeletal
 CC muscle. Mutations in the CHRNE gene are associated with congenital
 CC myasthenic syndrome (CMS). CHRNE gene sequences can therefore be used in
 CC gene therapy. The CHRNE gene is also useful for studying the expression
 CC and function of CHRNE, and in expressing CHRNE protein for use in
 CC screening for candidate drugs to treat diseases related to CHRNE. The
 CC method of the invention is useful for haplotyping the CHRNE gene in an
 CC individual, and can also be used in pharmaceutical research to validate
 CC CHRNE as a candidate target for, and in design of clinical trials of
 CC candidate drugs for, treating a specific condition or disease
 CC predicted to be associated with CHRNE activity such as CMS. Polymorphisms
 CC in the target region may be determined by the use of allele-specific
 CC oligonucleotides (ASOs; ABL88370-ABL88320) as probes and primers, and by
 CC primer extension using oligonucleotide primers comprising sequences
 CC ABL88371-ABL88354. The CHRNE protein is useful for improving the
 CC efficiency and reliability of several steps in the discovery and
 CC development of drugs for treating diseases associated with CHRNE
 CC activity, and may be used to screen drugs which target CHRNE. Sequences
 CC ABL88321-ABL88354 represent sequences that are specifically claimed as
 CC components of primers used to detect polymorphisms in the CHRNE gene by
 CC primer extension
 XX
 XX Sequence 10 BP; 2 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 44.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 TGTGGCGAAG 18
 Db ||||| |||||
 10 TGTGGGGAAG 1
 RESULT 75
 ABN87962
 ID ABN87962 standard; DNA; 10 BP.
 XX
 AC ABN87962;
 XX
 XX 12-AUG-2002 (first entry)
 DT
 XX Human GSR preferred oligonucleotide detection primer SEQ ID NO:81.
 DE
 XX Human; glutathione reductase; GSR; enzyme; haemolytic anaemia;
 KW gene therapy; antianaemic; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200242320-A2.
 XX
 XX 30-MAY-2002.
 PD
 XX 13-NOV-2001; 2001WO-US046473.
 PF
 XX 10-NOV-2000; 2000US-0247202P.
 PR

XX (GENA-) GENAISSANCE PHARM INC.
 PA Bieglecki KM, Sanchis A, Sausker EA, Sun X;
 XX WPI; 2002-471719/50.
 XX
 XX New genetic variants of Glutathione reductase isogenes, useful for
 PT improving efficiency and reliability in drug development for treating
 PT hemolytic anemia.
 XX
 XX Claim 16; Page 15; 137pp; English.
 XX
 CC The present invention describes genetic variants of the human glutathione
 CC reductase (GSR) gene (I). (I) has antianaemic activity and can be used in
 CC gene therapy. (I) can be used in screening for drugs targeting (I) that
 CC are useful for treating haemolytic anaemia. Methods from the present
 CC invention can be used: for improving the efficiency and reliability of
 CC several steps in the discovery and development of drugs for treating
 CC diseases associated with GSR activity; for haplotyping, which is also
 CC used by the pharmaceutical research scientist to validate GSR as a
 CC candidate target for treating a specific condition or disease. Predicted
 CC to be associated with GSR activity, e.g. haemolytic anaemia, and in the
 CC design of clinical trials for treating a specific condition of disease
 CC associated with GSR activity; and for screening compounds targeting GSR.
 CC (I) is useful in studying the expression and function of GSR, and in
 CC expressing GSR protein for use in screening for candidate drugs to treat
 CC diseases related to GSR activity. (I) is also useful in studying the
 CC effect of the variation on the biological activity of GSR as well as on
 CC the binding affinity of candidate drugs targeting GSR for the treatment
 CC of haemolytic anaemia. The present sequence represents a preferred
 CC oligonucleotide detection primer for the human GSR gene, which is given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCGCTGTGGC 14
 Db ||||| |||||
 1 GCGCCGTGGC 10
 RESULT 76
 ABV78444/c
 ID ABV78444 standard; cDNA; 10 BP.
 XX
 AC ABV78444;
 XX
 XX 29-NOV-2002 (first entry)
 DT
 XX Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:155.
 DE
 XX SAGE tag; serial analysis of gene expression; human; Th1 cell;
 KW activated T cell; T lymphocyte; immune response; expression pattern;
 KW preferential expression; immune disorder; EST; expressed sequence tag;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002186482-A.
 XX
 PD 02-JUL-2002.
 XX
 XX 19-DEC-2000; 2000JP-00385816.
 PF
 XX 19-DEC-2000; 2000JP-00385816.
 PR
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA
 XX WPI; 2002-594261/64.
 DR

XX Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2-related diseases.
XX
XX
PS Claim 19; Page 10; 60pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are expressed in activated human Th1
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC lying nearest to the polyA region of cDNAs derived from a variety of
CC genes. These tags serve to uniquely identify each transcript and can thus
CC be used to analyse the pattern of gene expression in particular cell
CC types. The invention also relates to proteins encoded by the genes
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC inhibitors of the expression of groups of genes that are expressed in
CC either or both the two cell types. Groups of genes expressed in Th1
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC representing 171 genes which are more highly expressed in Th1 cells
XX compared with Th2 cells
XX
SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTCGCGCTG 10
DB 10 GGGCGCGCTG 1

RESULT 77
AAS97347/C
ID AAS97347 standard; DNA; 10 BP.
XX
AC AAS97347;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human CRYBB1 gene ASO primer extension PCR primer 3' end #6.
XX
KW Human; crystallin beta B1; CRYBB1; chromosome 22q12.1; ophthalmological;
KW cataract; allele specific oligonucleotide; ASO; ss; haplotype;
KW genotyping; transgenic animal; PCR primer; primer extension.
XX
OS Homo sapiens.
XX
PN WO200185998-A1.
XX
PD 15-NOV-2001.
XX
PF 07-MAY-2001; 2001WO-US014715.
XX
PR 05-MAY-2000; 2000US-0202253P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Kazemi A, Kliehm SE, Koshy B, Rounds E;
XX WPI; 2002-062253/08.
XX
DR Novel polymorphic variants of crystallin, beta B1 useful in studying
PT expression and function of the protein, useful for screening candidate
PT drugs to treat diseases e.g. cataract.
XX
PS Claim 17; Page 13; 94pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising a sequence
CC which is a polymorphic variant of a reference sequence for crystallin,
CC beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their fragment,
CC where the polymorphic variant comprises a CRYBB1 isogene defined by a

CC haplotype from haplotypes 1-16 as given in the specification. Also
CC included are a transgenic non-human animal transformed or transfected
CC with the polymorphic variant, a computer system for storing and analysing
CC polymorphism data for CRYBB1 gene, a genome anthology for the CRYBB1 gene
CC which comprises the defined CRYBB1 isogenes, methods of determining the
CC individuals haplotype or genotype as well as methods of determining an
CC association of a particular haplotype with a disease or trait and a
CC composition comprising at least one genotyping oligonucleotide
CC (especially allele-specific oligonucleotides (ASO)) for detecting a
CC polymorphism in the CRYBB1. The isogenes or haplotypes are useful for
CC improving the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated with
CC CRYBB1 activity, e.g. cataract, and can also be used by the
CC pharmaceutical research scientist to validate CRYBB1 as a candidate
CC target for, and in design of clinical trials of candidate drugs for,
CC treating a specific condition drugs or disease predicted to be associated
CC with CRYBB1 activity. The ASOs are useful as probes and primers, and for
CC assaying a polymorphism in the target region. The present sequence is the
CC allele specific 3' end of a PCR primer used in primer extension
CC experiment to detect polymorphisms in CRYBB1
XX
SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GCGCTGTGGC 14
DB 10 GCGCAGTGGC 1

RESULT 78
ABL45886
ID ABL45886 standard; DNA; 10 BP.
XX
AC ABL45886;
XX
DT 26-APR-2002 (first entry)
XX
DE Human EDG6 gene allele specific primer extension oligo SEQ ID NO: 80.
XX
KW Human; endothelial differentiation, G-protein coupled receptor 6; EDG6;
KW haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;
KW cytostatic; antiinflammatory; gene therapy; SNP;
KW single nucleotide polymorphism; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200206446-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022523.
XX
PR 17-JUL-2000; 2000US-0218727P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kliehm SE, Koshy B;
XX WPI; 2002-171804/22.
XX
DR New genetic variants of endothelial differentiation, G-protein coupled
PT receptor-6 gene for studying expression, function of the gene and
PT expressing EDG6 protein for use in screening drugs to treat cancer,
PT inflammation.
XX
PS Claim 18; Page 14; 111pp; English.
XX
XX The present invention provides the gene, protein and cDNA sequences of
CC the human endothelial differentiation, G-protein coupled receptor 6
CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found

CC within the sequences. The sequences can be used in the identification of
 CC the haplotype of an individual, and in the treatment of cancer,
 CC angiogenesis and inflammation. The present sequence is an allele specific
 CC primer extension oligonucleotide for the EDG6 gene, which is found on
 CC chromosome 19p13.3

XX SQ Sequence 10 BP; 0 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
 |||||
 DB 1 GCGCTGGGC 10

RESULT 79
 AB199149/c
 ID AB199149 standard; DNA; 10 BP.
 XX AC AB199149;
 XX DT 27-FEB-2002 (first entry)
 XX DE Human PCDH2 ASO PCR primer SEQ ID NO 106.
 XX KW Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;
 KW single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31;
 KW allele-specific oligonucleotide; ASO; PCR primer; ss.
 XX OS Homo sapiens.

XX PN WO200194361-A2.
 XX PD 13-DEC-2001.
 XX PF 06-JUN-2001; 2001WO-US018321.
 XX PR 06-JUN-2000; 2000US-0209564P.
 XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Kliem SE, Koshy B, Tanguay DA;
 XX WPI; 2002-097928/13.
 XX PT New protocadherin 2 (PCDH2) polymorphic variants and encoding genes,
 PT useful in expressing PCDH2 protein for screening candidate drugs to treat
 PT diseases related to PCDH2 activity.

XX PS Claim 18; Page 14; 127pp; English.
 XX CC The invention relates to haplotyping the protocadherin 2 (PCDH2) gene,
 CC comprising determining which of the haplotypes given in the specification
 CC defines one or both copies of the individual's PCDH2 gene. The
 CC polymorphisms are within a 30244 base pair sequence (ABA05413), fully
 CC defined in the specification. The polymorphic variants are useful in
 CC studying the expression and function of PCDH2, in expressing PCDH2
 CC protein for use in screening for candidate drugs to treat diseases such
 CC as cancer, related to PCDH2 activity, in studying the effect of the
 CC variation on the biological activity of PCDH2 and the binding affinity of
 CC candidate drugs targeting PCDH2. The haplotyping methods are useful in
 CC validating PCDH2 as a candidate target for treating a specific condition
 CC or disease predicted to be associated with PCDH2 activity or in the
 CC design of clinical trials of candidate drugs for treating a specific
 CC condition or disease associated with PCDH2 activity. The present sequence
 CC is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of
 CC the invention

XX SQ Sequence 10 BP; 2 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 81

Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCGCTGTGGC 14
 |||||
 DB 10 GCGCTGTGGC 1

RESULT 80
 AAD52054
 ID AAD52054 standard; DNA; 10 BP.
 XX AC AAD52054;
 XX DT 02-MAY-2003 (first entry)
 XX DE Human CES2 gene polymorphism detecting primer #8.

XX KW Human; carboxylesterase 2; CES2; drug screening; antiaddictive; cancer;
 KW transgenic; gene therapy; polymorphism; cytostatic; primer; ss.

XX OS Homo sapiens.
 XX PN WO200290378-A2.
 XX PD 14-NOV-2002.

XX PF 09-MAY-2002; 2002WO-US014813.
 XX PR 09-MAY-2001; 2001US-0289886P.
 XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Gilson CR, Kazemi A, Russo DP;
 XX WPI; 2003-148336/14.

XX PT New genetic variants of human carboxylesterase 2 (CES2) gene having
 PT polymorphisms, useful for screening drugs for treating disorders
 PT associated with CES2 isogene activity e.g. cancer or substance
 PT abuse/addiction.

XX PS Claim 32; Page 15; 85pp; English.

XX CC The invention relates to genetic variants of human carboxylesterase 2
 CC (CES2) gene. Polymorphic variants of CES2 gene are useful in studying the
 CC expression and function of CES2, and in expressing CES2 proteins for use
 CC in screening candidate drugs to treat diseases associated with CES2
 CC activity, e.g. cancer or substance abuse/addiction. Establishing CES2
 CC haplotype or haplotype pair of an individual is useful for improving the
 CC efficiency and reliability of several steps in the discovery and
 CC development of drugs for treating diseases associated with CES2 activity.
 CC Haplotype information is useful in improving the efficiency and output of
 CC several steps in drug discovery and development process, including target
 CC validation, identifying lead compounds, and early phase clinical trials.
 CC The transgenic animals are useful for studying expression of the CES2
 CC isogenes in vivo, for in vivo screening and testing of drugs targeted
 CC against CES2 protein, and for testing the efficacy of the therapeutic
 CC agents and compounds. CES2 gene is used in gene therapy. The present
 CC sequence is a primer used for detecting human CES2 gene polymorphisms

XX SQ Sequence 10 BP; 0 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCGCTGTGG 13
 |||||
 DB 1 CCGCTGTGG 10

ACA94569
 ID ACA94569 standard; DNA; 10 BP.
 XX AC
 XX ACA94569;
 XX 18-JUL-2003 (first entry)
 XX DE
 XX DNA tag from human transcript repressed in adenomas/cancers #102.
 XX KW
 XX Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.
 XX OS
 XX Homo sapiens.
 XX WO2003022863-A1.
 XX 20-MAR-2003.
 XX PF
 XX 09-SEP-2002; 2002WO-US028518.
 XX PR
 XX 07-SEP-2001; 2001US-0317494P.
 XX PR
 XX 30-MAY-2002; 2002US-0383805P.
 XX PA
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX PI
 XX Buckhaults P, Kinzler KW, Vogelstein B;
 XX WIPI; 2003-313220/30.
 XX DR
 XX Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.
 XX PS
 XX Disclosure; Page 29; 59pp; English.
 XX CC
 XX The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA
 CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
 CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces by
 CC detection of increased reaction product or decreased RDP substrate, and
 CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a
 CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or RDP substrate
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC repressed in colorectal cancer or colorectal adenoma
 XX SQ
 Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
 DB 1 CGCTGTGGCG 10

RESULT 82
 ADK13021
 ID ADK13021 standard; DNA; 10 BP.
 XX AC
 XX ADK13021;
 XX 20-MAY-2004 (first entry)
 XX DE
 XX Human glioma endothelial marker (GEM) standard tag SEQ ID NO:199.
 XX KW
 XX glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;
 KW anticancer; antiglioma; immune response; cytostatic;
 KW multi-drug sensitive glioma; human; standard tag; ss.
 XX OS
 XX Homo sapiens.
 XX OS
 XX Synthetic.
 XX PN
 XX WO2004016758-A2.
 XX PD
 XX 26-FEB-2004.
 XX XX
 XX 15-AUG-2003; 2003WO-US025614.
 XX PF
 XX 15-AUG-2002; 2002US-0403390P.
 XX PR
 XX 01-APR-2003; 2003US-0458978P.
 XX PA
 XX (GENZ) GENZYME CORP.
 XX PI
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX PI
 XX Madden SI, Wang CJ, Cook BP, Lattera J, Walter K;
 XX WIPI; 2004-247973/23.
 XX DR
 XX Diagnosing glioma by detecting expression product of any one of 255
 PT genes, glioma endothelial markers, in brain tissue sample suspected of
 PT being neoplastic, and comparing the expression with expression in normal
 PT brain tissue sample.

Example 2; SEQ ID NO 199; 114pp; English.

The present invention describes a method (M1) for aiding in the diagnosis
 of glioma. (M1) involves detecting an expression product of at least one
 gene (I) in a first brain tissue sample (T) suspected of being
 neoplastic, where (I) is chosen from any one of 255 genes (Glioma
 endothelial markers (GEMs)) as given in specification, and comparing the
 expression of (I) in (T) with expression of (I) in a second normal brain
 tissue sample (R), where increased expression of (I) in (T) relative to
 (R), identifies (T) as likely to be neoplastic. Also described: (1)
 treating (M2) glioma involves contacting cells of the glioma with an
 antibody that specifically binds to an extracellular epitope; (2)
 identifying (M3) a test compound as potential anticancer or antiglioma
 drug involves contacting a test compound with the cell which expresses
 (I), monitoring an expression product of the at least one gene and
 identifying test compound as a potential anticancer drug if it decreases
 the expression of at least one gene; (3) identifying (M4) a test compound
 as potential anticancer or antiglioma drug involves contacting a test
 compound with the cell which expresses mRNA of at least one gene
 identified by a tag as described above, monitoring mRNA of the gene, and
 identifying the test compound as a potential anticancer drug if it
 decreases the expression of at least one gene; and (4) inducing (M5) an
 immune response to glioma involves administering to a mammal, a protein
 or (I). (I) have cytostatic activities, and can be used to trigger immune
 destruction of glioma cells, and as immune response inducers. (M1) is
 useful for aiding in diagnosing glioma. (M2) is useful for treating multi

CC -drug sensitive glioma in a human. (MS) is useful for inducing an immune
 CC response to a glioma in a mammal having glioma or in a mammal who has had
 CC a glioma surgically removed. The present sequence represents a human GEM
 CC standard tag oligonucleotide, which is used in the exemplification of the
 CC present invention.

XX Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
 Db 1 CGCTGTGGGG 10

RESULT 83

AAN20067/c
 ID AAN20067 standard; DNA; 11 BP.

XX AC AAN20067;

XX 25-MAR-2003 (revised)

DT 21-SEP-1992 (first entry)

XX DNA primer for HLA-B locus.

XX DNA primer; HLA-B; ss.

XX Homo sapiens.

XX W08202060-A.

XX 24-JUN-1982.

XX 18-DEC-1980; 80US-00217643.

XX 18-DEC-1980; 80US-00217643.

PR 13-JUL-1983; 83US-00513524.

PR 31-MAR-1986; 86US-00846481.

XX (UYVA) UNIV YALE.

XX Weiseman SM, Pereira D, Sood A;

XX WPI; 1982-54906E/26.

XX Isolating and identifying recombinant clones - contg. DNA derived from
 PT one component of a messenger RNA mixt.

XX Claim 11; Page 33; 40pp; English.

XX The DNA primer is complementary to a region of target mRNA coding for a
 CC portion of the HLA-B antigen. (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 11 BP; 2 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
 Db 10 TGTGGAGAAG 1

RESULT 84

AAZ18995
 ID AAZ18995 standard; DNA; 11 BP.

XX AC AAZ18995;

XX

DT 22-OCT-1999 (first entry)

XX Murine MRL SAGE tag 2603602.

XX Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;

KW healing response; microsatellite marker; treatment; central nerve;

KW peripheral nerve; nerve injury; SAGE tag; murine; ss.

XX Mus sp.

XX W09941364-A2.

XX 19-AUG-1999.

XX 12-FEB-1999; 99WO-US002962.

XX 13-FEB-1998; 98US-0074737P.

PR 26-AUG-1998; 98US-0097937P.

PR 28-SEP-1998; 98US-0102051P.

XX (WIST-) WISTAR INST.

XX Heber-Katz E;

XX WPI; 1999-494533/41.

XX New mammalian model for enhanced wound healing - useful for identifying
 PT enhanced wound healing genes.

XX Claim 13; Page 74; 136pp; English.

XX This invention describes a novel non-MRL healer mouse (M) having at least
 CC one quantitative trait locus selected from those given in the
 CC specification, exhibiting an enhanced healing response to a wound
 CC compared to mice (m) without the locus. The invention describes a novel
 CC method of identifying a gene involved in enhanced wound healing by
 CC identifying DNA microsatellite markers which can distinguish healer mice
 CC from non-healer mice and identifying microsatellite markers which
 CC segregate with enhanced wound healing in progeny of the mice, where a
 CC chromosomal locus containing at least one enhanced wound healing gene is
 CC identified. A method of treating a wound in a mammal is also disclosed.

XX The new methods are useful for treating wounds, especially central and
 CC peripheral nerve wound. The methods of the invention are useful for
 CC restoring function after nerve injury in a mammal. (M) is useful as a
 CC mammalian model of enhanced wound healing, useful for identifying genes
 CC and gene products involved in enhanced wound healing, and to provide
 CC methods for wound healing. AAZ18691-219036 represent murine SAGE tags
 CC from C57BL/6 and MRL mice which are used to illustrate the method of the
 CC invention

XX Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCGA 16
 Db 1 GCTGTGGCGA 10

RESULT 85

ABQ86261

ID ABQ86261 standard; cDNA; 11 BP.

XX AC ABQ86261;

XX 10-SEP-2002 (first entry)

XX Human skin stress/ageing related EST SEQ ID NO 16.

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

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XX OS Homo sapiens.
XX PN WO200253773-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-528865/56.
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT expression.
XX PS Claim 8; Page 36; 325pp; German.
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
XX CC or animals, are important for skin ageing and/or skin stress by serial
XX CC analysis of gene expression between mixtures of transcribed and
XX CC optionally translated, genetically encoded factors (A) obtained from
XX CC young and aged skin, to identify that genes that show strong differential
XX CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX CC useful for: identifying markers of skin ageing and/or stress; determining
XX CC skin ageing and/or stress; and identifying or determining the effects of
XX CC pharmaceutical or cosmetic agents for control of skin ageing. The present
XX CC sequence is one of a group of human skin ageing/stress related expressed
XX CC sequence tags (ABQ86246-ABQ87680) of the invention
XX SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
DB 1 GTGGCGAATG 10

RESULT 86
ABQ87168/c
ID ABQ87168 standard; cDNA; 11 BP.
XX AC ABQ87168;
XX DT 10-SEP-2002 (first entry)
XX DE Human skin stress/ageing related EST SEQ ID NO 923.
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253773-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-528865/56.

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
DB 1 GTGGCGAATG 10

RESULT 87
ABV65931
ID ABV65931 standard; cDNA; 11 BP.
XX AC ABV65931;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 3717.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 128; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin

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XX PT Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT expression.
XX PS Claim 8; Page 75; 325pp; German.
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
XX CC or animals, are important for skin ageing and/or skin stress by serial
XX CC analysis of gene expression between mixtures of transcribed and
XX CC optionally translated, genetically encoded factors (A) obtained from
XX CC young and aged skin, to identify that genes that show strong differential
XX CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX CC useful for: identifying markers of skin ageing and/or stress; determining
XX CC skin ageing and/or stress; and identifying or determining the effects of
XX CC pharmaceutical or cosmetic agents for control of skin ageing. The present
XX CC sequence is one of a group of human skin ageing/stress related expressed
XX CC sequence tags (ABQ86246-ABQ87680) of the invention
XX SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
DB 11 GTGGGAGG 2

RESULT 87
ABV65931
ID ABV65931 standard; cDNA; 11 BP.
XX AC ABV65931;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 3717.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 128; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin

```

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX

SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GTGGCGAAG 18

Db 1 GTGGCGAAG 10

RESULT 88

ABV69764

ID ABV69764 standard; cDNA; 11 BP.

XX

AC ABV69764;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human skin EST 7550.

XX

KW Human; skin; dermatological; vulnery; antipsoriatic; antisborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX

OS Homo sapiens.

XX

FN WO200253774-A2.

XX

PD 11-JUL-2002.

XX

PF 20-DEC-2001; 2001WO-EP015179.

XX

PR 03-JAN-2001; 2001DE-01000127.

XX

PA (HENK) HENKEL KGAA.

XX

PI Petersohn D, Conradt M, Hofmann K;

XX

DR WPI; 2002-590638/63.

XX

PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX

PS Claim 24; Page 238; 1345pp; German.

XX

CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.

CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX

SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match

Best Local Similarity 44.2%; Score 8.4; DB 1; Length 11;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 19

Db 1 GTGGCGAATG 10

RESULT 89

ABV70774

ID ABV70774 standard; cDNA; 11 BP.

XX

AC ABV70774;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human skin EST 8560.

XX

KW Human; skin; dermatological; vulnery; antipsoriatic; antisborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX

OS Homo sapiens.

XX

FN WO200253774-A2.

XX

PD 11-JUL-2002.

XX

PF 20-DEC-2001; 2001WO-EP015179.

XX

PR 03-JAN-2001; 2001DE-01000127.

XX

PA (HENK) HENKEL KGAA.

XX

PI Petersohn D, Conradt M, Hofmann K;

XX

DR WPI; 2002-590638/63.

XX

PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX

PS Claim 24; Page 274; 1345pp; German.

XX

CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.

CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX

SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 93;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 19

Db 1 GTGGCGAATG 10

RESULT 90

ABV69072/c

ID ABV69072 standard; cDNA; 11 BP.

XX

AC ABV69072;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human skin EST 6858.

```
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 216; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
XX Query Match 44.2%; Score 8.4; DB 1; Length 11;
XX Best Local Similarity 90.0%; Pred. No. 93;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GTGGCGAAGG 19
Db 11 GTGGAGAGG 2
RESULT 91
ABV69619/C
ID ABV69619 standard; cDNA; 11 BP.
AC ABV69619;
XX 21-OCT-2002 (first entry)
XX Human skin EST 7405.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Claim 24; Page 296; 1345pp; German.
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PR 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 232; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX SQ Sequence 11 BP; 1 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
XX Query Match 44.2%; Score 8.4; DB 1; Length 11;
XX Best Local Similarity 90.0%; Pred. No. 93;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTCTGGCGCTG 10
Db 10 GGGCGCGCTG 1
RESULT 92
ABV71417
ID ABV71417 standard; cDNA; 11 BP.
XX AC ABV71417;
XX 21-OCT-2002 (first entry)
XX Human skin EST 9203.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Claim 24; Page 296; 1345pp; German.
```

XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX CC
 SQ Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CGCTGTGGCG 15
 || |||||
 Db 2 CGATGTGGCG 11
 RESULT 93
 ABV63353 ID ABV63353 standard; cDNA; 11 BP.
 AC AC
 XX ABV63353;
 XX 21-OCT-2002 (first entry)
 DT 21-OCT-2002 (first entry)
 DE Human skin EST 1139.
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 PR (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 56; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GTGGCGAAGG 19
 |||||
 Db 1 GTGGCGAATG 10
 RESULT 94
 ABV66009/c ID ABV66009 standard; cDNA; 11 BP.
 XX AC
 XX ABV66009;
 DT 21-OCT-2002 (first entry)
 XX Human skin EST 3795.
 DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 PR (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 130; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 2 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCGCTGTGGC 14
 |||||
 Db 11 GCGCAGTGGC 2
 RESULT 95

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ABV67796
ID ABV67796 standard; cDNA; 11 BP.
XX
AC ABV67796;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 5582.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 208; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
Db 2 GCGCTGTGGC 11
| | | | |
| | | | |

RESULT 96
ABV68820
ID ABV68820 standard; cDNA; 11 BP.
XX
AC ABV68820;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6606.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX

ABV63996
ID ABV63996 standard; cDNA; 11 BP.
XX
AC ABV63996;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 1782.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 208; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 15
Db 1 CGCTGTGGC 10
| | | | |
| | | | |

RESULT 97
ABV63996
ID ABV63996 standard; cDNA; 11 BP.
XX
AC ABV63996;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 1782.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;

```

XX WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 XX Disclosure; Page 74; 1345pp; German.
 XX
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CGCTGTGGCG 15
 || |||||
 Db 2 CGATGTGGCG 11
 RESULT 98
 ABV62343
 ID ABV62343 standard; cDNA; 11 BP.
 XX
 AC ABV62343;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX Human skin EST 129.
 DE
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrheic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200253774-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 PR
 XX (HENK) HENKEL KGAA.
 PA
 XX Petersohn D, Conradt M, Hofmann K;
 PI
 XX WPI; 2002-590638/63.
 DR
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 PT
 XX Disclosure; Page 29; 1345pp; German.
 PS
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.

CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GTGGCGAAGG 19
 |||||
 Db 1 GTGGCGAATG 10
 RESULT 99
 ADQ35656/c
 ID ADQ35656 standard; DNA; 11 BP.
 XX
 AC ADQ35656;
 XX
 DT 23-SEP-2004 (first entry)
 DT
 XX Human hair-bearing skin-associated DNA fragment SEQ ID NO 473.
 DE
 XX hair-bearing skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
 KW
 XX Homo sapiens.
 OS
 XX DE10260931-A1.
 PN
 XX 08-JUL-2004.
 PD
 XX 20-DEC-2002; 2002DE-01060931.
 PF
 XX 20-DEC-2002; 2002DE-01060931.
 PR
 XX (HENK) HENKEL KGAA.
 PA
 XX Petersohn D, Schlottmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 PI
 XX WPI; 2004-518857/50.
 DR
 XX
 XX In vitro identification of genes important for hair-bearing skin, useful
 PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.
 PT
 XX Claim 5; SEQ ID NO 473; 250pp; German.
 PS
 XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for hair-bearing skin in humans. The method
 CC comprises recovering, from hair-bearing skin, a first mixture of
 CC genetically expressed (transcribed and optionally translated) factors
 CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
 CC mixture from skin on which hair does not grow and subjecting both
 CC mixtures to serial analysis of gene expression (SAGE) to identify those
 CC genes for which expression is markedly different between the two types of
 CC skin. The invention also describes in vitro methods for determining
 CC homeostasis of human hair-bearing skin and for determining activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
 CC a test kit comprising a solid support (flexible or rigid) with
 CC immobilised probes are also described for determining homeostasis. The
 CC hair-bearing skin is from the scalp and the other skin is from the face.
 CC The method allows identification of as many as possible of the genes
 CC important for hair-bearing skin, and therefore, of a very wide range of

CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
 CC human DNA Tag fragments used to identify genes associated with hair-
 CC bearing skin.

XX Sequence 11 BP; 1 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
 SQ

Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCTGGCTG 10
 |||||
 Db 10 GGGCGGCTG 1

RESULT 100

ADQ36012
 ID ADQ36012 standard; DNA; 11 BP.

XX AC ADQ36012;

XX DT 23-SEP-2004 (first entry)

XX DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 829.

XX KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; cosmetic; pharmaceutical; biochip; ds.

XX OS Homo sapiens.

XX PN DE10260931-AL.

XX PD 08-JUL-2004.

XX PF 20-DEC-2002; 2002DE-01060931.

XX PR 20-DEC-2002; 2002DE-01060931.

XX PA (HENK) HENKEL KGAA.

XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;

XX WPI; 2004-518857/50.

XX In vitro identification of genes important for hair-bearing skin, useful
 PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 5; SEQ ID NO 829; 250pp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for hair-bearing skin in humans. The method
 CC comprises recovering, from hair-bearing skin, a first mixture of
 CC genetically expressed (transcribed and optionally translated) factors
 CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
 CC mixture from skin on which hair does not grow and subjecting both
 CC mixtures to serial analysis of gene expression (SAGE) to identify those
 CC genes for which expression is markedly different between the two types of
 CC skin. The invention also describes in vitro methods for determining
 CC homeostasis of human hair-bearing skin and for determining activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
 CC a test kit comprising a solid support (flexible or rigid) with
 CC immobilised probes are also described for determining homeostasis. The
 CC hair-bearing skin is from the scalp and the other skin is from the face.
 CC The method allows identification of as many as possible of the genes
 CC important for hair-bearing skin, and therefore, of a very wide range of
 CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
 CC human DNA Tag fragments used to identify genes associated with hair-
 CC bearing skin.

XX Sequence 11 BP; 0 A; 2 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
 |||||
 Db 2 GGGCTGTGGC 11

RESULT 101

ADQ35381
 ID ADQ35381 standard; DNA; 11 BP.

XX AC ADQ35381;

XX DT 23-SEP-2004 (first entry)

XX DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 198.

XX KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; cosmetic; pharmaceutical; biochip; ds.

XX OS Homo sapiens.

XX PN DE10260931-AL.

XX PD 08-JUL-2004.

XX PF 20-DEC-2002; 2002DE-01060931.

XX PR 20-DEC-2002; 2002DE-01060931.

XX PA (HENK) HENKEL KGAA.

XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;

XX WPI; 2004-518857/50.

XX In vitro identification of genes important for hair-bearing skin, useful
 PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 6; SEQ ID NO 198; 250pp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for hair-bearing skin in humans. The method
 CC comprises recovering, from hair-bearing skin, a first mixture of
 CC genetically expressed (transcribed and optionally translated) factors
 CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
 CC mixture from skin on which hair does not grow and subjecting both
 CC mixtures to serial analysis of gene expression (SAGE) to identify those
 CC genes for which expression is markedly different between the two types of
 CC skin. The invention also describes in vitro methods for determining
 CC homeostasis of human hair-bearing skin and for determining activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
 CC a test kit comprising a solid support (flexible or rigid) with
 CC immobilised probes are also described for determining homeostasis. The
 CC hair-bearing skin is from the scalp and the other skin is from the face.
 CC The method allows identification of as many as possible of the genes
 CC important for hair-bearing skin, and therefore, of a very wide range of
 CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
 CC human DNA Tag fragments used to identify genes associated with hair-
 CC bearing skin.

XX Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      9 TGTGGCGAAG 18
DB      1 TGTGGCAAG 10

RESULT 102
ADQ32141/c
ID ADQ32141 standard; DNA; 11 BP.
XX AC ADQ32141;
XX DT 23-SEP-2004 (first entry)
XX DE Human facial skin-associated DNA fragment SEQ ID NO 231.
XX KW facial skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX OS Homo sapiens.
XX PN DE10260928-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060928.
XX PR 20-DEC-2002; 2002DE-01060928.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX DR WPI; 2004-518855/50.
XX PT In vitro identification of genes important for facial skin, useful for
XX PT assessing homeostasis and in screening for pharmaceutical or cosmetic
XX PT agents, based on differential expression analysis.
XX PS Claim 9; SEQ ID NO 231; 577pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
XX CC that are significant for facial skin in humans. The method comprises
XX CC recovering, from facial skin, a first mixture of genetically expressed
XX CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
XX CC their fragments), recovering a second, similar mixture from some other
XX CC human tissue, preferably skin from a protected area, especially from the
XX CC breast and subjecting the mixtures to serial analysis of gene expression
XX CC (SAGE) to identify those genes for which expression is markedly different
XX CC between facial skin and the other tissue. The invention also describes an
XX CC in vitro method for determining homeostasis of human facial skin; a test
XX CC kit which comprises a solid support (flexible or rigid) on which are
XX CC immobilised probes that bind specifically to the factors of interest and
XX CC of the invention are also used in a method which determines activity of
XX CC cosmetic and pharmaceutical agents for use against disorders or
XX CC disturbances of the homeostasis of human skin and a screening method for
XX CC identifying cosmetic and pharmaceutical agents. The method allows
XX CC identification of as many as possible of the genes important for facial
XX CC skin and thus of a very wide range of potential therapeutic and cosmetic
XX CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
XX CC identify the facial skin-associated genes described in the invention.
SQ Sequence 11 BP; 2 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GGCCTGTGGC 14
DB      11 GGCAGTGGC 2

RESULT 104
ADQ35029
ID ADQ35029 standard; DNA; 11 BP.

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RESULT 103
ADQ34986
ID ADQ34986 standard; DNA; 11 BP.
XX AC ADQ34986;
XX DT 23-SEP-2004 (first entry)
XX DE Human facial skin-associated DNA fragment SEQ ID NO 3076.
XX KW facial skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX OS Homo sapiens.
XX PN DE10260928-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060928.
XX PR 20-DEC-2002; 2002DE-01060928.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX DR WPI; 2004-518855/50.
XX PT In vitro identification of genes important for facial skin, useful for
XX PT assessing homeostasis and in screening for pharmaceutical or cosmetic
XX PT agents, based on differential expression analysis.
XX PS Claim 4; SEQ ID NO 3076; 577pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
XX CC that are significant for facial skin in humans. The method comprises
XX CC recovering, from facial skin, a first mixture of genetically expressed
XX CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
XX CC their fragments), recovering a second, similar mixture from some other
XX CC human tissue, preferably skin from a protected area, especially from the
XX CC breast and subjecting the mixtures to serial analysis of gene expression
XX CC (SAGE) to identify those genes for which expression is markedly different
XX CC between facial skin and the other tissue. The invention also describes an
XX CC in vitro method for determining homeostasis of human facial skin; a test
XX CC kit which comprises a solid support (flexible or rigid) on which are
XX CC immobilised probes that bind specifically to the factors of interest and
XX CC of the invention are also used in a method which determines activity of
XX CC cosmetic and pharmaceutical agents for use against disorders or
XX CC disturbances of the homeostasis of human skin and a screening method for
XX CC identifying cosmetic and pharmaceutical agents. The method allows
XX CC identification of as many as possible of the genes important for facial
XX CC skin and thus of a very wide range of potential therapeutic and cosmetic
XX CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
XX CC identify the facial skin-associated genes described in the invention.
SQ Sequence 11 BP; 0 A; 2 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GGCCTGTGGC 14
DB      2 GGCCTGTGGC 11

RESULT 104
ADQ35029
ID ADQ35029 standard; DNA; 11 BP.

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XX AC ADQ35029;
XX DT 23-SEP-2004 (first entry)
XX DE Human facial skin-associated DNA fragment SEQ ID NO 3119.
XX DE facial skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX OS Homo sapiens.
XX PN DE10260928-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060928.
XX PR 20-DEC-2002; 2002DE-01060928.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX DR WPI; 2004-518855/50.
XX PT In vitro identification of genes important for facial skin, useful for
XX PT assessing homeostasis and in screening for pharmaceutical or cosmetic
XX PT agents, based on differential expression analysis.
XX PS Claim 4; SEQ ID NO 3119; 577pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
XX CC that are significant for facial skin in humans. The method comprises
XX CC recovering from facial skin, a first mixture of genetically expressed
XX CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
XX CC their fragments), recovering a second, similar mixture from some other
XX CC human tissue, preferably skin from a protected area, especially from the
XX CC breast and subjecting the mixtures to serial analysis of gene expression
XX CC (SAGE) to identify those genes for which expression is markedly different
XX CC between facial skin and the other tissue. The invention also describes an
XX CC in vitro method for determining homeostasis of human facial skin; a test
XX CC kit which comprises a solid support (flexible or rigid) on which are
XX CC immobilised probes that bind specifically to the factors of interest and
XX CC a biochip for determining homeostasis of human facial skin. The products
XX CC of the invention are also used in a method which determines activity of
XX CC cosmetic and pharmaceutical agents for use against disorders or
XX CC disturbances of the homeostasis of human skin and a screening method for
XX CC identifying cosmetic and pharmaceutical agents. The method allows
XX CC identification of as many as possible of the genes important for facial
XX CC skin and thus of a very wide range of potential therapeutic and cosmetic
XX CC agents. ADQ31911-ADQ35111 represent human DNA tag fragments used to
XX CC identify the facial skin-associated genes described in the invention.
XX SQ Sequence 11 BP; 0 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
DB 1 CGCTGTGGCG 10

RESULT 105
ADQ34095/c
ID ADQ34095 standard; DNA; 11 BP.
XX AC ADQ34095;
XX DT 23-SEP-2004 (first entry)

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XX DE Human facial skin-associated DNA fragment SEQ ID NO 2185.
XX KW facial skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX OS Homo sapiens.
XX PN DE10260928-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060928.
XX PR 20-DEC-2002; 2002DE-01060928.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX DR WPI; 2004-518855/50.
XX PT In vitro identification of genes important for facial skin, useful for
XX PT assessing homeostasis and in screening for pharmaceutical or cosmetic
XX PT agents, based on differential expression analysis.
XX PS Claim 4; SEQ ID NO 2185; 577pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
XX CC that are significant for facial skin in humans. The method comprises
XX CC recovering from facial skin, a first mixture of genetically expressed
XX CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
XX CC their fragments), recovering a second, similar mixture from some other
XX CC human tissue, preferably skin from a protected area, especially from the
XX CC breast and subjecting the mixtures to serial analysis of gene expression
XX CC (SAGE) to identify those genes for which expression is markedly different
XX CC between facial skin and the other tissue. The invention also describes an
XX CC in vitro method for determining homeostasis of human facial skin; a test
XX CC kit which comprises a solid support (flexible or rigid) on which are
XX CC immobilised probes that bind specifically to the factors of interest and
XX CC a biochip for determining homeostasis of human facial skin. The products
XX CC of the invention are also used in a method which determines activity of
XX CC cosmetic and pharmaceutical agents for use against disorders or
XX CC disturbances of the homeostasis of human skin and a screening method for
XX CC identifying cosmetic and pharmaceutical agents. The method allows
XX CC identification of as many as possible of the genes important for facial
XX CC skin and thus of a very wide range of potential therapeutic and cosmetic
XX CC agents. ADQ31911-ADQ35111 represent human DNA tag fragments used to
XX CC identify the facial skin-associated genes described in the invention.
XX SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
DB 11 GTGGCGAAGG 2

RESULT 106
AAV65451
ID AAV65451 standard; DNA; 12 BP.
XX AC AAV65451;
XX DT 08-DEC-1998 (first entry)
XX DE Primer pBS900-23E used in the course of the invention.
XX KW Nucleic acid determination; hybridisation; probe; mismatch; SBH;

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SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCTGGCTG 10
Db 2 GGTCTGGCTG 11

RESULT 109
AAV65546
ID AAV65546 standard; DNA; 12 BP.
XX AC
XX AAV65546;
XX DT
XX 08-DEC-1998 (first entry)
XX DE
XX Forward primer 16 used in the course of the invention.
XX KW
XX Nucleic acid determination; hybridisation; probe; mismatch; SBH;
XX KW sequencing by hybridisation; PCR primer; ss.
XX OS
XX Synthetic.
XX PN
XX JP10243785-A.
XX PD
XX 14-SEP-1998.
XX PF
XX 03-MAR-1997; 97JP-00047821.
XX PR
XX 03-MAR-1997; 97JP-00047821.
XX PA
XX (BUNS-) BUNSHI BIOHOTOONICS KENKYUSHO KK.
XX DR
XX WPI; 1998-549781/47.
XX PT
XX Determination of nucleic acid base sequence - is sensitive and rapid
XX PT without mismatch in hybridisation as in sequencing by hybridisation
XX PT method.
XX PS
XX Example; Page 12; 20pp; Japanese.
XX CC
XX Sequences shown in AAV65401 to AAV65580 represent PCR primers used in the
XX CC course of the invention which provides a method for determining a single
XX CC stranded nucleic acid base sequence. The method comprises separation of
XX CC 4k oligonucleotide probe as a primer from all combinations of k base
XX CC sequences and hybridising the probe and the nucleic acid to be tested.
XX CC The probe is elongated to make a primer using the nucleic acid to be
XX CC tested as a template and the elongated primer is determined. The base
XX CC sequence of the nucleic acid is determined based on the elongated amount.
XX CC The method allows sensitive and rapid determination of nucleic acid base
XX CC sequence without mismatch in hybridisation as in sequencing by
XX CC hybridisation (SBH) method
XX SQ
XX Sequence 12 BP; 0 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCTGGCTG 10
Db 3 GGTCTGGCTG 12

RESULT 110
AAA74607
ID AAA74607 standard; DNA; 12 BP.
XX AC
XX AAA74607;
XX XX

SQ Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
Db 1 CCCTGTGGCG 10

RESULT 111
ABI23621
ID ABI23621 standard; DNA; 12 BP.
XX AC
XX ABI23621;
XX XX
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 323594 for detecting SNP TSC0031477.
XX KW
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN
XX WO200177384-A2.
XX PD
XX 18-OCT-2001.
XX PF
XX 06-APR-2001; 2001WO-IB000713.
XX XX

```

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PR 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 323594; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ASC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GTGGCGAAGG 19
Db 1 GTGGCGAAGG 10
RESULT 112
ABI12916
ID ABI12916 standard; DNA; 12 BP.
XX
AC ABI12916;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 312889 for detecting SNP TSC0025347.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 312889; 29pp + Sequence Listing; German.

```

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XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ASC00010
XX -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GTGGCGAAGG 19
Db 3 GTAGCGAAGG 12
RESULT 113
ABI06621/C
ID ABI06621 standard; DNA; 12 BP.
XX
AC ABI06621;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 306594 for detecting SNP TSC0022080.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 306594; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ASC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

```


CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 0 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 85;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCGCGTGTGG 13
 DB 2 CGCGCGTGTGG 11

RESULT 119

ABH72007
 ID ABH72007 standard; DNA; 12 BP.

XX
 AC ABH72007;

XX
 DT 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 271986 for detecting SNP TSC0002677.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 271986; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 85;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GTGGCGAAGG 19
 DB 2 GAGGCGAAGG 11

RESULT 120

ABI25686
 ID ABI25686 standard; DNA; 12 BP.

XX
 AC ABI25686;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 325659 for detecting SNP TSC0032649.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 325659; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 1 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 85;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGCGAAG 18
 DB 3 TGTGCGGAGG 12

RESULT 121

ABI26828
 ID ABI26828 standard; DNA; 12 BP.

XX
 AC ABI26828;

XX

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DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 326801 for detecting SNP TSC0033283.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 326801; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
Db 1 GTGGCGAAGG 10

RESULT 122
ABH90031/c
ID ABH90031 standard; DNA; 12 BP.
XX
AC ABH90031;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 290024 for detecting SNP TSC0014187.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 290024; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
Db 1 GTGGCGAAGG 10

RESULT 123
ABI29748/c
ID ABI29748 standard; DNA; 12 BP.
XX
AC ABI29748;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 329721 for detecting SNP TSC0035109.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine

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XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 290024; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
XX
Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
Db 12 TGTGGCGAGG 3

RESULT 123
ABI29748/c
ID ABI29748 standard; DNA; 12 BP.
XX
AC ABI29748;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 329721 for detecting SNP TSC0035109.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine

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methylation status.

Claim 1; SEQ ID NO 329721; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCGAAG 18
Db 11 TGTGGAGAAG 2

RESULT 124
ABI12040
ID ABI12040 standard; DNA; 12 BP.
AC ABI12040;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
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PN WO200177384-A2.
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PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.

PA (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 290346; 29pp + Sequence Listing; German.
 PS
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC000010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the invention. NOTE: The sequence
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 85;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 TGTGGCGAAG 18
 Db 12 TGTGGCGAAG 3
 RESULT 129
 ID ADC3639/c
 XX ADC3639 standard; DNA; 12 BP.
 XX
 AC ADC3639;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE M. tuberculosis PCR primer #6.
 XX
 KW ss; PCR; primer; rifampin resistance; rpoB; tuberculosis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 XX US2003104387-A1.
 XX
 XX 05-JUN-2003.
 XX
 XX 07-SEP-2001; 2001US-00949041.
 XX
 XX 07-SEP-2001; 2001US-00949041.
 XX
 XX (YANG/) YANG M.
 PA (WOH/) WOO H S.
 XX
 XX Yang M, Woo HS;
 XX
 XX WPI; 2003-787043/74.
 DR
 XX
 XX Detecting tendency to rifampin resistance caused by mutation in RNA
 PT polymerase beta-subunit gene of Mycobacterium tuberculosis.
 PT
 XX
 XX Claim 50; SEQ ID NO 50; 27pp; English.
 PS
 XX
 XX The invention relates to a method of detecting a tendency to rifampin
 CC resistance caused by mutations in rpoB gene of Mycobacterium tuberculosis
 CC comprising extracting DNA from M. tuberculosis cells, amplifying rpoB

CC gene to produce fluorescently labelled product, contacting the labelled
 CC product with first and second array of oligonucleotide probes, detecting
 CC fluorescent hybridisation signal and correlating with tendency to
 CC rifampin resistance. The method is useful for detecting a tendency to
 CC rifampin resistance caused by mutations in a rpoB gene of M.
 CC tuberculosis. The method is easy to perform and is cost effective to be
 CC performed on a large-scale basis. The results produced is reliable and
 CC readily detectable. The method is easily adaptable to automation. The
 CC present sequence represents a M. tuberculosis PCR primer.
 XX
 SQ Sequence 12 BP; 1 A; 7 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 85;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GGCCTGTGGC 14
 Db 11 GGCCTGTGGC 2
 RESULT 130
 ID ADZ45204/c
 XX ADZ45204 standard; DNA; 12 BP.
 XX
 AC ADZ45204;
 XX
 DT 14-JUL-2005 (first entry)
 XX
 DE Parallel stranded hairpin component oligonucleotide SEQ ID NO:28.
 XX
 KW aptamer; ss.
 XX
 OS Synthetic.
 XX
 XX US2005089893-A1.
 XX
 XX 28-APR-2005.
 XX
 XX 04-AUG-2004; 2004US-00912032.
 XX
 XX 06-AUG-2003; 2003US-0493092P.
 XX
 XX (LOPE/) LOPEZ M J.
 PA (MUNZ/) MUNZER M.
 PA (ERIT/) ERITJA R.
 XX
 XX Lopez MJ, Munzer M, Eritja R;
 XX
 XX WPI; 2005-314086/32.
 XX
 XX New nucleic acid ligand comprising a parallel-stranded hairpin, useful as
 PT aptamers, as artificial nucleic acid ligands and for detecting and
 PT eliminating molecules of interest.
 XX
 XX Disclosure; SEQ ID NO 28; 25pp; English.
 PS
 XX
 XX The invention relates to a nucleic acid ligand comprising a parallel-
 CC stranded hairpin. Also described: (1) a method for preparing a parallel-
 CC oligonucleotide duplex; and (2) a method for binding a target molecule.
 CC The parallel-stranded hairpin sequences or oligonucleotide triplexes are
 CC useful as aptamers. They are useful for detecting and eliminating
 CC molecules of interest. The ligand is useful as artificial nucleic acid
 CC ligand. The present sequence represents a parallel stranded hairpin
 CC component oligonucleotide from the present invention.
 XX
 SQ Sequence 12 BP; 0 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 44.2%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 85;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GTGGCGAAG 19

```

Db      | |||||
        12 GAGGCGAAG 3

RESULT 131
AAZ79106
ID  AAZ79106 standard; DNA; 10 BP.
AC  AAZ79106;
XX
XX
DT  10-APR-2000 (first entry)
XX
XX  Human dendritic cell SAGE tag, SEQ ID NO:1534.
XX
XX  SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW  APC; monocyte-derived dendritic cell; differential gene expression;
KW  immunostimulatory cofactor; costimulatory factor; CTL;
KW  cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX  Homo sapiens.
XX
XX  WO9965924-A2.
XX
XX  23-DEC-1999.
XX
XX  18-JUN-1999; 99WO-US013800.
XX
XX  19-JUN-1998; 98US-0089833P.
XX  19-JUN-1998; 98US-0089844P.
XX  19-JUN-1998; 98US-0089853P.
XX  19-JUN-1998; 98US-0089878P.
XX  19-JUN-1998; 98US-0089911P.
XX  19-JUN-1998; 98US-0089922P.
XX  19-JUN-1998; 98US-0089933P.
XX  19-JUN-1998; 98US-0089944P.
XX  19-JUN-1998; 98US-0089977P.
XX  19-JUN-1998; 98US-0089999P.
XX  19-JUN-1998; 98US-0090000P.
XX  19-JUN-1998; 98US-0090035P.
XX  19-JUN-1998; 98US-0090036P.
XX  19-JUN-1998; 98US-0090039P.
XX  19-JUN-1998; 98US-0090040P.
XX  19-JUN-1998; 98US-0090041P.
XX  19-JUN-1998; 98US-0090042P.
XX  19-JUN-1998; 98US-0090043P.
XX  19-JUN-1998; 98US-0090044P.
XX  19-JUN-1998; 98US-0090045P.
XX  19-JUN-1998; 98US-0090047P.
XX  19-JUN-1998; 98US-0090048P.
XX  19-JUN-1998; 98US-0090072P.
XX  19-JUN-1998; 98US-0090076P.
XX  19-JUN-1998; 98US-0090077P.
XX  19-JUN-1998; 98US-0090078P.
XX  19-JUN-1998; 98US-0090079P.
XX  19-JUN-1998; 98US-0090080P.
XX  08-DEC-1998; 98US-0111715P.
XX
XX  (GENZ ) GENZYME CORP.
PA  (ROBE/) ROBERTS B L.
PA  (SHAN/) SHANKARA S.
XX
XX  Roberts BL, Shankara S;
XX
XX  WPI; 2000-106077/09.
XX
XX  Isolated polynucleotides differentially expressed in antigen-presenting
PT  cells, useful in gene vaccines against cancer.
XX
XX  Claim 1; Page 109; 130pp; English.
XX
XX  Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC  expression) tags used to identify mRNA transcripts encoding
CC  immunostimulatory cofactor proteins which are preferentially or

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CC  differentially expressed in monocyte-derived dendritic cells compared
CC  with monocytes. Some of the transcripts correspond to known genes or ESTs
CC  (expressed sequence tags) which were previously unknown to be
CC  preferentially or differentially expressed in dendritic cells, while
CC  other transcripts correspond to novel genes. Antigen-presenting cell
CC  (APC)-associated costimulatory factors play an important role in the
CC  activation of the cytotoxic immune response, particularly against tumour
CC  cells. Tumour antigen presentation via the MHC (major histocompatibility
CC  complex) and subsequent recognition by T-cell receptors is alone
CC  insufficient to activate a robust cytotoxic immune response that can lyse
CC  the tumour cells, immunostimulatory cofactors also being required for
CC  efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC  sequences identified using the SAGE tags have several potential uses.
CC  They may be used in vaccines to induce an immune response, particularly
CC  against a tumour antigen; to modulate the genotype of an APC; to screen
CC  for agents that modulate expression of differentially expressed genes in
CC  an APC; and as hybridisation probes/amplification primers for the
CC  diagnosis, prognosis and monitoring of diseases related to abnormal
CC  expression of these genes. Detection of the dendritic cell differentially
CC  expressed genes, or of their encoded proteins, can be used to identify
CC  cells as belonging to the monocyte lineage. Cells containing these genes
CC  can be used in active immunotherapy (or to stimulate production of a
CC  population of antigen-specific effector cells) and vectors containing
CC  them are used in gene therapy. Co-administration of tumour antigens and
CC  APC-associated costimulatory factors ensures adequate antigen
CC  presentation to endogenous APCs and upregulates the APCs for the
CC  presentation of co-stimulatory signals, migration to T cell-rich sites,
CC  secretion of T cell growth factors and secretion of chemokines for
CC  recruitment of immune effector cells
XX
XX  Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
SQ

```

```

Query Match      42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCGAAG 18
        |||||
DB       3 TGGCGAAG 10

RESULT 132
AAZ81742
ID  AAZ81742 standard; DNA; 10 BP.
XX
XX  AAZ81742;
XX
XX  07-APR-2000 (first entry)
XX
XX  Metastatic breast tumour cell upregulated transcript tag #976.
DE
XX
XX  Human; metastatic breast tumour tissue; tag; primer;
KW  non-metastatic breast tumour tissue; gene therapy; anticancer;
KW  antimetastatic; vaccine; diagnosis; ss.
XX
XX  Homo sapiens.
XX
XX  WO9965928-A2.
XX
XX  23-DEC-1999.
XX
XX  18-JUN-1999; 99WO-US013647.
XX
XX  19-JUN-1998; 98US-0089853P.
XX  19-JUN-1998; 98US-0089977P.
XX  19-JUN-1998; 98US-0090039P.
XX  19-JUN-1998; 98US-0090040P.
XX  19-JUN-1998; 98US-0090041P.
XX
XX  (GENZ ) GENZYME CORP.
PA  (ROBE/) ROBERTS B L.
PA  (SHAN/) SHANKARA S.
XX
XX
XX

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PI Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 84; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX
XX Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 42.1%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 GCTGTGGC 14
XX |||||
XX Db 2 GCTGTGGC 9
XX
XX RESULT 133
XX AAZ85240
XX ID AAZ85240 standard; DNA; 10 BP.
XX AC AAZ85240;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell downregulated transcript tag #4474.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX anti-metastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.

```

```

PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 179; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX
XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 42.1%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 CTGTGGCG 15
XX |||||
XX Db 2 CTGTGGCG 9
XX
XX RESULT 134
XX AAZ85260/c
XX ID AAZ85260 standard; DNA; 10 BP.
XX AC AAZ85260;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell downregulated transcript tag #4494.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX anti-metastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.

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PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 179; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GCGCTGTG 12
Db 8 GCGCTGTG 1
RESULT 135
AAZ84921
ID AAZ84921 standard; DNA; 10 BP.
XX
XX AAZ84921;
AC
XX
XX 07-APR-2000 (first entry)
DT
XX
XX Metastatic breast tumour cell downregulated transcript tag #415.
DE
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
OS
XX WO9965928-A2.
PN
XX
XX 23-DEC-1999.
PD
XX
XX 18-JUN-1999; 99WO-US013647.
PF
XX 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR

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PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
PI
XX
XX WPI; 2000-106079/09.
DR
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 169; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TGGCGAAG 18
Db 3 TGGCGAAG 10
RESULT 136
AAZ84042
ID AAZ84042 standard; DNA; 10 BP.
XX
XX AAZ84042;
AC
XX
XX 07-APR-2000 (first entry)
DT
XX
XX Metastatic breast tumour cell downregulated transcript tag #3276.
DE
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
OS
XX WO9965928-A2.
PN
XX
XX 23-DEC-1999.
PD
XX
XX 18-JUN-1999; 99WO-US013647.
PF
XX 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089997P.
PR

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PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 146; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCTG 10
Db |||||
2 TCGCGCTG 9

RESULT 137
AAZ79746
ID AAZ79746 standard; DNA; 10 BP.
AC
AC AAZ79746;
XX
XX 10-APR-2000 (first entry)
XX
XX Human colon preferentially expressed gene SAGE tag, SEQ ID NO:37.
XX
XX SAGE tag; serial analysis of gene expression; diagnosis;
KW differential gene expression; characterisation; targeted expression;
KW tumour; cancer; immunotherapy; ss.
XX
XX Homo sapiens.
OS
XX
XX WO966303-A2.
XX
XX 23-DEC-1999.
XX
XX 17-JUN-1999; 99WO-US013820.
XX

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PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089911P.
PR 19-JUN-1998; 98US-0089922P.
PR 19-JUN-1998; 98US-0089933P.
PR 19-JUN-1998; 98US-0089944P.
PR 19-JUN-1998; 98US-0089979P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106132/09.
XX
XX New polynucleotide useful in cancer immunotherapy.
XX
XX Claim 1; Page 53; 97pp; English.
XX
XX Sequences AAZ79710-279916 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts which are
XX differentially expressed in a variety of normal or malignant cell types.
XX Some of the transcripts correspond to known genes or ESTs (expressed
XX sequence tags) which were previously unknown to be preferentially or
XX differentially expressed in that particular cell type, while other
XX transcripts correspond to novel genes. The invention also provides a
XX nucleotide comprising a promoter sequence derived from one of the
XX differentially expressed genes, which may optionally be operably linked
XX to a foreign nucleotide sequence, and gene delivery vehicles and host
XX cells comprising the polynucleotides of the invention. A nucleotide
XX comprising sequences AAZ79710-279916 may be used in diagnostic procedures
XX to characterise a cell of a specific tissue type and to determine whether
XX it is normal or malignant. They may be used to screen for agents that
XX modulate expression of differentially expressed genes compound. The
XX promoter/foreign gene construct of the invention may be used for
XX targeted expression of the foreign gene in a particular cell type. For
XX example, a promoter derived from a gene preferentially expressed in
XX dendritic cells (antigen-presenting cells, or APCs), may be operably
XX linked to a sequence encoding an immunostimulatory molecule and a
XX sequence encoding an antigen. Such a construct could be transduced into
XX APCs and would be useful for inducing an immune response by educating
XX immune effector cells in vivo, or in cancer immunotherapy
XX
XX Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCTG 10

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```

Db      2 TCGCGCTG 9
|||||
RESULT 138
AAH63878
ID AAH63878 standard; cDNA; 10 BP.
XX
AC AAH63878;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 718.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velulescu VE, Vogelstein B, Kinzler KW;
XX
PWPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 13; Page 55; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGTG 12
DB 3 GCGCTGTG 10
|||||

RESULT 139
AAH32681
ID AAH32681 standard; cDNA; 10 BP.
XX
AC AAH32681;
XX
DT 13-AUG-2001 (first entry)
XX
DE LPS activated human monocyte expression gene cDNA tag SEQ:54.
XX
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.

Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGCG 15
DB 2 CTGTGGCG 9
|||||

RESULT 140
ABA06193
ID ABA06193 standard; cDNA; 10 BP.
XX
AC ABA06193;
XX
DT 10-JAN-2002 (first entry)
XX
DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 170.
XX
KW Human; hepatocyte; gene expression; hepatopathy; ss.
XX
OS Homo sapiens.
XX
PN JP2001211883-A.
XX
PD 07-AUG-2001.
XX
PF 31-JAN-2000; 2000JP-00023170.
XX
PR 31-JAN-2000; 2000JP-00023170.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
PWPI; 2001-629566/73.
XX
DE Human normal hepatocyte expression gene group.
XX
PT Claim 1; Page 9; 26pp; Japanese.
XX
PS The invention relates to a human normal hepatocyte expression gene group
CC comprising 200 genes in the human normal hepatocyte. The cDNA of each

```

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XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
PF 28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
PWPI; 2001-304369/32.
XX
DE LPS activated human monocyte expression gene group.
XX
PT Claim 10; Page 18; 52pp; Japanese.
XX
CC The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CC CATG-3' nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role. AAH32628
CC to AAH32943 represent specifically claimed LPS activated human monocyte
CC expression gene cDNA tags from the present invention. AAH32944 represents
CC an LPS activated human monocyte expression gene cDNA sequence encoding
CC AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGCG 15
DB 2 CTGTGGCG 9
|||||

RESULT 140
ABA06193
ID ABA06193 standard; cDNA; 10 BP.
XX
AC ABA06193;
XX
DT 10-JAN-2002 (first entry)
XX
DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 170.
XX
KW Human; hepatocyte; gene expression; hepatopathy; ss.
XX
OS Homo sapiens.
XX
PN JP2001211883-A.
XX
PD 07-AUG-2001.
XX
PF 31-JAN-2000; 2000JP-00023170.
XX
PR 31-JAN-2000; 2000JP-00023170.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
PWPI; 2001-629566/73.
XX
DE Human normal hepatocyte expression gene group.
XX
PT Claim 1; Page 9; 26pp; Japanese.
XX
PS The invention relates to a human normal hepatocyte expression gene group
CC comprising 200 genes in the human normal hepatocyte. The cDNA of each

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CC gene comprises one of 200 fully defined nucleotide sequences as given in
 CC the specification. The gene group and the cDNAs corresponding to each of
 CC the genes in the group are useful in the diagnosis and treatment of human
 CC hepatopathy. The present sequence is a cDNA corresponding to a gene
 CC expressed by normal human hepatocytes
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGTG 12
 |||||
 DB 3 GCGCTGTG 10

RESULT 141

ABA83148

ID ABA83148 standard; cDNA; 10 BP.

XX

AC ABA83148;

XX

08-FEB-2002 (first entry)

XX

XX

DE Claudin 2 ovarian tumour marker gene SAGE tag, SEQ ID NO:108.

XX

Ovarian tumour marker gene; human; overexpression; upregulation;
 epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
 identification; serous cystadenoma; borderline serous tumour;
 serous cystadenocarcinoma; mucinous cystadenocarcinoma;
 mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
 undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
 adenofibroma; Brenner tumour; serial analysis of gene expression;
 immune response pathway; cell proliferation regulation; protein folding;
 membrane localised; secreted; therapeutic target; cytostatic;
 gene therapy; vaccine; SAGE tag; ss.

XX
 OS Homo sapiens.

XX
 PN WO200175177-A2.

XX
 PD 11-OCT-2001.

XX
 PF 03-APR-2001; 2001WO-US010947.

XX
 PR 03-APR-2000; 2000US-0194336P.

XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
 PI Morin PU, Sherman-Baust CA, Pizer ES, Hough CD;

XX
 DR WPI; 2001-626450/72.

XX
 PT Detecting and identifying ovarian tumor, identifying increased risk for
 PT developing ovarian cancer, and determining effectiveness of ovarian
 PT cancer treatment, by measuring expression level of ovarian tumor marker
 PT gene.

XX
 PS Claim 26; Page 41; 140pp; English.

XX
 CC The invention relates to methods for diagnosing and prognosing ovarian
 CC tumours in an individual via the detection and measurement of the
 CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183). The methods of the invention are useful for
 CC detecting an ovarian tumour in a patient, for identifying an individual
 CC at increased risk for developing ovarian cancer, in prognostic tests for
 CC assessing the relative severity of ovarian cancer, in tests for
 CC monitoring a patient in remission from ovarian cancer and in tests for
 CC monitoring disease status in a patient being treated for ovarian cancer.
 CC The methods can additionally be used to identify a particular tumour as
 CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from

CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
 CC mucinous cystadenoma, borderline mucinous tumour, mucinous
 CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
 CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
 CC tumour. The ovarian tumour marker genes of the invention were identified
 CC using SAGE (serial analysis of gene expression) and were found to be
 CC overexpressed in a broad variety of ovarian epithelial tumour cells
 CC relative to normal ovarian epithelial cells. The marker genes are
 CC implicated in immune response pathways, in the regulation of cell
 CC proliferation and in protein folding, and many of these are membrane-
 CC localised or secreted. In addition to their use as diagnostic and
 CC prognostic markers, the ovarian tumour marker genes or their encoded
 CC proteins may be used as therapeutic targets for the treatment and
 CC prevention of ovarian cancer. Sequences ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183 represent SAGE tags derived from the ovarian tumour
 CC marker genes of the invention
 XX

SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCTG 10
 |||||
 DB 2 TCGCGCTG 9

RESULT 142

AAF43250

ID AAF43250 standard; DNA; 10 BP.

XX

AC AAF43250;

XX

DT 23-MAR-2001 (first entry)

XX

XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11389.

XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX
 OS Saccharomyces cerevisiae.

XX
 PN WO200077214-A2.

XX
 PD 21-DEC-2000.

XX
 PF 14-JUN-2000; 2000WO-US016223.

XX
 PR 16-JUN-1999; 99US-00335032.

XX
 PA (UYJO) UNIV JOHNS HOPKINS.

XX
 PI Velculescu V, Vogelstein B, Kinzler K;

XX
 DR WPI; 2001-061874/07.

XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX
 PS Example; Page 356; 419pp; English.

XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAAG 18
 |||||
 Db 1 TGGCGAAG 8

RESULT 143

ABL42674

ID ABL42674 standard; cDNA; 10 BP.

AC ABL42674;

DT 12-APR-2002 (first entry)

DE Human maturation/activation dendritic cell expression gene tag #48.

KW Human; maturation/activation dendritic cell expression gene; tag;
 maturation; activation; dendritic cell; ss.

XX Homo sapiens.

XX JP2001327293-A.

XX 27-NOV-2001.

XX 22-MAY-2000; 2000JP-00150562.

XX 22-MAY-2000; 2000JP-00150562.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-127070/17.

XX Human maturation/activation dendritic cell expression gene group.

XX Claim 1; Page 9; 41pp; Japanese.

XX The present invention describes a human maturation/activation dendritic
 CC cell (DC) expression gene group consisting of 100 genes which show the
 CC highest expression among the genes expressed in human maturation/
 CC activation DC. Also described are: (1) a protein expressed by the above
 CC human maturation/activation DC expression gene; (2) an antibody against
 CC the protein; and (3) an antagonist against the expression of each gene
 CC belonging to the above gene group. The gene group is useful for the
 CC treatment and the diagnosis of various human diseases related to human
 CC DC. ABL42627 to ABL42926 represent specifically claimed human
 CC maturation/activation DC expression gene tags from the present invention

SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGCG 15
 |||||
 Db 2 CTGTGGCG 9

RESULT 144

ABL42776

ID ABL42776 standard; cDNA; 10 BP.

XX ABL42776;

DT 12-APR-2002 (first entry)

XX Human maturation/activation dendritic cell expression gene tag #150.

KW Human; maturation/activation dendritic cell expression gene; tag;
 maturation; activation; dendritic cell; ss.

XX Homo sapiens.

XX JP2001327293-A.

XX 27-NOV-2001.

XX 22-MAY-2000; 2000JP-00150562.

XX 22-MAY-2000; 2000JP-00150562.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-127070/17.

XX Human maturation/activation dendritic cell expression gene group.

XX Claim 10; Page 13; 41pp; Japanese.

XX The present invention describes a human maturation/activation dendritic
 CC cell (DC) expression gene group consisting of 100 genes which show the
 CC highest expression among the genes expressed in human maturation/
 CC activation DC. Also described are: (1) a protein expressed by the above
 CC human maturation/activation DC expression gene; (2) an antibody against
 CC the protein; and (3) an antagonist against the expression of each gene
 CC belonging to the above gene group. The gene group is useful for the
 CC treatment and the diagnosis of various human diseases related to human
 CC DC. ABL42627 to ABL42926 represent specifically claimed human
 CC maturation/activation DC expression gene tags from the present invention

XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGCG 15
 |||||
 Db 2 CTGTGGCG 9

RESULT 145

ABK96054

ID ABK96054 standard; DNA; 10 BP.

XX ABK96054;

XX 24-SEP-2002 (first entry)

XX Human LIPE gene polymorphism detection oligonucleotide primer #29.

XX Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;
 KW polymorphism; primer; ss.
 XX Homo sapiens.
 XX WO200240502-A2.
 XX 23-MAY-2002.
 XX 16-NOV-2001; 2001WO-US043518.
 XX 16-NOV-2000; 2000US-0249302P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Anastasio AE, Bentivegna SC, Chew A, Koshy B, Rounds E;
 XX WPI; 2002-519369/55.
 XX Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for
 PT improving efficiency and reliability in drug development for treating
 PT diseases associated with LIPE activity, e.g. obesity and male sterility.
 XX Claim 17; Page 16; 142pp; English.
 XX The present invention relates to a new polynucleotide comprising a
 CC nucleotide sequence which comprises lipase, hormone sensitive (LIPE)
 CC isogenes. The invention is useful in screening for drugs targeting LIPE
 CC isogenes that are useful for treating obesity and male sterility. The
 CC methods of the invention are useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with LIPE activity. The polynucleotide
 CC is useful in studying the expression and function of LIPE, and in
 CC expressing LIPE protein for use in screening for candidate drugs to treat
 CC diseases related to LIPE activity. It is also useful in studying the
 CC effect of the variation on the biological activity of LIPE as well as on
 CC the binding affinity of candidate drugs targeting LIPE for the treatment
 CC of obesity and male sterility. The invention is useful for studying the
 CC expression of LIPE isogenes in vivo, for in vivo screening and testing of
 CC drugs targeted against LIPE protein, and for testing the efficacy of
 CC therapeutic agents and compounds for treating obesity and male sterility
 CC in a biological system. The present nucleic acid sequence represents one
 CC of a collection (ABK96026-ABK96083) of oligonucleotide primers that were
 CC used in the invention to detect polymorphisms in the human LIPE gene
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GCTGTGGC 14
 Db 2 GCTGTGGC 9
 RESULT 146
 AAL48073
 ID AAL48073 standard; DNA; 10 BP.
 XX
 AC AAL48073;
 XX
 DT 27-SEP-2002 (first entry)
 XX
 DE Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 51.
 XX Human; colony stimulating factor 3 (granulocyte); CSF3; SNP; isogene;
 KW chromosome 17q11-12; single nucleotide polymorphism; immunostimulant;
 KW neutropenia; promyelocytic leukaemia; haematological disorder;
 KW gene therapy; PCR; primer extension oligonucleotide; ss.
 XX Homo sapiens.
 OS

XX WO200194364-A2.
 XX 13-DEC-2001.
 XX 11-JUN-2001; 2001WO-US018813.
 XX 09-JUN-2000; 2000US-0210380P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Duda A, Kazemi A, Messer C, Sausker EA;
 XX WPI; 2002-566435/60.
 XX New variants of colony stimulating factor 3 (CSF3) isogenes, useful for
 PT improving efficiency and reliability in the development of drugs for
 PT treating diseases associated with CSF3 activity e.g. neutropenia.
 XX Claim 19; Page 13; 68pp; English.
 XX The present invention provides the protein, gene and cDNA sequences of
 CC human colony stimulating factor 3 (granulocyte) CSF3. Also described are
 CC single nucleotide polymorphisms (SNPs) identified within these sequences.
 CC The sequences can be used in the treatment of neutropenia, promyelocytic
 CC leukaemia and haematological disorders. The present sequence is an allele
 CC specific primer extension oligonucleotide used to isolate the coding
 CC sequences of the invention
 XX
 SQ Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 GCGGAGG 19
 Db 2 GCGGAGG 9
 RESULT 147
 ABK23699
 ID ABK23699 standard; DNA; 10 BP.
 XX
 AC ABK23699;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Transcript tag DNA sequence #288 induced or suppressed by N-myc.
 XX
 KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
 KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;
 KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
 XX Homo sapiens.
 XX
 PN WO200185941-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 11-MAY-2001; 2001WO-NL000361.
 XX
 PR 11-MAY-2000; 2000EP-00201698.
 PR 29-JUN-2000; 2000EP-00202284.
 XX
 PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
 XX
 PI Versteeg R, Caron HN;
 XX WPI; 2002-066603/09.
 XX A new nucleic acid library of myc-dependent downstream genes capable of
 PT supporting a neoplastic characteristic of cancer is useful to find new

PT therapies and diagnoses for cancer.
 XX
 PS Disclosure; Page 57; 69pp; English.
 XX

CC The present invention relates to a nucleic acid library comprising myc-
 CC dependent downstream genes or their functional fragments essentially
 CC capable of supporting a neoplastic character of cancer such as growth,
 CC invasion or spread. These myc target or tag sequences are identified by
 CC SAGE (serial analysis of gene expression). The library is useful to find
 CC new diagnoses and treatments for cancer. The invention is also useful to
 CC enhance production of recombinant proteins in a production system with
 CC high expression of endogenous or transfected myc oncogenes. ABK23412-
 CC ABK23828 represent transcript tag DNA sequences that are activated or
 CC repressed by N-myc in human neuroblastoma
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGTG 12
 Db 3 GCGCTGTG 10

RESULT 148
 ACA94662
 ID ACA94662 standard; DNA; 10 BP.
 XX
 AC ACA94662;
 XX
 DT 18-JUL-2003 (first entry)
 XX
 DE DNA tag from human transcript repressed in adenomas/cancers #195.
 XX
 KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.
 XX
 OS Homo sapiens.
 XX
 PN WO2003022863-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 09-SEP-2002; 2002WO-US028518.
 XX
 PR 07-SEP-2001; 2001US-0317494P.
 PR 30-MAY-2002; 2002US-0383805P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Buckhaults P, Kinzler KW, Vogelstein B;
 XX
 DR WPI; 2003-313220/30.
 XX
 PT Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.
 XX
 PS Disclosure; Page 32; 59pp; English.
 XX

CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA

CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces by
 CC detection of increased reaction product or decreased RDP substrate, and
 CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a
 CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or decreased
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC repressed in colorectal cancer or colorectal adenoma
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGTG 12
 Db 3 GCGCTGTG 10

RESULT 149
 ACA94515
 ID ACA94515 standard; DNA; 10 BP.
 XX
 AC ACA94515;
 XX
 DT 18-JUL-2003 (first entry)
 XX
 DE DNA tag from human transcript repressed in adenomas/cancers #48.
 XX
 KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.
 XX
 OS Homo sapiens.
 XX
 PN WO2003022863-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 09-SEP-2002; 2002WO-US028518.
 XX
 PR 07-SEP-2001; 2001US-0317494P.
 PR 30-MAY-2002; 2002US-0383805P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Buckhaults P, Kinzler KW, Vogelstein B;
 XX
 DR WPI; 2003-313220/30.
 XX
 PT Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.
 XX
 PS Disclosure; Page 27; 59pp; English.
 XX

CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA
 CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
 CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces by
 CC detection of increased reaction product or decreased RDP substrate, and
 CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a
 CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or RDP substrate
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC repressed in colorectal cancer or colorectal adenoma
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGCG 15
 Db 2 CTGTGGCG 9
 |||||

RESULT 150
 ADS76513
 ID ADS76513 standard; DNA; 10 BP.
 AC
 XX ADS76513;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Breast cancer detection oligonucleotide #295.
 XX
 KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
 KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
 KW cathepsin L inhibitor; cathepsin F inhibitor;
 KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
 KW collagen antagonist; diagnosis; breast tissue; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2004085621-A2.
 XX
 PD 07-OCT-2004.
 XX
 PF 22-MAR-2004; 2004WO-US008866.
 XX
 PR 20-MAR-2003; 2003US-0456735P.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX Polyak K, Porter D, Allinen M;
 XX WPI; 2004-728732/71.
 DR
 XX Diagnosing breast cancer comprises determining expression levels of a
 XX gene selected from those differentially expressed in normal or cancerous
 XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
 XX and cystatin C.
 XX
 PS Example 2; SEQ ID NO 295; 149pp; English.
 XX
 CC The invention relates to a method of diagnosis (M1) comprising: (a)
 CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
 CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCTG 10
 Db 2 TCGCGCTG 9
 |||||

RESULT 151
 ADS78031
 ID ADS78031 standard; DNA; 10 BP.
 AC
 XX ADS78031;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Breast cancer detection oligonucleotide #1813.
 XX
 KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
 KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
 KW cathepsin L inhibitor; cathepsin F inhibitor;
 KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
 KW collagen antagonist; diagnosis; breast tissue; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2004085621-A2.
 XX
 PD 07-OCT-2004.
 XX
 PF 22-MAR-2004; 2004WO-US008866.
 XX
 PR 20-MAR-2003; 2003US-0456735P.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX Polyak K, Porter D, Allinen M;
 XX WPI; 2004-728732/71.
 DR
 XX Diagnosing breast cancer comprises determining expression levels of a
 XX gene selected from those differentially expressed in normal or cancerous
 XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
 XX and cystatin C.
 XX
 PS Example 6; SEQ ID NO 1813; 149pp; English.
 XX
 CC The invention relates to a method of diagnosis (M1) comprising: (a)

XX Polyak K, Porter D, Allinen M;
 PI WPI; 2004-728732/71.
 DR
 XX Diagnosing breast cancer comprises determining expression levels of a
 XX gene selected from those differentially expressed in normal or cancerous
 XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
 XX and cystatin C.
 XX
 PS Example 2; SEQ ID NO 295; 149pp; English.
 XX
 CC The invention relates to a method of diagnosis (M1) comprising: (a)
 CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
 CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCTG 10
 Db 2 TCGCGCTG 9
 |||||

RESULT 151
 ADS78031
 ID ADS78031 standard; DNA; 10 BP.
 AC
 XX ADS78031;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Breast cancer detection oligonucleotide #1813.
 XX
 KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
 KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
 KW cathepsin L inhibitor; cathepsin F inhibitor;
 KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
 KW collagen antagonist; diagnosis; breast tissue; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2004085621-A2.
 XX
 PD 07-OCT-2004.
 XX
 PF 22-MAR-2004; 2004WO-US008866.
 XX
 PR 20-MAR-2003; 2003US-0456735P.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX Polyak K, Porter D, Allinen M;
 XX WPI; 2004-728732/71.
 DR
 XX Diagnosing breast cancer comprises determining expression levels of a
 XX gene selected from those differentially expressed in normal or cancerous
 XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
 XX and cystatin C.
 XX
 PS Example 6; SEQ ID NO 1813; 149pp; English.
 XX
 CC The invention relates to a method of diagnosis (M1) comprising: (a)

CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
 CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing the
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.

XX Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCTG 10
 |||||
 Db 2 TCGCGCTG 9

RESULT 152

ADS76514

ID ADS76514 standard; DNA; 10 BP.

XX AC ADS76514;

XX 30-DEC-2004 (first entry)

XX Breast cancer detection oligonucleotide #296.

XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
 KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
 KW cathepsin L inhibitor; cathepsin F inhibitor;
 KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
 KW collagen antagonist; diagnosis; breast tissue; cancer.

XX Homo sapiens.

XX WO2004085621-A2.

XX 07-OCT-2004.

XX 22-MAR-2004; 2004WO-US008866.

XX 20-MAR-2003; 2003US-0456735P.

XX (DAND) DANA FARBER CANCER INST INC.

XX Polyak K, Porter D, Allinen M;

XX WPI; 2004-728732/71.

XX Diagnosing breast cancer comprises determining expression levels of a
 PT gene selected from those differentially expressed in normal or cancerous
 PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
 PT and cystatin C.

XX Example 2; SEQ ID NO 296; 149pp; English.

XX The invention relates to a method of diagnosis (M1) comprising: (a)
 CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
 CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.

XX Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCTG 10
 |||||
 Db 2 TCGCGCTG 9

RESULT 153

ADU19803

ID ADU19803 standard; DNA; 10 BP.

XX AC ADU19803;

XX 13-JAN-2005 (first entry)

XX Hypoxia-related tumorigenesis-related SAGE tag #1594.

XX screening; hypoxia-related tumorigenesis;
 KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.

XX Unidentified.

XX WO2004092198-A2.

XX 28-OCT-2004.

XX 09-APR-2004; 2004WO-US011087.

XX 09-APR-2003; 2003US-0461712P.

XX (GENZ) GENZYME CORP.

XX Nacht M;

XX WPI; 2004-758333/74.

XX Identifying agents that alter biological activity of a polypeptide
 PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis
 PT comprises contacting an agent with a target cell and monitoring activity
 PT of expressed product.

XX Disclosure; Page 88; 100pp; English.

XX The invention comprises a method of screening for candidate agents
 CC capable of altering the biological activity of a protein encoded by a
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the
 CC invention involves: contacting a test agent with a target cell expressing
 CC the nucleotide, and monitoring the activity of the expressed protein
 CC product; if the test agent modifies the activity of the expressed protein
 CC then this is a candidate agent. The method of the invention is useful for
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
 CC or treating tumours. The present DNA sequence represents a SAGE tag that
 CC was used in the exemplification of the invention.

XX Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCTG 10
 |||||
 Db 2 TCGCGCTG 9

RESULT 154

ABV69823/C

ID ABV69823 standard; cDNA; 11 BP.

XX AC ABV69823;

XX 21-OCT-2002 (first entry)

XX


```

DE Human skin EST 7609.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP015179.
PF
XX
XX 03-JAN-2001; 2001DE-01000127.
PR
XX (HENK ) HENKEL KGAA.
PA
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Claim 24; Page 241; 1345pp; German.
PS
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 42.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGGC 14
Db 8 GCTGTGGC 1
|||||

RESULT 155
ABV62402/c
ID ABV62402 standard; cDNA; 11 BP.
XX
XX AC ABV62402;
XX
XX 21-OCT-2002 (first entry)
DT
XX Human skin EST 188.
DE
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP015179.
PF
XX
XX 03-JAN-2001; 2001DE-01000127.
PR
XX (HENK ) HENKEL KGAA.
PA
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 42.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGGC 14
Db 8 GCTGTGGC 1
|||||

RESULT 156
ABV67604/c
ID ABV67604 standard; cDNA; 11 BP.
XX
XX AC ABV67604;
XX
XX 21-OCT-2002 (first entry)
DT
XX Human skin EST 5390.
DE
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP015179.
PF
XX
XX 03-JAN-2001; 2001DE-01000127.
PR
XX (HENK ) HENKEL KGAA.
PA
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 42.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGGC 14
Db 8 GCTGTGGC 1
|||||

RESULT 155
ABV62402/c
ID ABV62402 standard; cDNA; 11 BP.
XX
XX AC ABV62402;
XX
XX 21-OCT-2002 (first entry)
DT
XX Human skin EST 188.
DE
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP015179.
PF

```

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

PS Disclosure; Page 174; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed

CC in the skin of humans or animals by subjecting a mixture of genetically

CC encoded factors from skin, to serial analysis of gene expression (SAGE)

CC so as to identify skin-expressed genes and quantify their expression.

CC (M1) is useful for identifying genes involved in skin homeostasis; to

CC determine skin homeostasis and to test agent (A) that maintains or

CC promotes skin homeostasis or that can be used for treating skin

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

CC skin. The present sequence is that of a human expressed sequence tag

CC (EST) of the invention

XX

XX Sequence 11 BP; 3 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGGC 14

DB 8 GCTGTGGC 1

RESULT 157

AAC85261

ID AAC85261 standard; DNA; 11 BP.

XX

AC AAC85261;

XX

DT 22-MAR-2001 (first entry)

XX

DE mutD promoter sequence pOS102.

XX

XX E. coli; mutD; evolved microorganism; heterologous; mutator gene;

KW mutation rate; DNA repair gene; proof reading; selective pressure; ss.

KW

OS Synthetic.

OS

XX WO200070037-A2.

PN

XX 23-NOV-2000.

PD

XX

XX 15-MAY-2000; 2000WO-US013337.

PF

XX

XX 19-MAY-1999; 99US-00314847.

PR

XX (GEMV) GENENCOR INT INC.

PA

XX Schellenberger V, Liu AD, Selifonova OV;

PI

XX WPI; 2001-070775/08.

DR

XX Directing evolution of microorganisms to produce microorganisms able to

PT grow under conditions suitable for production of useful products,

PT comprises using mutator genes and extreme conditions.

XX

XX Disclosure; Page 12; 47pp; English.

XX

XX The sequences given in AAC85259-64 represent mutated promoter sequences

CC which were used with the E. coli mutD coding sequence in the method of

CC the invention to prepare an evolved microorganism. The method comprises

CC culturing a microorganism having a heterologous mutator gene, for at

CC least 20 doublings to select an evolved microorganism, where the gene

CC generates a mutation rate of at least 5 - 100 000 fold relative to wild

CC type. The evolved microorganism is then restored to a wild type mutation

CC rate. A mutator gene is defined in the specification as being a DNA

CC repair gene which comprises a mutation and which has impaired proof

CC reading function. The method is useful for directing the evolution of a

CC microorganism, i.e., directing desired genetic change in microorganisms

CC in response to selective pressure. Microorganisms are produced that are

CC

CC capable of producing, e.g., enzymes, growth factors, hormones, vitamins,

CC amino acids, dyes or other chemicals. The method can be used to produce

CC microorganisms which can grow under extreme conditions, e.g., high

CC temperature, pH extremes, high salt concentrations or the presence of

CC solvent

XX

XX Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGGCTGTG 12

DB 1 GTGCCCTGTG 11

RESULT 158

ABQ87267

ID ABQ87267 standard; cDNA; 11 BP.

XX

AC ABQ87267;

XX

DT 10-SEP-2002 (first entry)

XX

XX Human skin stress/ageing related EST SEQ ID NO 1022.

DE

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

KW

XX Homo sapiens.

OS

XX WO200253773-A2.

PN

XX 11-JUL-2002.

PD

XX

XX 20-DEC-2001; 2001WO-EP015178.

PF

XX

XX 03-JAN-2001; 2001DE-01000121.

PR

XX (HENK) HENKEL KGAA.

PA

XX Petersohn D, Conradt M, Hofmann K;

PI

XX WPI; 2002-528865/56.

DR

XX Identifying genes involved in skin stress and aging, useful e.g. in

PT screening for cosmetic or therapeutic agents, based on differential gene

PT expression.

XX

XX Claim 8; Page 79; 325pp; German.

PS

XX The invention relates to identifying (M1) genes in vitro that, in humans

CC or animals, are important for skin ageing and/or skin stress by serial

CC analysis of gene expression between mixtures of transcribed and

CC optionally translated, genetically encoded factors (A) obtained from

CC young and aged skin, to identify that genes that show strong differential

CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is

CC useful for: identifying markers of skin ageing and/or stress; determining

CC skin ageing and/or stress; and identifying or determining the effects of

CC pharmaceutical or cosmetic agents for control of skin ageing. The present

CC sequence is one of a group of human skin ageing/stress related expressed

CC sequence tags (ABQ86246-ABQ87680) of the invention

XX

XX Sequence 11 BP; 2 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGCGGAAG 18

DB 1 CTGGGGGGAAG 11

```

RESULT 159
ABQ87096/c
ID ABQ87096 standard; cDNA; 11 BP.
XX
XX AC ABQ87096;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Human skin stress/ageing related EST SEQ ID NO 851.
XX
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253773-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015178.
XX
XX PR 03-JAN-2001; 2001DE-01000121.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX
XX PS Claim 8; Page 72; 325pp; German.
XX
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX SQ Sequence 11 BP; 2 A; 5 C; 4 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 1.3e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4 CGCGTGTGGC 14
XX | | | | |
XX 11 CTCGCTGGGCG 1
XX
XX RESULT 160
ABQ87230/c
ID ABQ87230 standard; cDNA; 11 BP.
XX
XX AC ABQ87230;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Human skin stress/ageing related EST SEQ ID NO 985.
XX
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253773-A2.
XX
XX Query Match 41.1%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 1.3e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4 CGCGTGTGGC 14
XX | | | | |
XX 11 CTCGCTGGGCG 1
XX
XX RESULT 161
ABV68460/c
ID ABV68460 standard; cDNA; 11 BP.
XX
XX AC ABV68460;
XX
XX DT 21-OCT-2002 (first entry)
XX
XX DE Human skin EST 6246.
XX
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253774-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015179.
XX
XX PR 03-JAN-2001; 2001DE-01000127.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-590638/63.
XX
XX PT In vitro identification of skin-expressed genes, useful for determining

```

```

XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015178.
XX
XX PR 03-JAN-2001; 2001DE-01000121.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX
XX PS Claim 8; Page 78; 325pp; German.
XX
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 1.3e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 8 CTGTGGCGGAAG 18
XX | | | | |
XX 11 CTGGGGCTAAG 1
XX
XX Db
XX
XX RESULT 161
ABV68460/c
ID ABV68460 standard; cDNA; 11 BP.
XX
XX AC ABV68460;
XX
XX DT 21-OCT-2002 (first entry)
XX
XX DE Human skin EST 6246.
XX
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253774-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015179.
XX
XX PR 03-JAN-2001; 2001DE-01000127.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-590638/63.
XX
XX PT In vitro identification of skin-expressed genes, useful for determining

```

PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 198; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGGCGCTGT 11
DB 11 GGTACCCCTGT 1

RESULT 162
ABV69665
ID ABV69665 standard; cDNA; 11 BP.
XX
AC ABV69665;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7451.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 234; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14
DB 1 CACGAGTGGC 11

RESULT 163
ABV65281
ID ABV65281 standard; cDNA; 11 BP.
XX
AC ABV65281;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3067.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 110; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGCGGAAG 18
|||||

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Db      1 CTGGGGCGAAG 11
RESULT 164
ABV67742/c
ID      ABV67742 standard; cDNA; 11 BP.
AC      ABV67742;
XX
XX      21-OCT-2002 (first entry)
XX
XX      Human skin EST 5528.
XX
XX      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX      Homo sapiens.
XX
XX      WO200253774-A2.
XX
XX      11-JUL-2002.
XX
XX      20-DEC-2001; 2001WO-EP015179.
XX
XX      03-JAN-2001; 2001DE-01000127.
XX
XX      (HENK ) HENKEL KGAA.
XX
XX      Petersohn D, Conradt M, Hofmann K;
XX
XX      WPI; 2002-590638/63.
XX
XX      In vitro identification of skin-expressed genes, useful for determining
PT      homeostasis and identifying cosmetic or pharmaceutical agents against
PT      e.g. skin cancer.
XX
XX      Claim 24; Page 177; 1345pp; German.
XX
XX      The invention relates to in vitro identification (M1) of genes expressed
CC      in the skin of humans or animals by subjecting a mixture of genetically
CC      encoded factors from skin, to serial analysis of gene expression (SAGE)
CC      so as to identify skin-expressed genes and quantify their expression.
CC      (M1) is useful for identifying genes involved in skin homeostasis; to
CC      determine skin homeostasis and to test agent (A) that maintains or
CC      promotes skin homeostasis or that can be used for treating skin
CC      disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC      ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC      rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC      skin. The present sequence is that of a human expressed sequence tag
CC      (EST) of the invention
XX
XX      Sequence 11 BP; 2 A; 5 C; 4 G; 0 T; 0 U; 0 Other;
XX
XX      Query Match      41.1%; Score 7.8; DB 1; Length 11;
XX      Best Local Similarity 81.8%; Pred. NO. 1.3e+02;
XX      Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      QY      4 CCGGCTGTGGC 14
XX      DB      11 CTGGCTGGGC 1
XX
XX      RESULT 165
XX      ABV70868/c
XX      ID      ABV70868 standard; cDNA; 11 BP.
XX
XX      AC      ABV70868;
XX
XX      21-OCT-2002 (first entry)
XX
XX      Human skin EST 8654.
XX
XX      1 CTGGGGCGAAG 11
XX
XX      RESULT 166
XX      ABV63447/c
XX      ID      ABV63447 standard; cDNA; 11 BP.
XX
XX      AC      ABV63447;
XX
XX      21-OCT-2002 (first entry)
XX
XX      Human skin EST 1233.
XX
XX      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX      Homo sapiens.
XX
XX      WO200253774-A2.
XX
XX      11-JUL-2002.
XX
XX      20-DEC-2001; 2001WO-EP015179.
XX
XX      03-JAN-2001; 2001DE-01000127.

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KW      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX      Homo sapiens.
XX
XX      WO200253774-A2.
XX
XX      11-JUL-2002.
XX
XX      20-DEC-2001; 2001WO-EP015179.
XX
XX      03-JAN-2001; 2001DE-01000127.
XX
XX      (HENK ) HENKEL KGAA.
XX
XX      Petersohn D, Conradt M, Hofmann K;
XX
XX      WPI; 2002-590638/63.
XX
XX      In vitro identification of skin-expressed genes, useful for determining
PT      homeostasis and identifying cosmetic or pharmaceutical agents against
PT      e.g. skin cancer.
XX
XX      Claim 24; Page 277; 1345pp; German.
XX
XX      The invention relates to in vitro identification (M1) of genes expressed
CC      in the skin of humans or animals by subjecting a mixture of genetically
CC      encoded factors from skin, to serial analysis of gene expression (SAGE)
CC      so as to identify skin-expressed genes and quantify their expression.
CC      (M1) is useful for identifying genes involved in skin homeostasis; to
CC      determine skin homeostasis and to test agent (A) that maintains or
CC      promotes skin homeostasis or that can be used for treating skin
CC      disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC      ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC      rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC      skin. The present sequence is that of a human expressed sequence tag
CC      (EST) of the invention
XX
XX      Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      41.1%; Score 7.8; DB 1; Length 11;
XX      Best Local Similarity 81.8%; Pred. NO. 1.3e+02;
XX      Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      QY      8 CTGGCGGAAG 18
XX      DB      11 CTGGCGCTAAG 1
XX
XX      RESULT 166
XX      ABV63447/c
XX      ID      ABV63447 standard; cDNA; 11 BP.
XX
XX      AC      ABV63447;
XX
XX      21-OCT-2002 (first entry)
XX
XX      Human skin EST 1233.
XX
XX      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX      Homo sapiens.
XX
XX      WO200253774-A2.
XX
XX      11-JUL-2002.
XX
XX      20-DEC-2001; 2001WO-EP015179.
XX
XX      03-JAN-2001; 2001DE-01000127.

```


SQ Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAG 18
 |||||
 Db 1 CTGTGTCCAAG 11
 |||||

RESULT 169
 ABV62244
 ID ABV62244 standard; cDNA; 11 BP.
 XX
 AC ABV62244;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 30.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 26; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14
 |||||
 Db 1 CACGCAGTGGC 11
 |||||

RESULT 170
 ADQ36355
 ID ADQ36355 standard; DNA; 11 BP.
 XX
 AC ADQ36355;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 1172.
 XX
 KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
 XX
 OS Homo sapiens.
 XX
 PN DE10260931-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 20-DEC-2002; 2002DE-01060931.
 XX
 PR 20-DEC-2002; 2002DE-01060931.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 XX
 DR WPI; 2004-518857/50.
 XX
 PT In vitro identification of genes important for hair-bearing skin, useful
 PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.
 XX
 PS Claim 4; SEQ ID NO 1172; 250pp; German.
 XX
 CC This invention describes a novel in vitro method for identifying genes
 CC that are significant for hair-bearing skin in humans. The method
 CC comprises recovering, from hair-bearing skin, a first mixture of
 CC genetically expressed (transcribed and optionally translated) factors
 CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
 CC mixture from skin on which hair does not grow and subjecting both
 CC mixtures to serial analysis of gene expression (SAGE) to identify those
 CC genes for which expression is markedly different between the two types of
 CC skin. The invention also describes in vitro methods for determining
 CC homeostasis of human hair-bearing skin and for determining activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
 CC a test kit comprising a solid support (flexible or rigid) with
 CC immobilised probes are also described for determining homeostasis. The
 CC hair-bearing skin is from the scalp and the other skin is from the face.
 CC The method allows identification of as many as possible of the genes
 CC important for hair-bearing skin, and therefore of a very wide range of
 CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
 CC human DNA tag fragments used to identify genes associated with hair-
 CC bearing skin.
 XX
 SQ Sequence 11 BP; 1 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCTGTGGCG 15
 |||||
 Db 1 GCGCTGTGGAG 11
 |||||

RESULT 171
 ADQ35677
 ID ADQ35677 standard; DNA; 11 BP.
 XX
 AC ADQ35677;
 XX
 DT 23-SEP-2004 (first entry)

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XX DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 494.
XX KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX OS Homo sapiens.
XX XX DE10260931-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060931.
XX PR 20-DEC-2002; 2002DE-01060931.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX XX WPI; 2004-518857/50.
XX PS Claim 5; SEQ ID NO 494; 250pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
XX CC that are significant for hair-bearing skin in humans. The method
XX CC comprises recovering, from hair-bearing skin, a first mixture of
XX CC genetically expressed (transcribed and optionally translated) factors
XX CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
XX CC mixture from skin on which hair does not grow and subjecting both
XX CC mixtures to serial analysis of gene expression (SAGE) to identify those
XX CC genes for which expression is markedly different between the two types of
XX CC skin. The invention also describes in vitro methods for determining
XX CC homeostasis of human hair-bearing skin and for determining activity of
XX CC cosmetic and pharmaceutical agents for use against disorders or
XX CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
XX CC a test kit comprising a solid support (flexible or rigid) with
XX CC immobilised probes are also described for determining homeostasis. The
XX CC hair-bearing skin is from the scalp and the other skin is from the face.
XX CC The method allows identification of as many as possible of the genes
XX CC important for hair-bearing skin, and therefore, of a very wide range of
XX CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
XX CC human DNA Tag fragments used to identify genes associated with hair-
XX CC bearing skin.
XX SQ Sequence 11 BP; 3 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
DB 1 TGTGGGGAAG 11

RESULT 172
ADQ34103/c
ID ADQ34103 standard; DNA; 11 BP.
XX AC ADQ34103;
XX XX 23-SEP-2004 (first entry)
XX DT Human facial skin-associated DNA fragment SEQ ID NO 2193.
XX DE facial skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; biochip; cosmetic; pharmaceutical; ds.

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XX OS Homo sapiens.
XX PN DE10260928-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060928.
XX PR 20-DEC-2002; 2002DE-01060928.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX XX WPI; 2004-518855/50.
XX PS Claim 4; SEQ ID NO 2193; 577pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
XX CC that are significant for facial skin in humans. The method comprises
XX CC recovering, from facial skin, a first mixture of genetically expressed
XX CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
XX CC their fragments), recovering a second, similar mixture from some other
XX CC human tissue, preferably skin from a protected area, especially from the
XX CC breast and subjecting the mixtures to serial analysis of gene expression
XX CC (SAGE) to identify those genes for which expression is markedly different
XX CC between facial skin and the other tissue. The invention also describes an
XX CC in vitro method for determining homeostasis of human facial skin; a test
XX CC kit which comprises a solid support (flexible or rigid) on which are
XX CC immobilised probes that bind specifically to the factors of interest and
XX CC a biochip for determining homeostasis of human facial skin. The products
XX CC of the invention are also used in a method which determines activity of
XX CC cosmetic and pharmaceutical agents for use against disorders or
XX CC disturbances of the homeostasis of human skin and a screening method for
XX CC identifying cosmetic and pharmaceutical agents. The method allows
XX CC identification of as many as possible of the genes important for facial
XX CC skin and thus of a very wide range of potential therapeutic and cosmetic
XX CC agents. ADQ31911-ADQ35111 represent human DNA tag fragments used to
XX CC identify the facial skin-associated genes described in the invention.
XX SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGCGGCTGT 11
DB 11 GGTACCCCTGT 1

RESULT 173
ADT79188
ID ADT79188 standard; DNA; 11 BP.
XX AC ADT79188;
XX XX 30-DEC-2004 (first entry)
XX DT Oligonucleotide #1 used in detection of Cx26 35deltaG mutation.
XX DE Connexin 26; Cx26; non-syndromic hearing impairment; NSHI;
XX KW gap-junction beta 2; GJB2; ss.
XX OS Unidentified.
XX XX US2004203035-A1.

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XX PD 14-OCT-2004.
XX PF
XX PP 09-JAN-2004; 2004US-00754408.
XX PR 09-JAN-2003; 2003US-0438963P.
XX PT (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX PA Mast AL, Dorn E, Kwiatkowski RJ, Accola M, Wigdal SS;
XX PI WPI; 2004-746972/73.
XX DR
XX XX
XX PT New kit comprises non-amplified oligonucleotide detection assay
XX PT configured for detecting at least one Connexin 26 allele, useful for
XX PT screening nucleic acid samples for the presence of mutations in the
XX PT connexin 26 or gap-junction beta 2 gene.
XX XX
XX PS Disclosure; SEQ ID NO 8; 25pp; English.
XX XX
XX CC The present invention relates to a method which comprises of a non-
XX CC amplified oligonucleotide detection assay configured for detecting at
XX CC least one Connexin 26 (Cx26) allele. The method of the invention is
XX CC useful for the detection and characterisation of mutations associated
XX CC with non-syndromic hearing impairment (NSHI). The invention is also
XX CC useful for using invasive cleavage structure assays to screen nucleic
XX CC acid samples for the presence of mutations in the connexin 26 or gap-
XX CC junction beta 2 gene (GJB2) associated with non-syndromic hearing loss.
XX CC The present sequence is an oligonucleotide used in the detection of Cx26
XX CC 35deltaG mutation.
XX XX
XX SQ Sequence 11 BP; 1 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. NO. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CGCGCTGTGGC 14
DB 1 CGCGCGGAGGC 11
RESULT 174
ADZ24827/c
ID ADZ24827 standard; DNA; 11 BP.
XX AC
XX ADZ24827;
XX DT 16-JUN-2005 (first entry)
XX DE Human SNP detection related oligonucleotide #1794.
XX KW ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;
XX KW immune disorder; cardiovascular disease; metabolic disorder;
XX KW respiratory disease; musculoskeletal disease; renal disease;
XX KW nephrotropic; endocrine disease; genitourinary disease.
XX XX
XX OS Homo sapiens.
XX XX WO2005030952-A1.
XX PN
XX PD 07-APR-2005.
XX XX
XX PF 30-SEP-2004; 2004WO-JP014784.
XX XX
XX PR 30-SEP-2003; 2003JP-00342519.
XX PR 28-MAY-2004; 2004JP-00158717.
XX XX
XX XX (RIKE ) RIKEN KK.
XX PA (STAG-) STAGEN CO LTD.
XX PA (SEKI/) SEKINE A.
XX PA (IIDA/) IIDA A.
XX PA (SAIT/) SAITO S.

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XX PI Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;
XX DR WPI; 2005-305936/31.
XX XX
XX PT Analyzing haplotype, by detecting polymorphism in drug-related genes,
XX PT electing common polymorphism (CP), building haplotype block using CP,
XX PT specifying CP within block, specifying tag polymorphism from CP within
XX PT block.
XX XX
XX PS Disclosure; SEQ ID NO 1794; 1290pp; Japanese.
XX XX
XX CC The invention relates to a method of analyzing haplotype, by detecting
XX CC gene polymorphism in drug-related genes such as aryl acetylamide
XX CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
XX CC sub-family A (ABCA), member 1. The method is useful for analyzing
XX CC haplotype. The method is useful for estimating the sensitivity or disease
XX CC of a medicine or a foreign material, for selecting the medicine for
XX CC preventing or treating diseases, for determining appropriate dosage of
XX CC medicine for preventing or treating a disease, for analyzing a drug
XX CC interaction, and for determining the related polymorphism relative to the
XX CC sensitivity of the medicine, foreign material or disease. The diseases
XX CC include malignant tumor, immune disorder circulatory disease, metabolic
XX CC disease, kidney disease, respiratory disease and muscle associated
XX CC disease. The method enables analysis of the individual differences
XX CC related to the sensitivity of a medicine, using a haplotype, without
XX CC using each single nucleotide polymorphism. The present sequence
XX CC represents a human SNP detection related oligonucleotide.
XX XX
XX SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. NO. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTGCGCTGT 11
DB 11 GGTGCGCACTGT 1
RESULT 175
AAQ71089/c
ID AAQ71089 standard; cDNA; 10 BP.
XX AC
XX AAQ71089;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 20-APR-1995 (first entry)
XX XX
XX DE Merlin exon 7 splice acceptor site.
XX XX
XX KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;
XX KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;
XX KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;
XX KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;
XX KW merlin-associated tumour; D22S1; posterior capsular lens opacity;
XX KW deafness; balance disorder; paralysis; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN EP613945-A2.
XX XX
XX PD 07-SEP-1994.
XX XX
XX PF 25-FEB-1994; 94EP-00301367.
XX XX
XX PR 25-FEB-1993; 93US-00022034.
XX PR 04-MAR-1993; 93US-00026063.
XX PR 19-AUG-1993; 93US-00108808.
XX PR 22-DEC-1993; 93US-00171718.
XX XX
XX PA (GEO ) GEN HOSPITAL CORP.
XX XX

```

PI Trofatter JA, Maccollin MM, Gusella JF;
 XX
 DR WPI; 1994-272992/34.
 XX
 PT The tumour suppressor gene merlin - for treatment and diagnosis of
 PT tumours and neurofibromatosis (NF2).
 XX
 PS Example 6; Page 26; 86pp; English.
 XX
 CC The sequences given in AAQ71078-109 represent the splice donor and
 CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-
 CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2
 CC "gene" has been shown by linkage studies to be assigned to chromosome 22.
 CC The missing or mutated gene in NF2 patients has been shown to be the
 CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-
 CC like protein), which possesses tumour suppressor activity, and whose
 CC tumour suppressor activity is mediated by inter- actions with the
 CC cytoskeleton. The merlin gene is found on chromosome 22 between the known
 CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene
 CC is either lost or mutated. A mutant merlin protein may be encoded by a
 CC gene in which a mutation of A to T at the first position of the codon
 CC encoding amino acid 220 causes the substitution of Tyr for Asn. The
 CC merlin gene may be used in gene therapy for the treatment of a merlin-
 CC associated tumour or NF2, or for prevention of schwannoma, meningioma,
 CC posterior capsular lens opacities, deafness or hearing loss, balance
 CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CTGTGGCGA 16
 DB 10 CTGTGGCGA 2
 RESULT 176
 AAQ71095/c
 ID AAQ71095 standard; cDNA; 10 BP.
 XX
 AC AAQ71095;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-APR-1995 (first entry)
 XX
 DE Merlin exon 10 splice acceptor site.
 XX
 KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;
 KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;
 KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;
 KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;
 KW merlin-associated tumour; D22S1; posterior capsular lens opacity;
 KW deafness; balance disorder; paralysis; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP613945-A2.
 XX
 PD 07-SEP-1994.
 XX
 PF 25-FEB-1994; 94EP-00301367.
 XX
 PR 25-FEB-1993; 93US-00022034.
 PR 04-MAR-1993; 93US-00026063.
 PR 19-AUG-1993; 93US-00108808.
 PR 22-DEC-1993; 93US-00171718.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Trofatter JA, Maccollin MM, Gusella JF;
 XX

DR WPI; 1994-272992/34.
 XX
 PT The tumour suppressor gene merlin - for treatment and diagnosis of
 PT tumours and neurofibromatosis (NF2).
 XX
 PS Example 6; Page 26; 86pp; English.
 XX
 CC The sequences given in AAQ71078-109 represent the splice donor and
 CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-
 CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2
 CC "gene" has been shown by linkage studies to be assigned to chromosome 22.
 CC The missing or mutated gene in NF2 patients has been shown to be the
 CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-
 CC like protein), which possesses tumour suppressor activity, and whose
 CC tumour suppressor activity is mediated by inter- actions with the
 CC cytoskeleton. The merlin gene is found on chromosome 22 between the known
 CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene
 CC is either lost or mutated. A mutant merlin protein may be encoded by a
 CC gene in which a mutation of A to T at the first position of the codon
 CC encoding amino acid 220 causes the substitution of Tyr for Asn. The
 CC merlin gene may be used in gene therapy for the treatment of a merlin-
 CC associated tumour or NF2, or for prevention of schwannoma, meningioma,
 CC posterior capsular lens opacities, deafness or hearing loss, balance
 CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CTGTGGCGA 16
 DB 10 CTGTGGCGA 2
 RESULT 177
 AAQ96664/c
 ID AAQ96664 standard; DNA; 10 BP.
 XX
 AC AAQ96664;
 XX
 DT 16-OCT-2003 (revised)
 DT 22-MAR-1996 (first entry)
 XX
 DE HIV-1 NL4-3 nef gene nucleotide deletion 259.
 XX
 KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN W09521912-A1.
 XX
 PD 17-AUG-1995.
 XX
 PF 14-FEB-1995; 95WO-AU0000063.
 XX
 PR 14-FEB-1994; 94AU-00003864.
 PR 21-FEB-1994; 94AU-00004002.
 PR 23-DEC-1994; 94AU-00000284.
 XX
 PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
 PA (AURE-) AUSTRALIAN RED CROSS SOC.
 XX
 PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
 XX
 DR WPI; 1995-293115/38.
 XX
 PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
 PT LTR region - can be used in a vaccine to inhibit/reduce productive
 PT infection in an individual by a pathogenic strain.
 XX
 PS Claim 13; Page 191; 301pp; English.


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AAZ79074/c
ID  AAZ79074 standard; DNA; 10 BP.
XX
AC  AAZ79074;
XX
DT  10-APR-2000 (first entry)
XX
DE  Human dendritic cell SAGE tag, SEQ ID NO:1502.
XX
XX  SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW  APC; monocyte-derived dendritic cell; differential gene expression;
KW  immunostimulatory cofactor; costimulatory factor; CTL;
KW  cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS  Homo sapiens.
XX
PN  WO9965924-A2.
XX
PD  23-DEC-1999.
XX
PF  18-JUN-1999; 99WO-US013800.
XX
PR  19-JUN-1998; 98US-0089833P.
PR  19-JUN-1998; 98US-0089844P.
PR  19-JUN-1998; 98US-0089853P.
PR  19-JUN-1998; 98US-0089878P.
PR  19-JUN-1998; 98US-0089918P.
PR  19-JUN-1998; 98US-0089922P.
PR  19-JUN-1998; 98US-0089933P.
PR  19-JUN-1998; 98US-0089944P.
PR  19-JUN-1998; 98US-0089977P.
PR  19-JUN-1998; 98US-0089992P.
PR  19-JUN-1998; 98US-0090008P.
PR  19-JUN-1998; 98US-0090035P.
PR  19-JUN-1998; 98US-0090036P.
PR  19-JUN-1998; 98US-0090039P.
PR  19-JUN-1998; 98US-0090041P.
PR  19-JUN-1998; 98US-0090042P.
PR  19-JUN-1998; 98US-0090043P.
PR  19-JUN-1998; 98US-0090044P.
PR  19-JUN-1998; 98US-0090045P.
PR  19-JUN-1998; 98US-0090047P.
PR  19-JUN-1998; 98US-0090048P.
PR  19-JUN-1998; 98US-0090072P.
PR  19-JUN-1998; 98US-0090076P.
PR  19-JUN-1998; 98US-0090077P.
PR  19-JUN-1998; 98US-0090078P.
PR  19-JUN-1998; 98US-0090079P.
PR  19-JUN-1998; 98US-0090080P.
PR  08-DEC-1998; 98US-0111715P.
XX
(GENZ ) GENZYME CORP.
PA  (ROBE/) ROBERTS B L.
PA  (SHAN/) SHANKARA S.
XX
PI  Roberts BL, Shankara S;
XX
XX  WPI; 2000-106077/09.
XX
XX  Isolated polynucleotides differentially expressed in antigen-presenting
PT  cells, useful in gene vaccines against cancer.
PT
PT
XX  Claim 1; Page 108; 130pp; English.
XX
XX  Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC  expression) tags used to identify mRNA transcripts encoding
CC  immunostimulatory cofactor proteins which are preferentially or
CC  differentially expressed in monocyte-derived dendritic cells compared
CC  with monocytes. Some of the transcripts correspond to known genes or ESTs
CC  (expressed sequence tags) which were previously unknown to be
CC  preferentially or differentially expressed in dendritic cells, while
CC  other transcripts correspond to novel genes. Antigen-presenting cell

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CC  (APC)-associated costimulatory factors play an important role in the
CC  activation of the cytotoxic immune response, particularly against tumour
CC  cells. Tumour antigen presentation via the MHC (major histocompatibility
CC  complex) and subsequent recognition by T-cell receptors is alone
CC  insufficient to activate a robust cytotoxic immune response that can lyse
CC  the tumour cells, immunostimulatory cofactors also being required for
CC  efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC  sequences identified using the SAGE tags have several potential uses.
CC  They may be used in vaccines to induce an immune response, particularly
CC  against a tumour antigen; to modulate the genotype of an APC; to screen
CC  for agents that modulate expression of differentially expressed genes in
CC  an APC; and as hybridisation probes/amplification primers for the
CC  diagnosis, prognosis and monitoring of diseases related to abnormal
CC  expression of these genes. Detection of the dendritic cell differentially
CC  expressed genes, or of their encoded proteins, can be used to identify
CC  cells as belonging to the monocyte lineage. Cells containing these genes
CC  can be used in active immunotherapy (or to stimulate production of a
CC  population of antigen-specific effector cells) and vectors containing
CC  them are used in gene therapy. Co-administration of tumour antigens and
CC  APC-associated costimulatory factors ensures adequate antigen
CC  presentation to endogenous APCs and upregulates the APCs for the
CC  presentation of co-stimulatory signals, migration to T cell-rich sites,
CC  secretion of T cell growth factors and secretion of chemokines for
CC  recruitment of immune effector cells
XX
SQ  Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCTGTGGCG 15
Db 10 GCTGTGGCG 2
RESULT 181
AAZ79675
ID  AAZ79675 standard; DNA; 10 BP.
XX
AC  AAZ79675;
XX
DT  10-APR-2000 (first entry)
XX
DE  Human dendritic cell SAGE tag, SEQ ID NO:2103.
XX
KW  SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW  APC; monocyte-derived dendritic cell; differential gene expression;
KW  immunostimulatory cofactor; costimulatory factor; CTL;
KW  cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS  Homo sapiens.
XX
PN  WO9965924-A2.
XX
PD  23-DEC-1999.
XX
PF  18-JUN-1999; 99WO-US013800.
XX
PR  19-JUN-1998; 98US-0089833P.
PR  19-JUN-1998; 98US-0089844P.
PR  19-JUN-1998; 98US-0089853P.
PR  19-JUN-1998; 98US-0089878P.
PR  19-JUN-1998; 98US-0089918P.
PR  19-JUN-1998; 98US-0089922P.
PR  19-JUN-1998; 98US-0089933P.
PR  19-JUN-1998; 98US-0089944P.
PR  19-JUN-1998; 98US-0089977P.
PR  19-JUN-1998; 98US-0089992P.
PR  19-JUN-1998; 98US-0090008P.
PR  19-JUN-1998; 98US-0090035P.
PR  19-JUN-1998; 98US-0090036P.
PR  19-JUN-1998; 98US-0090039P.
PR  19-JUN-1998; 98US-0090041P.
PR  19-JUN-1998; 98US-0090042P.
PR  19-JUN-1998; 98US-0090043P.
PR  19-JUN-1998; 98US-0090044P.
PR  19-JUN-1998; 98US-0090045P.
PR  19-JUN-1998; 98US-0090047P.
PR  19-JUN-1998; 98US-0090048P.
PR  19-JUN-1998; 98US-0090072P.
PR  19-JUN-1998; 98US-0090076P.
PR  19-JUN-1998; 98US-0090077P.
PR  19-JUN-1998; 98US-0090078P.
PR  19-JUN-1998; 98US-0090079P.
PR  19-JUN-1998; 98US-0090080P.
PR  08-DEC-1998; 98US-0111715P.
XX
(GENZ ) GENZYME CORP.
PA  (ROBE/) ROBERTS B L.
PA  (SHAN/) SHANKARA S.
XX
PI  Roberts BL, Shankara S;
XX
XX  WPI; 2000-106077/09.
XX
XX  Isolated polynucleotides differentially expressed in antigen-presenting
PT  cells, useful in gene vaccines against cancer.
PT
PT
XX  Claim 1; Page 108; 130pp; English.
XX
XX  Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC  expression) tags used to identify mRNA transcripts encoding
CC  immunostimulatory cofactor proteins which are preferentially or
CC  differentially expressed in monocyte-derived dendritic cells compared
CC  with monocytes. Some of the transcripts correspond to known genes or ESTs
CC  (expressed sequence tags) which were previously unknown to be
CC  preferentially or differentially expressed in dendritic cells, while
CC  other transcripts correspond to novel genes. Antigen-presenting cell

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PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090046P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 DR
 XX
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX
 XX Claim 1; Page 124; 130pp; English.
 XX
 CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the immune response, particularly
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 5 GGCCTGTGG 13
 Db 2 GGGCTGTGG 10

RESULT 182
 AAZ79480
 ID AAZ79480 standard; DNA; 10 BP.
 XX
 AC AAZ79480;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:1908.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO965924-A2.
 XX
 XX 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089911P.
 PR 19-JUN-1998; 98US-0089922P.
 PR 19-JUN-1998; 98US-0089933P.
 PR 19-JUN-1998; 98US-0089944P.
 PR 19-JUN-1998; 98US-0089978P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 DR
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX
 XX Claim 1; Page 119; 130pp; English.
 CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while

other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

Sequence 10 BP; 0 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
|||||||
DB 2 GCTGTGGCG 10

RESULT 183

AAZ78781/C
ID AAZ78781 standard; DNA; 10 BP.

AC AAZ78781;

XX 10-APR-2000 (first entry)

XX Human dendritic cell SAGE tag, SEQ ID NO:1209.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

XX 19-JUN-1998; 98US-0089833P.

XX 19-JUN-1998; 98US-0089844P.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089878P.

XX 19-JUN-1998; 98US-0089991P.

XX 19-JUN-1998; 98US-0089992P.

XX 19-JUN-1998; 98US-0089993P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0089999P.

XX 19-JUN-1998; 98US-0090000P.

19-JUN-1998; 98US-0090039P.
19-JUN-1998; 98US-0090040P.
19-JUN-1998; 98US-0090041P.
19-JUN-1998; 98US-0090042P.
19-JUN-1998; 98US-0090043P.
19-JUN-1998; 98US-0090044P.
19-JUN-1998; 98US-0090045P.
19-JUN-1998; 98US-0090047P.
19-JUN-1998; 98US-0090048P.
19-JUN-1998; 98US-0090072P.
19-JUN-1998; 98US-0090076P.
19-JUN-1998; 98US-0090077P.
19-JUN-1998; 98US-0090078P.
19-JUN-1998; 98US-0090079P.
19-JUN-1998; 98US-0090080P.
08-DEC-1998; 98US-011715P.

(GENZ) GENZYME CORP.

(ROBE/) ROBERTS B L.

(SHAN/) SHANKARA S.

Roberts BL, Shankara S;

WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.

Claim 1; Page 99; 130pp; English.

Sequences AAZ7573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

|||||

DB 10 TGGAGAAGG 2

```

RESULT 184
AAZ82348/c
ID AAZ82348 standard; DNA; 10 BP.
XX AC AAZ82348;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #1582.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX PS Claim 1; Page 100; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
| | | | | | | |

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Db 10 CTCTGTGGC 2

RESULT 185
AAZ81963/c
ID AAZ81963 standard; DNA; 10 BP.
XX AC AAZ81963;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #1197.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX PS Claim 1; Page 90; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      6 CGCTGTGGC 14
Db      9 CTCTGTGGC 1

RESULT 186
AAZ85441/c
ID  AAZ85441 standard; DNA; 10 BP.
XX
AC  AAZ85441;
DT  07-APR-2000 (first entry)
XX
DE  Metastatic breast tumour cell downregulated transcript tag #4675.
XX
KW  Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW  non-metastatic breast tumour tissue; gene therapy; anticancer;
KW  antimetastatic; vaccine; diagnosis; ss.
XX
OS  Homo sapiens.
XX
PN  WO9965928-A2.
XX
PD  23-DEC-1999.
XX
PF  18-JUN-1999; 99WO-US013647.
XX
PR  19-JUN-1998; 98US-0089853P.
PR  19-JUN-1998; 98US-0089997P.
PR  19-JUN-1998; 98US-0090039P.
PR  19-JUN-1998; 98US-0090040P.
PR  19-JUN-1998; 98US-0090041P.
XX
PA  (GENZ ) GENZYME CORP.
PA  (ROBE/) ROBERTS B L.
PA  (SHAN/) SHANKARA S.
XX
PI  Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
Isolated polynucleotides differentially expressed between metastatic and
non-metastatic breast cancer cells, useful for diagnosis, prevention and
treatment of cancer.
XX
Claim 1; Page 184; 219pp; English.
XX
AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy
XX
Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      2 GTCGCGCTG 10
      | | | | |
Db     10 GCGCGCTG 2

RESULT 187
AAZ83525
ID  AAZ83525 standard; DNA; 10 BP.
XX
AC  AAZ83525;
XX
DT  07-APR-2000 (first entry)
XX
DE  Metastatic breast tumour cell upregulated transcript tag #2759.
XX
KW  Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW  non-metastatic breast tumour tissue; gene therapy; anticancer;
KW  antimetastatic; vaccine; diagnosis; ss.
XX
OS  Homo sapiens.
XX
PN  WO9965928-A2.
XX
PD  23-DEC-1999.
XX
PF  18-JUN-1999; 99WO-US013647.
XX
PR  19-JUN-1998; 98US-0089853P.
PR  19-JUN-1998; 98US-0089997P.
PR  19-JUN-1998; 98US-0090039P.
PR  19-JUN-1998; 98US-0090040P.
PR  19-JUN-1998; 98US-0090041P.
XX
PA  (GENZ ) GENZYME CORP.
PA  (ROBE/) ROBERTS B L.
PA  (SHAN/) SHANKARA S.
XX
PI  Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
Isolated polynucleotides differentially expressed between metastatic and
non-metastatic breast cancer cells, useful for diagnosis, prevention and
treatment of cancer.
XX
Claim 1; Page 133; 219pp; English.
XX
AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy
XX
Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

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Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
    |||||
Db 2 CGCGTGGC 10

RESULT 188
AAZ82033
ID AAZ82033 standard; DNA; 10 BP.
AC AAZ82033;
DT 07-APR-2000 (first entry)
DE Metastatic breast tumour cell upregulated transcript tag #1267.
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
OS Homo sapiens.
XX WO9965928-A2.
XX 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013647.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 92; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy

SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
    |||||
Db 1 GTGGCAAG 9

RESULT 189
AAZ84603
ID AAZ84603 standard; DNA; 10 BP.
AC AAZ84603;
DT 07-APR-2000 (first entry)
DE Metastatic breast tumour cell downregulated transcript tag #3837.
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
OS Homo sapiens.
XX WO9965928-A2.
XX 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013647.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 161; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy

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CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
    Query Match      38.9%; Score 7.4; DB 1; Length 10;
    Best Local Similarity 88.9%; Pred. No. 1.7e+02;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGCCTGTGG 13
    | |||||
Db 2 GGCCTGTGG 10

RESULT 190
AAZ81044/c
ID AAZ81044 standard; DNA; 10 BP.
XX
AC AAZ81044;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #278.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
(GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
Isolated polynucleotides differentially expressed between metastatic and
non-metastatic breast cancer cells, useful for diagnosis, prevention and
treatment of cancer.
XX
Claim 1; Page 65; 219pp; English.
XX
AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand

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CC and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy
XX
SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
    Query Match      38.9%; Score 7.4; DB 1; Length 10;
    Best Local Similarity 88.9%; Pred. No. 1.7e+02;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
    |||||
Db 10 GCTGTGGCG 2

RESULT 191
AAZ81349
ID AAZ81349 standard; DNA; 10 BP.
XX
AC AAZ81349;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #583.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
(GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
Isolated polynucleotides differentially expressed between metastatic and
non-metastatic breast cancer cells, useful for diagnosis, prevention and
treatment of cancer.
XX
Claim 1; Page 74; 219pp; English.
XX
AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand

```

CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
 |||||
 Db 1 GCGTGGCG 9

RESULT 192

AAZ82759/c
 ID AAZ82759 standard; DNA; 10 BP.

XX AC AAZ82759;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #1993.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX PN WO9965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX PI Roberts BL, Shankara S;

XX PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and

PT treatment of cancer.

XX Claim 1; Page 113; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the metastatic breast tumour

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

CC to AAZ86677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour

CC tissue (i.e. are downregulated in metastatic breast tumour cells). These

CC transcripts can be used for diagnosis, prognosis, monitoring and

CC treatment of breast cancer, particularly where metastatic. Diagnosis is

CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from

CC e.g. therapeutic genes (also ribozymes or antisense sequences),

CC particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX

SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14

|||||

Db 9 CGCTGGGC 1

RESULT 193

AAZ81572/c

ID AAZ81572 standard; DNA; 10 BP.

XX AC AAZ81572;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #806.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX PN WO9965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX PI Roberts BL, Shankara S;

XX PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and

PT treatment of cancer.

XX Claim 1; Page 79; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the metastatic breast tumour

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

CC to AAZ86677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour

CC tissue (i.e. are downregulated in metastatic breast tumour cells). These

CC transcripts can be used for diagnosis, prognosis, monitoring and

CC treatment of breast cancer, particularly where metastatic. Diagnosis is

CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from

CC the transcripts are used to direct expression, in selected cell types, of

CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCGAAGG 19
 |||||
 Db 10 TGGGAGAAG 2
 RESULT 194
 AAZ81415/c
 ID AAZ81415 standard; DNA; 10 BP.
 XX
 AC AAZ81415;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell upregulated transcript tag #649.
 XX
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 XX
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 75; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell in
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GTGGCGAAG 18
 |||||
 Db 10 GTGGGGAAG 2
 RESULT 195
 AAZ82829/c
 ID AAZ82829 standard; DNA; 10 BP.
 XX
 AC AAZ82829;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell upregulated transcript tag #2063.
 XX
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 XX
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 115; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is

CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 XX SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTCTGGCGCT 9
 |||||
 Db 10 GGTCTGGCGCT 2
 RESULT 196
 AAZ84942/c
 ID AAZ84942 standard; DNA; 10 BP.
 AC AAZ84942;
 XX
 DT 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell downregulated transcript tag #4176.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO9965928-A2.
 PN
 XX 23-DEC-1999.
 PD
 XX 18-JUN-1999; 99WO-US013647.
 PF
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 XX Roberts BL, Shankara S;
 PI
 XX WPI; 2000-106079/09.
 DR
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 170; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These

CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 XX SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CGCTGTGGC 14
 |||||
 Db 10 CGCAGTGGC 2
 RESULT 197
 AAZ80867/c
 ID AAZ80867 standard; DNA; 10 BP.
 AC AAZ80867;
 XX
 DT 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell upregulated transcript tag #101.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO9965928-A2.
 PN
 XX 23-DEC-1999.
 PD
 XX 18-JUN-1999; 99WO-US013647.
 PF
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 XX Roberts BL, Shankara S;
 PI
 XX WPI; 2000-106079/09.
 DR
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 61; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 SQ Sequence 10 BP; 3 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
 |||||
 Db 10 TGGTGAAGG 2

RESULT 198
 AAC74122
 ID AAC74122 standard; cDNA; 10 BP.
 XX
 AC AAC74122;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human monocyte and dendritic cell expressed gene oligonucleotide #209.
 XX
 KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW autoimmune disease; tumour; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200060074-A1.
 XX

PD 12-OCT-2000.
 XX
 PF 30-MAR-2000; 2000WO-JP002019.
 XX
 PR 01-APR-1999; 99JP-00095481.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Hashimoto S, Matsushima K, Suzuki T;
 XX
 DR WPI; 2000-619172/59.
 XX
 PT Groups of genes expressed in human dendritic cells at a greater or lesser
 PT extent than in monocytes for investigation and diagnosis of autoimmune
 PT disease and tumors.
 XX
 PS Claim 19; Page 15; 95pp; Japanese.

XX The present invention describes a group of genes consisting of 100 genes
 CC which are highly expressed in human dendritic cells; a group of genes
 CC which are expressed at a higher frequency in human dendritic cells than
 CC in human monocytes; and a group of genes which are expressed at lower
 CC frequency in human dendritic cells than in human monocytes. Each group of
 CC genes are characterised in that cDNAs of these genes respectively have
 CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
 CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
 CC to AAC74213), each is continuous with the base sequence 5'-CATG-3'

CC located most closely to the poly-A region. The sequences can be used for
 CC the investigation of the role and mechanism of the involvement of
 CC dendritic cells in the immune system and for the study and diagnosis of
 CC diseases in which dendritic cells play a significant role, e.g. cancers
 CC and autoimmune diseases
 XX

SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
 |||||
 Db 1 GCTGTGGCG 9

RESULT 199
 AAC73917
 ID AAC73917 standard; cDNA; 10 BP.
 XX
 AC AAC73917;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human dendritic cell cDNA base sequence oligonucleotide #4.
 XX
 KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW autoimmune disease; tumour; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200060074-A1.
 XX

PD 12-OCT-2000.
 XX
 PF 30-MAR-2000; 2000WO-JP002019.
 XX
 PR 01-APR-1999; 99JP-00095481.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Hashimoto S, Matsushima K, Suzuki T;
 XX
 DR WPI; 2000-619172/59.
 XX

PT Groups of genes expressed in human dendritic cells at a greater or lesser
 PT extent than in monocytes for investigation and diagnosis of autoimmune
 PT disease and tumors.
 XX

PS Claim 1; Page 9; 95pp; Japanese.

XX The present invention describes a group of genes consisting of 100 genes
 CC which are highly expressed in human dendritic cells; a group of genes
 CC which are expressed at a higher frequency in human dendritic cells than
 CC in human monocytes; and a group of genes which are expressed at lower
 CC frequency in human dendritic cells than in human monocytes. Each group of
 CC genes are characterised in that cDNAs of these genes respectively have
 CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
 CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
 CC to AAC74213), each is continuous with the base sequence 5'-CATG-3',
 CC located most closely to the poly-A region. The sequences can be used for
 CC the investigation of the role and mechanism of the involvement of
 CC dendritic cells in the immune system and for the study and diagnosis of
 CC diseases in which dendritic cells play a significant role, e.g. cancers
 CC and autoimmune diseases
 XX

SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      11 TGGCGAAGG 19
Db      ||| |||||
        2 TGGTGAAGG 10

RESULT 200
AAC74079/c
ID      AAC74079 standard; cDNA; 10 BP.
XX
AC      AAC74079;
XX
DT      02-FEB-2001 (first entry)
XX
DE      Human dendritic cell and monocyte expressed gene oligonucleotide #166.
XX
KW      Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW      autoimmune disease; tumour; ss.
XX
OS      Homo sapiens.
XX
PN      WO200060074-A1.
XX
PD      12-OCT-2000.
XX
PF      30-MAR-2000; 2000WO-JP002019.
XX
PR      01-APR-1999; 99JP-00095481.
XX
PA      (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI      Hashimoto S, Matsuhashima K, Suzuki T;
XX      WPI; 2000-619172/59.
XX
DR      Groups of genes expressed in human dendritic cells at a greater or lesser
PT      extent than in monocytes for investigation and diagnosis of autoimmune
PT      disease and tumors.
XX
PS      Claim 10; Page 13; 95pp; Japanese.
XX
CC      The present invention describes a group of genes consisting of 100 genes
CC      which are highly expressed in human dendritic cells; a group of genes
CC      which are expressed at a higher frequency in human dendritic cells than
CC      in human monocytes; and a group of genes which are expressed at lower
CC      frequency in human dendritic cells than in human monocytes. Each group of
CC      genes are characterised in that cDNAs of these genes respectively have
CC      the base sequences of SEQ ID NO:1 to 100 (AAC733914 to AAC74013), SEQ ID
CC      NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
CC      to AAC74213), each is continuous with the base sequence 5'-CATG-3',
CC      located most closely to the poly-A region. The sequences can be used for
CC      the investigation of the role and mechanism of the involvement of
CC      dendritic cells in the immune system and for the study and diagnosis of
CC      diseases in which dendritic cells play a significant role, e.g. cancers
CC      and autoimmune diseases
XX
SQ      Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 TGGCGAAGG 19
Db      ||| |||||
        2 TGGTGAAGG 10

RESULT 201
AAA56244
ID      AAA56244 standard; DNA; 10 BP.
XX
AC      AAA56244;
XX
DT      07-SEP-2000 (first entry)

```

```

XX      Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:138.
DE
XX
KW      Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW      granulocyte-macrophage colony-stimulating factor; characterisation;
KW      GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW      disease onset mechanism; genetic disease; drug development; ss.
XX
OS      Homo sapiens.
XX
PN      WO200024892-A1.
XX
PD      04-MAY-2000.
XX
PF      28-OCT-1999; 99WO-JP005982.
XX
PR      28-OCT-1998; 98JP-00307532.
XX
PA      (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI      Hashimoto S, Matsuhashima K, Suzuki T;
XX      WPI; 2000-350734/30.
XX
DR      Genes most frequently expressed in human monocytes and GM-macrophages and
PT      M-macrophages studied and with cDNAs characterized, for study of gene
PT      specificity, disease onset mechanism, drug development and diagnosis.
XX
PS      Claim 7; Page 66; 138pp; Japanese.
XX
CC      The present invention describes 100 human genes, which are expressed most
CC      frequently in human monocytes. The cDNA of each gene has a sequence fully
CC      defined in the specification, and lacking the CATG sequence located
CC      adjacent to polyA region. Also described are: (1) an antibody
CC      specifically for the protein encoded by any of the genes; (2)
CC      oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
CC      which are expressed most frequently in human macrophages, differentiated
CC      from human monocytes by granulocyte-macrophage colony-stimulating factor,
CC      the cDNA of each gene has a fully defined sequence, given in the
CC      specification, lacking the base sequence CATG located most closely to the
CC      poly A region; (4) an antibody specifically for the protein encoded by
CC      any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC      sequences of (3). The genes and cDNAs are used for the study of gene
CC      specificity and disease onset mechanism e.g. oncogenesis, genetic
CC      diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
CC      specifically claimed oligonucleotide tag sequences for human genes
CC      expressed in monocytes and macrophages
XX
SQ      Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 TGGCGAAGG 19
Db      ||| |||||
        2 TGGTGAAGG 10

RESULT 202
AAA56333
ID      AAA56333 standard; DNA; 10 BP.
XX
AC      AAA56333;
XX
DT      07-SEP-2000 (first entry)
XX
DE      Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:227.
XX
KW      Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW      granulocyte-macrophage colony-stimulating factor; characterisation;
KW      GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW      disease onset mechanism; genetic disease; drug development; ss.

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```

XX OS Homo sapiens.
XX PN WO200024892-A1.
XX PD 04-MAY-2000.
XX PF 28-OCT-1999; 99WO-JP005982.
XX PR 28-OCT-1998; 98JP-00307532.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PI Hashimoto S, Matsuhashima K, Suzuki T;
XX PS WPI; 2000-350734/30.
XX PT Genes most frequently expressed in human monocytes and GM-macrophages and
XX PT M-macrophages studied and with cDNAs characterized, for study of gene
XX PT specificity, disease onset mechanism, drug development and diagnosis.
XX PS Claim 13; Page 84; 138pp; Japanese.
XX CC The present invention describes 100 human genes, which are expressed most
XX CC frequently in human monocytes. The cDNA of each gene has a sequence fully
XX CC defined in the specification, and lacking the CATG sequence located
XX CC adjacent to polyA region. Also described are: (1) an antibody
XX CC specifically for the protein encoded by any of the genes; (2)
XX CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
XX CC which are expressed most frequently in human macrophages, differentiated
XX CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
XX CC the cDNA of each gene has a fully defined sequence, given in the
XX CC specification, lacking the base sequence CATG located most closely to the
XX CC poly A region; (4) an antibody specifically for the protein encoded by
XX CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
XX CC sequences of (3). The genes and cDNAs, are used for the study of gene
XX CC specificity and disease onset mechanism e.g. oncogenesis, genetic
XX CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
XX CC specifically claimed oligonucleotide tag sequences for human genes
XX CC expressed in monocytes and macrophages
XX SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 TGGCGAAGG 19
Db ||| |||||
2 TGGTGAAGG 10
RESULT 203
AAA56136
ID AAA56136 standard; DNA; 10 BP.
XX AC AAA56136;
XX DT 07-SEP-2000 (first entry)
XX DE Human monocyte gene Tag oligonucleotide sequence SEQ ID NO:30.
XX KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
XX KW granulocyte-macrophage colony-stimulating factor; characterization;
XX KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
XX KW disease onset mechanism; genetic disease; drug development; ss.
XX OS Homo sapiens.
XX PN WO200024892-A1.
XX PD 04-MAY-2000.

```

```

PF 28-OCT-1999; 99WO-JP005982.
XX PR 28-OCT-1998; 98JP-00307532.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PI Hashimoto S, Matsuhashima K, Suzuki T;
XX PS WPI; 2000-350734/30.
XX PT Genes most frequently expressed in human monocytes and GM-macrophages and
XX PT M-macrophages studied and with cDNAs characterized, for study of gene
XX PT specificity, disease onset mechanism, drug development and diagnosis.
XX PS Claim 1; Page 45; 138pp; Japanese.
XX CC The present invention describes 100 human genes, which are expressed most
XX CC frequently in human monocytes. The cDNA of each gene has a sequence fully
XX CC defined in the specification, and lacking the CATG sequence located
XX CC adjacent to polyA region. Also described are: (1) an antibody
XX CC specifically for the protein encoded by any of the genes; (2)
XX CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
XX CC which are expressed most frequently in human macrophages, differentiated
XX CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
XX CC the cDNA of each gene has a fully defined sequence, given in the
XX CC specification, lacking the base sequence CATG located most closely to the
XX CC poly A region; (4) an antibody specifically for the protein encoded by
XX CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
XX CC sequences of (3). The genes and cDNAs, are used for the study of gene
XX CC specificity and disease onset mechanism e.g. oncogenesis, genetic
XX CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
XX CC specifically claimed oligonucleotide tag sequences for human genes
XX CC expressed in monocytes and macrophages
XX SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 TGGCGAAGG 19
Db ||| |||||
2 TGGTGAAGG 10
RESULT 204
AAA14154
ID AAA14154 standard; DNA; 10 BP.
XX AC AAA14154;
XX DT 15-SEP-2003 (revised)
XX DT 21-JUL-2000 (first entry)
XX DE E. coli K-12 leading strand PCR primer, SEQ ID NO:52.
XX KW Polymorphism detection; over-represented sequence; strand bias;
XX KW organism identification; genomic mapping; octamer; leading strand;
XX KW Escherichia coli 0157:H7; PCR primer; ss.
XX OS Escherichia coli K12.
XX PN WO200017399-A2.
XX PD 30-MAR-2000.
XX PF 17-SEP-1999; 99WO-US021379.
XX PR 18-SEP-1998; 98US-01011P.
XX PA (UYNE-) UNIV NEBRASKA-LINCOLN.
XX PI Benson AK;

```


XX DR WPI; 2000-283618/24.

XX PT Detecting DNA polymorphisms, useful e.g. for identifying organisms by

XX PT species, strain or serotype, comprises amplification with primers based

XX PT on over-represented oligonucleotide sequences.

XX PS Example; Page 28; 49pp; English.

XX CC The invention relates to a novel method for the detection of

XX CC polymorphisms in a DNA sequence. Test DNA and a second DNA are amplified

XX CC with at least one pair of primers, and the sequence differences between

XX CC the amplicons are compared. The primers are based on oligonucleotide

XX CC sequences that are over-represented in the genome of the relevant

XX CC organism, and which are biased to one strand. The method can be used to

XX CC identify an organism by species, serotype or strain, in which case

XX CC amplicons are analysed for products, common to all members of the

XX CC species, and those specific for strain or serotype, and the results

XX CC compared with an existing database. The method can also be used to

XX CC identify an individual, by comparison of results for a test DNA with an

XX CC existing database. When applied to differential display analysis, pattern

XX CC differences in the amplicons are determined, particularly by a

XX CC quantitative method such as densitometry, fluorimetry or radiometry. The

XX CC method of the invention is used to identify individuals, to classify

XX CC organisms by species, strain or serotype, and to identify genes based on

XX CC differential display. The method can also be used for genomic mapping,

XX CC detecting changes in expression patterns, genetic linkage studies,

XX CC medical diagnosis, epidemiology, forensics, and agriculture. The method

XX CC uses over-represented sequences to prime amplification. These sequences

XX CC are distributed over the entire genome, so analysis is not restricted to

XX CC particular regions, and a single primer pair can amplify up to 5% of the

XX CC complete *Escherichia coli* genome. The primers are rationally designed, so

XX CC non-specific amplification is limited and the method does not require

XX CC restriction enzymes or adapters. Sequences AAA14149-A14154 represent PCR

XX CC primers based on over-represented octamer sequences biased to the leading

XX CC strand of the *E. coli* K-12 genome and are fluorescently labelled at the

XX CC 5' end. These primers, and lagging strand primers AAA14155-AAA14160 were

XX CC used in the exemplifications of the invention to differentiate and

XX CC further characterise two strains of *E. coli* O157:H7 (strains FR1K 1641

XX CC and FR1K 533) and two strains from the ECOR collection (ECOR 20 and ECOR

XX CC 50). (Updated on 15-SEP-2003 to standardise OS field)

XX SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAA 17

DB 2 TCTGGCGAA 10

RESULT 205

AAA73645/c

ID AAA73645 standard; DNA; 10 BP.

AC AAA73645;

XX 30-JAN-2001 (first entry)

DE Probe #14 for sequencing by hybridisation.

DE Nucleic acid sequencing; sequencing by hybridisation; SBH; probe; ss.

XX Synthetic.

OS

PN WO200040758-A2.

PD 13-JUL-2000.

XX 06-JAN-2000; 2000WO-US000458.

XX PF

XX PS

XX CC

XX CC The present sequence is a probe used to demonstrate the method of the

XX CC invention, which is concerned with the use of pools of probes to enable

XX CC sequencing by hybridisation, a process known as SBH. Overlapping probes

XX CC are used which allows the identification of sequences longer than the

XX CC probe length, and either the target nucleic acid or the probe is

XX CC labelled. The method of the invention is useful for assembling sequences

PR 06-JAN-1999; 99US-0115284P.

XX (HYSE-) HYSEQ INC.

XX Drmanac R, Drmanac S, Kita D, Cooke C, Xu C;

XX WPI; 2000-475839/41.

XX DR

XX PS Identifying one or more sequences of a target nucleic acid (NA), useful

XX PT for parallel analyses, comprises contacting the NA with a set of pools of

XX PT probes comprising mixture of probes with different information regions.

XX PS Disclosure; Page 53; 196pp; English.

XX CC The present sequence is a probe used to demonstrate the method of the

XX CC invention, which is concerned with the use of pools of probes to enable

XX CC sequencing by hybridisation, a process known as SBH. Overlapping probes

XX CC are used which allows the identification of sequences longer than the

XX CC probe length, and either the target nucleic acid or the probe is

XX CC labelled. The method of the invention is useful for assembling sequences

XX CC and in parallel analyses

XX SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16

DB 10 CTGTGGCGAA 2

RESULT 206

AAA73646/c

ID AAA73646 standard; DNA; 10 BP.

AC AAA73646;

XX 30-JAN-2001 (first entry)

DE Probe #15 for sequencing by hybridisation.

DE Nucleic acid sequencing; sequencing by hybridisation; SBH; probe; ss.

XX Synthetic.

OS

PN WO200040758-A2.

PD 13-JUL-2000.

XX 06-JAN-2000; 2000WO-US000458.

XX PR

XX PS

XX CC

XX CC The present sequence is a probe used to demonstrate the method of the

XX CC invention, which is concerned with the use of pools of probes to enable

XX CC sequencing by hybridisation, a process known as SBH. Overlapping probes

XX CC are used which allows the identification of sequences longer than the

XX CC probe length, and either the target nucleic acid or the probe is

XX CC labelled. The method of the invention is useful for assembling sequences

CC and in parallel analyses

XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

SQ Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16

|||||||

9 CTGTGGCGA 1

RESULT 207

AAI70450

ID AAI70450 standard; DNA; 10 BP.

XX AC

AAI70450;

XX DT

21-JAN-2002 (first entry)

XX DE

Oligonucleotide used in mismatch discrimination.

XX KW

Probe; hybridisation; array; microarray; mismatch; detection; ss.

XX OS

Synthetic.

XX PN

WO200164958-A2.

XX PD

07-SEP-2001.

XX PF

01-MAR-2001; 2001WO-US006900.

XX XX

01-MAR-2000; 2000US-0186046P.

XX PR

28-NOV-2000; 2000US-00724959.

XX XX

(EPOC-) EPOCH BIOSCIENCE INC.

XX PA

Dempsy RO, Gall AA, Lokhov SG, Afonina IA, Singer MJ;

PI Kutvavin IV, Vermeulen NMJ;

XX PI

WPI; 2001-648247/74.

XX DR

XX XX

New modified oligonucleotides containing pyrazolo-pyrimidine and/or 5-substituted pyrimidine bases, useful as probes or primers in assays, especially for mismatch discrimination.

XX PT

Example 9; Page 84; 116pp; English.

XX PS

XX CC

The present sequence is that of one of a set of oligonucleotides (see AAI70448-64) used in a mismatch discrimination experiment. The experiment compared the thermodynamic discrimination of mismatched base pairs formed by modified oligonucleotides containing 4-amino-3-(3-hydroxyprop-1-ynyl)pyrazolo(3,4-d)pyrimidine (HOPPPA) or 5-(3-hydroxyprop-1-ynyl)-1,3-dihydropyrimidine-2,4-dione (HOPU) versus those containing 4-amino-3-(prop-1-ynyl)pyrazolo(3,4-d)pyrimidine (PPPA) and 5-prop-1-ynyl-1,3-dihydropyrimidine-2,4-dione (PU) at 37 degree C. Oligonucleotides containing the modified bases and also including a 3' minor groove binder (MGB), were hybridised to their complements, such as the present sequence. HOPPPA and HOPU substitution generally increased mismatch discrimination compared to PPPA and PU. The invention provides modified oligonucleotides for mismatch discrimination. Also provides are methods for distinguishing related polynucleotides, detecting target sequences, sequencing, primer extension, for examining gene expression, and for identifying a mutation or polymorphism

XX SQ

Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16

Db 2 CAGTGGCGA 10

RESULT 208

AAH19999

ID AAH19999 standard; DNA; 10 BP.

XX AC

AAH19999;

XX XX

07-AUG-2001 (first entry)

XX XX

Mouse Treg immunoregulatory network related tag #70.

XX DE

Mouse; EST; expressed sequence tag; contig; immunoregulation;

XX KW

immunosuppression; Treg immunoregulatory network; inflammatory;

XX KW

immune disorder; T regulatory lymphocyte; T helper cell; dermatological;

XX KW

antiinflammatory; immunosuppressive; antiarteriosclerotic; antiallergic;

XX KW

antidiabetic; neuroprotective; osteopathic; antiarthritic; anti-ulcer;

XX KW

rheumatoid arthritis; osteoarthritis; glomerular nephritis; diabetes;

XX KW

inflammatory bowel disease; vascular disease; atherosclerosis; psoriasis;

XX KW

vasculitis; skin disease; dermatitis; Crohn's disease; lung disease;

XX KW

ulcerative colitis; lupus erythematosus; autoimmune disorder; emphysema;

XX KW

hypersensitivity; multiple sclerosis; chronic bronchitis; asthma;

XX KW

idiopathic pulmonary fibrosis; primer; probe; tag; ss.

XX OS

Mus musculus.

XX OS

Synthetic.

XX XX

WO200127267-A2.

XX XX

19-APR-2001.

XX PF

06-OCT-2000; 2000WO-GB003821.

XX XX

08-OCT-1999; 99GB-00023790.

XX PR

(ISIS-) ISIS INNOVATION LTD.

XX PA

Adams E, Waldmann H, Cobbold S, Zelenika D;

XX PI

WPI; 2001-300216/31.

XX DR

XX XX

Isolated genes differentially expressed in T helper 1 (Th1) and 2 (Th2)

XX PT

and T regulatory (Treg) lymphocytes useful in prophylaxis, diagnosis and

XX PT

therapy of inflammatory and immune diseases.

XX XX

Example 4; Page 5; 29pp; English.

XX PS

XX CC

The present invention describes an isolated gene (I) obtainable by: (a)

XX CC

comparing the expression of one or more genes in populations of T helper

XX CC

1 lymphocytes (Th1)-, Th2- and T regulatory cells (Treg)-enriched cell

XX CC

populations to identify a gene which is differentially expressed in the

XX CC

populations; and (b) isolating the gene. (I) can have dermatological,

XX CC

antiinflammatory, immunosuppressive, antiarteriosclerotic, antiallergic,

XX CC

antidiabetic, neuroprotective, osteopathic, antiarthritic and anti-ulcer

XX CC

activities. (I) can be used in anti-inflammatory and immunoregulatory

XX CC

compositions for use in therapy, prophylaxis, or diagnosis and/or in a

XX CC

pharmaceutical excipient, a unit dosage form or in a form suitable for

XX CC

local or systemic administration. Methods from the present invention can

XX CC

be used for detecting Th1 and/or Th2 and/or Treg cells in a biological

XX CC

sample, for cell typing or for determining the number of Th1 and/or Th2

XX CC

and/or Treg cells in a biological sample. Diseases which may be treated

XX CC

by compositions of the invention include rheumatoid and osteoarthritis,

XX CC

glomerular nephritis, diabetes, inflammatory bowel disease, vascular

XX CC

diseases e.g. atherosclerosis and vasculitis, skin diseases such as

XX CC

psoriasis and dermatitis, Crohn's disease, ulcerative colitis, lupus

XX CC

erythematosus, autoimmune disorders, hypersensitivity, multiple

XX CC

sclerosis, and lung diseases e.g. chronic bronchitis, emphysema,

XX CC

idiopathic pulmonary fibrosis and asthma. (I) can also be used as markers

XX CC

for analysis of serum, urine and biopsy, particularly during and after

XX CC

therapy for multiple sclerosis. AAH19930 to AAH20034 and AAH75133

XX CC

represent sequence used in the exemplification of the present invention

```

XX SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
Db 2 TGGTGAAGG 10
|||||

RESULT 209
AA167372
ID AA167372 standard; DNA; 10 BP.
XX
AC AA167372;
XX
DT 11-FEB-2002 (first entry)
XX
DE Human FKBP8 gene polymorphism detecting primer.
XX
KW FK506-binding protein 8; FKBP8; haplotyping; polymorphism; cancer;
KW immunosuppression; human; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200172965-A2.
XX
PD 04-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-US009718.
XX
PR 24-MAR-2000; 2000US-0192125P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Bentivegna SC, Choi JY, Kliem SE, Koshy B;
PI Stephens JC;
XX
DR WPI; 2001-626261/72.
XX
PT New haplotypes of the FK506-binding protein 8 gene, useful for genotyping
PT that gene in individual and to design new therapy for associated disease
PT such as immunosuppression and cancer.
XX
PS Claim 16; Page 14; 98pp; English.
XX
CC The invention relates to haplotyping the FK506-binding protein 8 (38kD)
CC (FKBP8) gene in an individual. The method involves determining the
CC identity of the nucleotide pair at one or more polymorphic sites selected
CC from P1 to P26 (described in the specification). The invention is useful
CC to improve the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated with
CC FKBP8 activity, for example immunosuppression and cancer. Sequences
CC AA167352-403 represent oligonucleotide primers for detecting FKBP8 gene
CC polymorphisms by primer extension techniques
XX
SQ Sequence 10 BP; 0 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
Db 1 GCTGGGCGC 9
|||||

RESULT 210
AA509210/C
ID AAS09210 standard; DNA; 10 BP.
XX

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```

AC AAS09210;
XX
DT 07-NOV-2001 (first entry)
XX
DE Oligonucleotide ON 10 relating to VEGF receptor-1 peptide ligand #1.
XX
KW Vascular endothelial growth factor receptor-1; VEGF; psoriasis;
KW angiogenesis mediated disease; birth control; neovascularisation;
KW inflammatory disorder; neoplastic disorder; anti tumour; anti rheumatic;
KW anti arthritic; anti psoriatic; anti diabetic; anti atherosclerotic;
KW anti ulcer; osteopathic; cytostatic; anti inflammatory; ophthalmological;
KW dermatological; ON 10; ss.
XX
OS Synthetic.
XX
PN WO200157067-A1.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-IB000135.
XX
PR 04-FEB-2000; 2000US-0180568P.
XX
PA (SUPR-) SUPRATEK PHARMA INC.
XX
PI Tchistiakova L, Li S, Pietrzynski G, Alakhov V;
XX
DR WPI; 2001-529780/58.
XX
PT Composition for treating angiogenesis mediated diseases such as tumor and
PT psoriasis, comprises a peptide or its derivative capable of specific
PT binding with high affinity vascular endothelial growth factor receptor-1.
XX
PS Example 16; Page 71; 86pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprising
CC of a peptide ligand, or its derivative, which is capable of specific
CC binding with high affinity to vascular endothelial growth factor (VEGF)
CC receptor-1 or its derivative and structurally similar receptors. The
CC invention also provides peptide ligands that are capable of inhibiting
CC angiogenesis induced by VEGF. The peptide ligands of the invention are
CC useful for treating a disease associated with angiogenesis in a patient.
CC They are also useful for treating angiogenesis mediated diseases e.g.
CC solid tumours, rheumatoid arthritis and psoriasis, for treating diseases
CC of excessive or abnormal stimulation of endothelial cells e.g. Crohn's
CC disease, atherosclerosis and scleroderma, for treating diseases that have
CC angiogenesis as a pathological consequence e.g. cat scratch disease and
CC ulcers, as a birth control agent, and for treating diseases associated
CC with neovascularisation of the eye e.g. atopic keratitis and Paget's
CC disease, inflammatory disorders e.g. ulcerative colitis and inflammatory
CC bowel disease, and neoplastic and non-neoplastic diseases and disorders.
CC The peptide ligands are also useful as a targeting group to improve the
CC delivery of a biological agent used for therapeutic or diagnostic
CC purpose. The present sequence for oligonucleotide ON 10 is used to
CC construct phage expressing VEGF receptor-1 peptide ligand #1 (AAU07801)
XX
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCCGGCT 9
Db 10 GGTGGCGCT 2
|||||

RESULT 211
AAH63607/C
ID AAH63607 standard; cDNA; 10 BP.
XX
AC AAH63607;
XX

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```
DT 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 447.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
OS
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
XX Claim 13; Page 49; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CGCTGTGGC 14
Db 9 CGCTGGGCG 1
RESULT 212
AAH63746/c
ID AAH63746 standard; cDNA; 10 BP.
XX
XX AAH63746;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 586.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
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XX Velculescu VE, Vogelstein B, Kinzler KW;
PI WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
XX Claim 11; Page 52; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CGCTGTGGC 14
Db 10 CGCAGTGGC 2
RESULT 213
AAH64224
ID AAH64224 standard; cDNA; 10 BP.
XX
XX AAH64224;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1064.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
XX Claim 13; Page 63; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
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PA (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptsomes expressed in particular
PT cell types.
XX
XX Claim 13; Page 62; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptsomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptsomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCTGTGGCG 15
Db ||||| |||||
1 GCTGTGGCG 9
RESULT 217
AAH63894/c
ID AAH63894 standard; cDNA; 10 BP.
XX
XX AAH63894;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptsomes sequence SEQ ID NO: 734.
XX
XX Human; transcriptsomes; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptsomes expressed in particular
PT cell types.
XX
XX Claim 13; Page 56; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptsomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC

CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptsomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 TGGCGAAGG 19
Db ||||| |||||
10 TGGAGAAGG 2
RESULT 218
AAD20721/c
ID AAD20721 standard; DNA; 10 BP.
XX
XX AAD20721;
XX
XX 03-JAN-2002 (first entry)
XX
XX Primer #13 used to detect human GPIBA gene polymorphism.
XX
XX Human; haplotyping; glycoprotein Ib (platelet) alpha protein; GPIBA;
KW Bernard-Soulier syndrome; platelet-type von Willebrand disease; HIV;
KW Alzheimer's disease; polymorphism; human immunodeficiency virus; primer;
KW ss.
XX
XX Homo sapiens.
XX
XX WO200175065-A2.
XX
XX 11-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US010671.
XX
XX 03-APR-2000; 2000US-0194341P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Bentivegna SC, Choi JY, Kliem SE, Koshy B, Parks KE;
XX WPI; 2001-626427/72.
XX
XX New haplotypes of the glycoprotein Ib platelet alpha polypeptide gene are
PT useful for diagnosis and drug discovery for treating Bernard Soulier
PT syndrome, platelet-type von Willebrand disease, HIV and Alzheimer's
PT disease.
XX
XX Claim 18; Page 14; 66pp; English.
XX
XX The invention relates to methods for haplotyping glycoprotein Ib
CC (platelet) alpha polypeptide (GPIBA) gene of an individual. The method
CC involves determining if the individual has one of the GPIBA haplotypes or
CC haplotype pairs. The methods of the invention are useful for disease
CC diagnosis and in the discovery and development of drugs for treating
CC diseases associated with GPIBA activity e.g. Bernard-Soulier syndrome,
CC platelet-type von Willebrand disease, HIV and Alzheimer's disease. The
CC present sequence is a primer used for detecting human GPIBA gene
CC polymorphisms
XX
XX Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GTCCGCGCTG 10
Db ||||| |||||
10 GTCCGCGCTG 2

```

RESULT 219
AAH32655
ID AAH32655 standard; cDNA; 10 BP.
XX
AC AAH32655;
XX
DT 13-AUG-2001 (first entry)
XX
DE LPS activated human monocyte expression gene cDNA tag SEQ:28.
XX
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
PF 28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
WPI; 2001-304369/32.
XX
LPS activated human monocyte expression gene group.
XX
Claim 1; Page 15; 52pp; Japanese.
XX
The present invention describes an lipopolysaccharide (LPS) activated
human monocyte expression gene group consisting of the high-ranking 50
genes of the highest expression among the genes expressed by human
monocyte stimulated by LPS in which the cDNA of each gene has the base
sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CATG-3', nearest to the polyA region. The gene group is useful for the
development of new means for the diagnosis and the treatment of various
human diseases in which human monocyte plays an important role. AAH32628
to AAH32943 represent specifically claimed LPS activated human monocyte
expression gene cDNA tags from the present invention. AAH32944 represents
an LPS activated human monocyte expression gene cDNA sequence encoding
AAB98009, which are given in the exemplification of the present invention
Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
PT LPS activated human monocyte expression gene group.
XX
PS Claim 1; Page 15; 52pp; Japanese.
XX
The present invention describes an lipopolysaccharide (LPS) activated
human monocyte expression gene group consisting of the high-ranking 50
genes of the highest expression among the genes expressed by human
monocyte stimulated by LPS in which the cDNA of each gene has the base
sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CATG-3', nearest to the polyA region. The gene group is useful for the
development of new means for the diagnosis and the treatment of various
human diseases in which human monocyte plays an important role. AAH32628
to AAH32943 represent specifically claimed LPS activated human monocyte
expression gene cDNA tags from the present invention. AAH32944 represents
an LPS activated human monocyte expression gene cDNA sequence encoding
AAB98009, which are given in the exemplification of the present invention
Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 TGGCGAAGG 19
Db |||||
2 TGGTGAAGG 10
RESULT 220
AAH32828
ID AAH32828 standard; cDNA; 10 BP.
XX
AC AAH32828;
XX
DT 13-AUG-2001 (first entry)
XX
DE LPS activated human monocyte expression gene cDNA tag SEQ:201.
XX
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
The present invention describes an lipopolysaccharide (LPS) activated
human monocyte expression gene group consisting of the high-ranking 50
genes of the highest expression among the genes expressed by human
monocyte stimulated by LPS in which the cDNA of each gene has the base
sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CATG-3', nearest to the polyA region. The gene group is useful for the
development of new means for the diagnosis and the treatment of various
human diseases in which human monocyte plays an important role. AAH32628
to AAH32943 represent specifically claimed LPS activated human monocyte
expression gene cDNA tags from the present invention. AAH32944 represents
an LPS activated human monocyte expression gene cDNA sequence encoding
AAB98009, which are given in the exemplification of the present invention
Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 TGGCGAAGG 19
Db |||||
2 TGGTGAAGG 10

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XX
PF 28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
WPI; 2001-304369/32.
XX
LPS activated human monocyte expression gene group.
XX
Claim 19; Page 36; 52pp; Japanese.
XX
The present invention describes an lipopolysaccharide (LPS) activated
human monocyte expression gene group consisting of the high-ranking 50
genes of the highest expression among the genes expressed by human
monocyte stimulated by LPS in which the cDNA of each gene has the base
sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CATG-3', nearest to the polyA region. The gene group is useful for the
development of new means for the diagnosis and the treatment of various
human diseases in which human monocyte plays an important role. AAH32628
to AAH32943 represent specifically claimed LPS activated human monocyte
expression gene cDNA tags from the present invention. AAH32944 represents
an LPS activated human monocyte expression gene cDNA sequence encoding
AAB98009, which are given in the exemplification of the present invention
Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCTGTGGCG 15
Db |||||
1 GCTGTGGCG 9
RESULT 221
AAH32746/C
ID AAH32746 standard; cDNA; 10 BP.
XX
AC AAH32746;
XX
DT 13-AUG-2001 (first entry)
XX
DE LPS activated human monocyte expression gene cDNA tag SEQ:119.
XX
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
PF 28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
WPI; 2001-304369/32.
XX
LPS activated human monocyte expression gene group.
XX
Claim 10; Page 26; 52pp; Japanese.
XX
The present invention describes an lipopolysaccharide (LPS) activated
human monocyte expression gene group consisting of the high-ranking 50
genes of the highest expression among the genes expressed by human
monocyte stimulated by LPS in which the cDNA of each gene has the base
sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CATG-3', nearest to the polyA region. The gene group is useful for the
development of new means for the diagnosis and the treatment of various
human diseases in which human monocyte plays an important role. AAH32628
to AAH32943 represent specifically claimed LPS activated human monocyte
expression gene cDNA tags from the present invention. AAH32944 represents
an LPS activated human monocyte expression gene cDNA sequence encoding
AAB98009, which are given in the exemplification of the present invention
Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCTGTGGCG 15
Db |||||
1 GCTGTGGCG 9

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CC CATG-3' nearest to the polyA region. The gene group is useful for the
 CC development of new means for the diagnosis and the treatment of various
 CC human diseases in which human monocyte plays an important role. AAH32628
 CC to AAH32943 represent specifically claimed LPS activated human monocyte
 CC expression gene cDNA tags from the present invention. AAH32944 represents
 CC an LPS activated human monocyte expression gene cDNA sequence encoding
 CC AAB98009, which are given in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
 ||| |||||
 DB 10 GCTTTGGCG 2

RESULT 222
 ABA81653/C
 ID ABA81653 standard; DNA; 10 BP.
 XX AC ABA81653;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human phospholipid transfer protein gene PCR primer SEQ ID NO: 102.
 XX
 KW Human; phospholipid transfer protein; PLTP; SNP; atherosclerosis;
 KW single nucleotide polymorphism; high-density lipoprotein metabolism;
 KW PCR primer; ss.
 XX

OS Homo sapiens.
 XX
 PN WO200172761-A2.
 XX
 PD 04-OCT-2001.

PF 15-MAR-2001; 2001WO-US008283.
 XX
 PR 24-MAR-2000; 2000US-0192127P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Choi JY, Koshy B;
 XX
 DR WPI; 2001-662922/76.

PT Genotyping phospholipid transfer protein gene of individual for
 PT haplotyping individual's gene, comprises determining identity of
 PT nucleotide pair at polymorphic sites for two copies of PLTP gene present
 PT in the individual.

PS Claim 17; Page 14; 98pp; English.
 XX
 CC The present invention relates to a method for haplotyping the human
 CC phospholipid transfer protein (PLTP) gene, involving determining the
 CC identity of the nucleotide present at one or more of the 25 polymorphic
 CC sites within the gene. This can be used to aid drug development for the
 CC treatment of diseases associated with different haplotypes of the PLTP
 CC gene, possibly including atherosclerosis. The present sequence is a PCR
 CC primer used for detecting polymorphisms in the PLTP gene

XX
 SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
 ||||| |||||
 DB 10 GTGGCCAAG 2

RESULT 223
 ABA06025

ID ABA06025 standard; cDNA; 10 BP.

XX AC ABA06025;

XX DT 10-JAN-2002 (first entry)

XX DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 2.

XX KW Human; hepatocyte; gene expression; hepatopathy; ss.

XX OS Homo sapiens.

XX PN JP2001211883-A.

XX PD 07-AUG-2001.

XX PF 31-JAN-2000; 2000JP-00023170.

XX PR 31-JAN-2000; 2000JP-00023170.

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX DR WPI; 2001-629566/73.

XX PT Human normal hepatocyte expression gene group.

XX PS Claim 1; Page 6; 26pp; Japanese.

XX CC The invention relates to a human normal hepatocyte expression gene group
 CC comprising 200 genes in the human normal hepatocyte. The cDNA of each
 CC gene comprises one of 200 fully defined nucleotide sequences as given in
 CC the specification. The gene group and the cDNAs corresponding to each of
 CC the genes in the group are useful in the diagnosis and treatment of human
 CC hepatopathy. The present sequence is a cDNA corresponding to a gene
 CC expressed by normal human hepatocytes

SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9
 ||| |||||
 DB 2 GGACGCGCT 10

RESULT 224
 ABA06218

ID ABA06218 standard; cDNA; 10 BP.

XX AC ABA06218;

XX DT 10-JAN-2002 (first entry)

XX DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 195.

XX KW Human; hepatocyte; gene expression; hepatopathy; ss.

XX OS Homo sapiens.

XX PN JP2001211883-A.

XX PD 07-AUG-2001.

XX PF 31-JAN-2000; 2000JP-00023170.

XX PR 31-JAN-2000; 2000JP-00023170.

XX

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2001-629566/73.
 XX Human normal hepatocyte expression gene group.
 XX
 XX
 PS Claim 1; Page 9; 26pp; Japanese.
 XX
 CC The invention relates to a human normal hepatocyte expression gene group comprising 200 genes in the human normal hepatocyte. The cDNA of each gene comprises one of 200 fully defined nucleotide sequences as given in the specification. The gene group and the cDNAs corresponding to each of the genes in the group are useful in the diagnosis and treatment of human CC hepatopathy. The present sequence is a cDNA corresponding to a gene CC expressed by normal human hepatocytes
 XX
 SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TTGGCGAAGG 19
 Db 2 TTGGTGAAGG 10
 RESULT 225
 AAA91471
 ID AAA91471 standard; DNA; 10 BP.
 XX
 AC AAA91471;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE Human CHRM5 gene, allele specific oligonucleotide #39.
 XX
 KW CHRM5; human; cholinergic receptor muscarinic 5; polymorphic variant;
 KW genotyping; haplotype; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200128995-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 19-OCT-2000; 2000WO-US029071.
 XX
 PR 21-OCT-1999; 99US-0160647P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Choi JY, Nandabalan K, Stephens JC;
 XX
 DR WPI; 2001-300313/31.
 XX
 CC Isolated polynucleotide encoding the cholinergic receptor, muscarinic 5 (CHRM5) used to genotype/haplotype the CHRM5 gene, and to identify an association between a trait and a polymorphism, comprises novel polymorphisms.
 XX
 PS Claim 15; Page 49; 53pp; English.
 XX
 CC This sequence is a the human cholinergic receptor, muscarinic 5 (CHRM5) gene, allele specific oligonucleotide. The invention relates to a polymorphic variant of the CHRM5 gene sequence. The polymorphic sequence is useful to genotype or haplotype the CHRM5 gene, to predict a haplotype pair for the CHRM5 gene, and for identifying an association between a trait (such as a clinical response to a drug targeting CHRM5). It is also useful in gene therapy in patients who lack the CHRM5 isogene or have only one copy of it, and in assays to measure the binding affinities of one or more candidate drugs targeting CHRM5. The DNA sequence is used in the treatment of disorders affected by expression or function of a novel CC

CC CHRM5 isogene of the invention. The protein encoded by the CHRM5 variant is useful to identify drugs which target the CHRM5 polymorphic variant protein. Antibodies against the protein can be used to neutralise the CHRM5 isoform activity expressed in an individual, and is useful in CC detection of CHRM5 in immunocytochemical, immunohistochemical and CC immunofluorescence. A composition containing a genotyping oligonucleotide CC for detecting a polymorphism in the CHRM5 gene is used to detect novel CC CHRM5 polymorphisms of the invention
 XX
 SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GTGGCGAAG 18
 Db 2 GTGGCGAAG 10
 RESULT 226
 AAF36041/C
 ID AAF36041 standard; DNA; 10 BP.
 XX
 AC AAF36041;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2780.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
 PT
 PS Example; Page 99; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCTGGCT 9
Db 10 GGTCTGGCT 2

RESULT 227
AAF43354
ID AAF43354 standard; DNA; 10 BP.
XX AAF43354;
DT 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11493.
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 360; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTG 10
Db 2 GTCGCGCTG 10

RESULT 228
AAF39191/c
ID AAF39191 standard; DNA; 10 BP.
XX AAF39191;
XX 23-MAR-2001 (first entry)
DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5930.
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 211; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising nucleotides of a NORF gene whose expression varies at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGTGT 11
 |||||
 Db 9 TCGCACTGT 1

RESULT 229

AAFP34571
 ID AAF34571 standard; DNA; 10 BP.

AC AAF34571;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1310.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 46; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13

||| |||||

Db 2 GCTCTGTGG 10

RESULT 230

AAFP35628

ID AAF35628 standard; DNA; 10 BP.

AC AAF35628;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2367.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 84; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log

described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. CCF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
Db 2 GTGGCGAGG 10
|||||||

RESULT 231

AAF37416
ID AAF37416 standard; DNA; 10 BP.

AC AAF37416;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4155.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

16-JUN-1999; 99US-00335032.

(UYJO) UNIV JOHNS HOPKINS.

Velculescu V, Vogelstein B, Kinzler K;

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 148; 419pp; English.

The present invention describes an isolated DNA molecule comprising a

coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. CCF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

Sequence 10 BP; 0 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCGCTGTG 12
Db 2 CGCGCTGCG 10
|||||||

RESULT 232

AAF36771/C

ID AAF36771 standard; DNA; 10 BP.

AC AAF36771;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3510.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

16-JUN-1999; 99US-00335032.

(UYJO) UNIV JOHNS HOPKINS.

Velculescu V, Vogelstein B, Kinzler K;

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

PS Example; Page 125; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGGA 16

DB 9 CTGAGGCGGA 1

RESULT 233

AAAF37531

ID AAF37531 standard; DNA; 10 BP.

XX AAF37531;

AC AAF37531;

XX 23-MAR-2001 (first entry)

DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4270.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX WO200077214-A2.

PN 21-DEC-2000.

PD 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PR (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

DR Yeast gene coding sequences comprising NORF genes with serial analysis of

XX PT

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 152; 419pp; English.

PS

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

DB 2 TGGCGAAGC 10

RESULT 234

AAAF43175/C

ID AAF43175 standard; DNA; 10 BP.

XX AAF43175;

AC AAF43175;

XX 23-MAR-2001 (first entry)

DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11314.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX WO200077214-A2.

PN 21-DEC-2000.

PD 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PR (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

PI

DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 354; 419pp; English.

PS The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

SQ Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14

DB 10 CGCTGAGC 2

RESULT 235

AAF43253

ID AAF43253 standard; DNA; 10 BP.

XX AAF43253;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11392.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 356; 419pp; English.

PS The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

SQ Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

DB 1 TGGCGATGG 9

RESULT 236

AAF43167

ID AAF43167 standard; DNA; 10 BP.

XX AAF43167;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11306.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PR 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 353; 419pp; English.
 PS
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GGCCTGTGG 13
 DB || |||||
 2 GCCCTGTGG 10
 RESULT 237
 AAS19671
 ID AAS19671 standard; DNA; 10 BP.
 XX
 AC AAS19671;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Primer-extension oligonucleotide #24 to detect human GHRHR polymorphisms.
 XX
 KW Human; single nucleotide polymorphism; SNP; GHRHR; chromosome 7p14;
 KW growth hormone releasing hormone receptor; haplotyping; genotyping;
 KW isolated growth hormone deficiency; IGHD; pituitary adenoma; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200179239-A2.
 XX
 XX 25-OCT-2001.
 XX
 XX Novel polymorphic variants of aldo-keto reductase family 1, member b1
 PT gene useful in studying expression and function of the protein, useful
 PT for screening drugs to treat diseases e.g. diabetes.

PF 17-APR-2001; 2001WO-US012453.
 XX
 PR 17-APR-2000; 2000US-0197978P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Choi JY, Denton RR, Nandabalan K, Sausker EA;
 XX WPI; 2002-066342/09.
 DR
 XX Genotyping human growth hormone releasing hormone receptor gene of
 PT individual for determining haplotype of individual by determining
 PT identity of nucleotide pair at specific polymorphic sites for two copies
 PT of gene.
 XX
 PS Claim 18; Page 15; 90pp; English.
 XX
 CC The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human growth hormone releasing hormone receptor (GHRHR)
 CC gene located on chromosome 7p14, and methods for haplotyping and/or
 CC genotyping the GHRHR gene. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the GHRHR gene
 CC polymorphisms. The polymorphisms and screened compounds are useful for
 CC the treatment of diseases associated with GHRHR activity, such as
 CC isolated growth hormone deficiency (IGHD) and pituitary adenomas.
 CC AAS19648-AAS19673 represent primer-extension oligonucleotides for
 CC detecting human GHRHR gene polymorphisms
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CTGTGCGCA 16
 DB || |||||
 1 CTGTGTGTA 9
 RESULT 238
 ABL01179/c
 ID ABL01179 standard; DNA; 10 BP.
 XX
 AC ABL01179;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human AKR1B1 gene polymorphism detection primer SEQ ID NO:76.
 XX
 KW Human; aldo-keto reductase family 1 member B1; aldose reductase; ss;
 KW AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer;
 KW allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes.
 XX
 OS Homo sapiens.
 XX
 PN WO200179223-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US011944.
 XX
 PR 12-APR-2000; 2000US-0196315P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Choi JY, Nandabalan K, Rounds E, Sanchis A;
 XX WPI; 2002-075056/10.
 DR
 XX Novel polymorphic variants of aldo-keto reductase family 1, member b1
 PT gene useful in studying expression and function of the protein, useful
 PT for screening drugs to treat diseases e.g. diabetes.

XX Claim 18; Page 15; 103pp; English.

PS The present invention describes an isolated polynucleotide (I) comprising

XX a sequence which is a polymorphic variant (PV) of a reference sequence

CC for aldo-keto reductase family 1, member B1 (AKR1B1) gene or its

CC fragment, having the 2214 base pair sequence given in ABL01105. AKR1B1

CC has antidiabetic activity and can be used in gene therapy. AKR1B1 can be

CC used in the treatment of diabetes. The human AKR1B1 gene is located on

CC chromosome 7q35. ABL01107 to ABL01129 represent allele-specific

CC oligonucleotide (ASO) probes used in the detection of polymorphisms in

CC the human AKR1B1 gene; ABL01130 to ABL01175 represent ASO primers used in

CC the detection of polymorphisms in the human AKR1B1 gene; and ABL01176 to

CC ABL01221 represent preferred primers used in the detection of

CC polymorphisms in the human AKR1B1 gene

XX

SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

Db 9 TGGCGAGGG 1

RESULT 239

AAS98835/C

ID AAS98835 standard; DNA; 10 BP.

AC AAS98835;

XX

XX 26-MAR-2002 (first entry)

XX

XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #201.

XX

XX Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;

KW cytostatic; gene therapy; malignant histiocytosis; isogene;

KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;

KW genotype; human; allele specific oligonucleotide; ASO; primer;

KW primer extension; ss.

XX

XX Homo sapiens.

OS

XX

XX WO200179225-A2.

PN

XX

XX 25-OCT-2001.

PD

XX

XX 12-APR-2001; 2001WO-US012044.

PF

XX

XX 12-APR-2000; 2000US-0196411P.

PR

XX

XX (GENA-) GENAISSANCE PHARM INC.

PA

XX

XX Chew A, Choi JY, Koshy B;

PI

XX

XX WPI; 2002-075058/10.

DR

XX

XX Novel polymorphic variants of colony stimulating factor 1 receptor useful

PT in studying expression and function of the protein, useful for screening

PT candidate drugs to treat diseases e.g. inflammatory disorders.

XX

XX Claim 17; Page 17; 164pp; English.

PS

XX The invention describes a novel isolated polynucleotide (I) comprising a

CC sequence which is a polymorphic variant (PV) of a reference sequence for

CC colony stimulating factor 1 receptor (CSF1R) gene, found on the

CC polypeptide are useful for improving the discovery and development of

CC drugs for treating diseases associated with CSF1R activity, e.g.,

CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders

CC and the haplotypes can be used to validate CSF1R as a candidate target

CC for treating a specific condition or disease predicted to be associated

CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also

CC be used in developing diagnostic tests and therapeutic treatments. (I) is

CC useful in studying the expression and function of CSF1R, and in

CC expressing CSF1R protein for use in screening for candidate drugs to

CC treat diseases related to CSF1R activity and in studying the effect of

CC the variation on the biological activity of CSF1R as well as on the

CC binding affinity of candidate drugs targeting CSF1R. Antibodies are

CC useful in a variety of diagnostic and prognostic formats and therapeutic

CC methods. A transgenic animal is useful in studying expression of the

CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs

CC targeted against CSF1R protein, and for testing the efficacy of

CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)

CC are useful as probes and primers, and for assaying a polymorphism in the

CC target region. Without requiring any a priori knowledge of the phenotypic

CC effect of any particular CSF1R or haplotype the invention provides a

CC method for identifying lead compounds that are more likely to show

CC efficacy in clinical trials. This sequence is a primer used to detect

CC CSF1R gene polymorphisms by primer extension, described in the method of

CC the invention

XX

SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15

Db 10 GGTGTGGCG 2

RESULT 240

ABL42636

ID ABL42636 standard; cDNA; 10 BP.

XX

XX ABL42636;

XX

XX 12-APR-2002 (first entry)

DT

XX Human maturation/activation dendritic cell expression gene tag #10.

DE

XX Human; maturation/activation dendritic cell expression gene; tag;

KW maturation; activation; dendritic cell; ss.

KW

XX

XX Homo sapiens.

OS

XX

XX JP2001327293-A.

PN

XX

XX 27-NOV-2001.

PD

XX

XX 22-MAY-2000; 2000JP-00150562.

PF

XX

XX 22-MAY-2000; 2000JP-00150562.

PR

XX

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA

XX

XX WPI; 2002-127070/17.

DR

XX

XX Human maturation/activation dendritic cell expression gene group.

PT

XX

XX Claim 1; Page 9; 41pp; Japanese.

PS

XX

XX The present invention describes a human maturation/activation dendritic

CC cell (DC) expression gene group consisting of 100 genes which show the

CC highest expression among the genes expressed in human maturation/

CC activation DC. Also described are: (1) a protein expressed by the above

CC human maturation/activation DC expression gene; (2) an antibody against

CC the protein; and (3) an antagonist against the expression of each gene

CC belonging to the above gene group. The gene group is useful for the

CC treatment and the diagnosis of various human diseases related to human

CC DC. ABL42627 to ABL42926 represent specifically claimed human

CC maturation/activation DC expression gene tags from the present invention

XX

SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
 |||||
 DB 2 TGGTGAAGG 10

RESULT 241
 AAD25385/C
 ID AAD25385 standard; DNA; 10 BP.
 XX AC
 XX AAD25385;
 DT 12-MAR-2002 (first entry)
 XX Human primer #2 to detect ADORA2A gene polymorphisms.
 DE Human; adenosine A2a receptor; ADORA2A; polymorphic site; PS; haplotype;
 XX drug screening; cellular stress; hypertension; antisense gene therapy;
 KW hypotensive; tranquilliser; chromosome 22q11.23; primer; ss.
 XX Homo sapiens.
 OS WO200187905-A2.
 PN 22-NOV-2001.
 PD 16-MAY-2001; 2001WO-US015789.
 PF 18-MAY-2000; 2000US-0205120P.
 PR (GENA-) GENAISSANCE PHARM INC.
 XX Bentivegna SC, Duda AE, Kliem SE, Koshy B, Lee HH, Sanchis A;
 XX WPI; 2002-055678/07.
 XX Genetic variants of human adenosine A2a receptors, ADORA2A gene useful
 PT for studying expression, function of the gene and expressing ADORA2A
 PT proteins for use in screening for drugs to treat hypertension and
 PT cellular stress.
 XX Claim 18; Page 13; 58pp; English.

The present invention relates to a polynucleotide comprising a sequence
 CC which comprises adenosine A2a receptor (ADORA2A) isogene chosen from
 CC isogenes 1-2 and 4 having polymorphisms at polymorphic sites (PS)
 CC corresponding to nucleotide position 531 (PS1) of a sequence of 997 bp,
 CC 1345 (PS2), 1794 (PS3) and 1833 (PS4) of a sequence of 1906 bp, or which
 CC is a polymorphic variant of a coding sequence for ADORA2A isogene.
 CC ADORA2A gene is located on chromosome 22q11.23. ADORA2A is useful for
 CC screening for drugs targeting the polypeptide, by contacting the ADORA2A
 CC polymorphic variant with a candidate agent and assaying for binding
 CC activity. The polymorphism and haplotype data are useful for validating
 CC whether ADORA2A is a suitable target for drugs to treat cellular stress
 CC and hypertension, screening for such drugs and reducing bias in clinical
 CC trials of such drugs. A polymorphic variant of ADORA2A is useful in
 CC studying the effect of the variation on the biological activity of
 CC ADORA2A, on the binding affinity of candidate drugs targeting ADORA2A
 CC for the treatment of cellular stress and hypertension and in assays to
 CC measure the binding affinities of one or more candidate drugs targeting
 CC the ADORA2A protein. The present sequence is human primer used for
 CC detecting ADORA2A gene polymorphisms

SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGCTGT 11
 |||||
 DB 1 TCGCGTGT 9

RESULT 243
 ABK96027

QY 8 CTGTGGCGA 16
 |||||
 DB 9 CTGTGGCCA 1

RESULT 242
 ABN81464
 ID ABN81464 standard; DNA; 10 BP.
 XX AC
 XX ABN81464;
 DT 16-AUG-2002 (first entry)
 XX Human HTATIP PCR primer SEQ ID NO 65.
 DE Human; HIV-1 Tat interactive protein; HTATIP; haplotyping; genotyping;
 KW transgenic; PCR; primer; ss.
 XX Homo sapiens.
 OS WO200229089-A2.
 PN 11-APR-2002.
 PD 05-OCT-2001; 2001WO-US031593.
 PF 06-OCT-2000; 2000US-0238655P.
 PR (GENA-) GENAISSANCE PHARM INC.
 XX Armstrong B, Bentivegna SC, Choi JY, Gilson CR, Parks KE;
 XX Sausker EA;
 XX WPI; 2002-330173/36.
 XX New HIV-1 tat interactive protein, 60 kDa (HTATIP) gene polymorphic
 PT variants, for studying the expression and function of HTATIP and
 PT screening candidate drugs for treating familial glucocorticoid deficiency
 PT and cancer.
 XX Claim 16; Page 14; 89pp; English.

The invention relates to novel genetic variants of the HIV-1 Tat
 CC interactive protein, 60 kDa (HTATIP) gene. The polymorphic variants are
 CC useful in studying the expression and function of HTATIP, in expressing
 CC HTATIP protein for use in screening for candidate drugs to treat diseases
 CC related to HTATIP activity, in studying the effect of the variation on
 CC the biological activity of HTATIP and the binding affinity of candidate
 CC drugs targeting HTATIP for the treatment of disorders. Haplotyping
 CC methods are useful in validating HTATIP as a candidate target for
 CC treating a specific condition or disease predicted to be associated with
 CC HTATIP activity or in the design of clinical trials of candidate drugs
 CC for treating a specific condition or disease associated with HTATIP
 CC activity. Transgenic animals are useful for studying expression of the
 CC HTATIP isogenes in vivo, for in vivo screening and testing of drugs
 CC targeted against HTATIP protein and for testing the efficacy of
 CC therapeutic agents and compounds for disorders. The present sequence is
 CC that of a HTATIP allele specific PCR primer of the invention

ID ABK96027 standard; DNA; 10 BP.
 XX
 AC ABK96027;
 XX
 XX 24-SEP-2002 (first entry)
 DT
 DE Human LIPE gene polymorphism detection oligonucleotide primer #2.
 XX
 DE
 XX Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;
 KW polymorphism; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200240502-A2.
 PN
 XX 23-MAY-2002.
 PD
 XX 16-NOV-2001; 2001WO-US043518.
 XX
 PF 16-NOV-2000; 2000US-0249302P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Anastasio AE, Bentivegna SC, Chew A, Koshy B, Rounds E;
 PI
 XX WPI; 2002-519369/55.
 DR
 XX Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for
 PT improving efficiency and reliability in drug development for treating
 PT diseases associated with LIPE activity, e.g. obesity and male sterility.
 PT
 XX Claim 17; Page 15; 142pp; English.
 PS
 XX The present invention relates to a new polynucleotide comprising a
 CC nucleotide sequence which comprises lipase, hormone sensitive (LIPE)
 CC isogenes. The invention is useful in screening for drugs targeting LIPE
 CC isogenes that are useful for treating obesity and male sterility. The
 CC methods of the invention are useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with LIPE activity. The polynucleotide
 CC is useful in studying the expression and function of LIPE, and in
 CC expressing LIPE protein for use in screening for candidate drugs to treat
 CC diseases related to LIPE activity. It is also useful in studying the
 CC effect of the variation on the biological activity of LIPE as well as on
 CC the binding affinity of candidate drugs targeting LIPE for the treatment
 CC of obesity and male sterility. The invention is useful for studying the
 CC expression of LIPE isogenes in vivo, for in vivo screening and testing of
 CC drugs targeted against LIPE protein, and for testing the efficacy of
 CC therapeutic agents and compounds for treating obesity and male sterility
 CC in a biological system. The present nucleic acid sequence represents one
 CC of a collection (ABK96026-ABK96083) of oligonucleotide primers that were
 CC used in the invention to detect polymorphisms in the human LIPE gene
 XX
 SQ Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GCTGTGGCG 15
 DB 2 GCTGTGGTG 10
 RESULT 244
 AAL48067
 ID AAL48067 standard; DNA; 10 BP.
 XX
 XX AAL48067;
 AC
 XX 27-SEP-2002 (first entry)
 DT
 XX Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 45.

XX Human; colony stimulating factor 3 (granulocyte); CSF3; SNP; isogene;
 KW chromosome 17q11-12; single nucleotide polymorphism; immunostimulant;
 KW neutropenia; promyelocytic leukaemia; haematological disorder;
 KW gene therapy; PCR; primer extension oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200194364-A2.
 PN
 XX 13-DEC-2001.
 PD
 XX 11-JUN-2001; 2001WO-US018813.
 XX
 PF 09-JUN-2000; 2000US-0210380P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Duda A, Kazemi A, Messer C, Sausker EA;
 PI
 XX WPI; 2002-566435/60.
 DR
 XX New variants of colony stimulating factor 3 (CSF3) isogenes, useful for
 PT improving efficiency and reliability in the development of drugs for
 PT treating diseases associated with CSF3 activity e.g. neutropenia.
 PT
 XX Claim 19; Page 13; 68pp; English.
 PS
 XX The present invention provides the protein, gene and cDNA sequences of
 CC human colony stimulating factor 3 (granulocyte) CSF3. Also described are
 CC single nucleotide polymorphisms (SNPs) identified within these sequences.
 CC The sequences can be used in the treatment of neutropenia, promyelocytic
 CC leukaemia and haematological disorders. The present sequence is an allele
 CC specific primer extension oligonucleotide used to isolate the coding
 CC sequences of the invention
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CGCTGTGGC 14
 DB 2 CGCCGTGGC 10
 RESULT 245
 AAL48068/c
 ID AAL48068 standard; DNA; 10 BP.
 XX
 XX AAL48068;
 AC
 XX 27-SEP-2002 (first entry)
 DT
 XX Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 46.
 DE
 XX Human; colony stimulating factor 3 (granulocyte); CSF3; SNP; isogene;
 KW chromosome 17q11-12; single nucleotide polymorphism; immunostimulant;
 KW neutropenia; promyelocytic leukaemia; haematological disorder;
 KW gene therapy; PCR; primer extension oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200194364-A2.
 PN
 XX 13-DEC-2001.
 PD
 XX 11-JUN-2001; 2001WO-US018813.
 XX
 PF 09-JUN-2000; 2000US-0210380P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA

XX Duda A, Kazemi A, Messer C, Sausker EA;
 XX WPI; 2002-566435/60.
 XX
 XX New variants of colony stimulating factor 3 (CSF3) isogenes, useful for
 PT improving efficiency and reliability in the development of drugs for
 PT treating diseases associated with CSF3 activity e.g. neutropenia.
 XX
 XX Claim 19; Page 13; 68pp; English.
 XX
 XX The present invention provides the protein, gene and cDNA sequences of
 CC human colony stimulating factor 3 (granulocyte) CSF3. Also described are
 CC single nucleotide polymorphisms (SNPs) identified within these sequences.
 CC The sequences can be used in the treatment of neutropenia, promyelocytic
 CC leukaemia and haematological disorders. The present sequence is an allele
 CC specific primer extension oligonucleotide used to isolate the coding
 CC sequences of the invention
 XX
 XX Sequence 10 BP; 3 A; 6 C; 1 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 7 GCTGTGGCG 15
 DB |||||
 9 GCTGTGGTG 1
 RESULT 246
 AAD27409/C
 ID AAD27409 standard; DNA; 10 BP.
 AC AAD27409;
 XX
 DT 18-APR-2002 (first entry)
 XX
 DE Oligo #2, to construct a phage that express ligand #4 of the invention.
 XX
 KW Small intestine; blood brain barrier; central nervous system; CNS;
 KW circulatory system; gastrointestinal tract; pharmaceutical; ligand; ss.
 XX
 OS Synthetic.
 XX
 XX WO200190139-A2.
 XX
 XX 29-NOV-2001.
 XX
 XX 07-MAY-2001; 2001WO-IB0000926.
 XX
 XX 07-MAY-2001; 2001WO-IB0000926.
 XX
 XX (SUPR-) SUPRATEK PHARMA INC.
 XX
 XX Tchistiakova L, Li S, Pietrzynski G, Alakhov V;
 XX WPI; 2002-130449/17.
 XX
 XX New polypeptide capable of crossing the blood brain or intestine barrier
 PT for increasing the absorption of an orally administered therapeutic from
 PT the gastrointestinal tract into the circulatory system.
 XX
 XX Example 3; Page 45; 60pp; English.
 XX
 XX The present invention relates to novel ligands comprising a peptide
 CC capable of crossing the small intestine and blood brain barrier. The
 CC ligand is capable of enhancing oral and central nervous system (CNS)
 CC bioavailability of biological agents or formulations. The invention also
 CC relates to pharmaceutical compositions in which the ligand is used as
 CC targeting moiety to improve the delivery of a biological agent used for
 CC diagnostic or therapeutic purpose. The polypeptide is used to increase
 CC absorption of an orally delivered therapeutic agent into the circulatory

CC system from the gastrointestinal tract. The present DNA sequence is an
 CC oligonucleotide which is used for constructing a phage that express
 CC ligand #4 used in the exemplification of the invention
 XX
 XX Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 GGTGCGCGCT 9
 DB |||||
 10 GGTGCGCGCT 2
 RESULT 247
 ABL39499
 ID ABL39499 standard; DNA; 10 BP.
 XX
 AC ABL39499;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Human ETVF primer-extension oligonucleotide 5.
 XX
 KW Human; electron-transfer flavoprotein beta polypeptide; ETVF;
 KW electron acceptor; mitochondrial matrix; glutaric acidemia type II;
 KW novel polymorphic site; novel polymorphism; ETVF genotype; ss; GAI1;
 KW ETVF haplotype; transgenic animal; primer; probe; chromosome 19q13;
 KW primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
 XX
 OS Homo sapiens.
 XX
 XX WO200202580-A2.
 XX
 XX 10-JAN-2002.
 XX
 XX 05-JUL-2001; 2001WO-US021306.
 XX
 XX 05-JUL-2000; 2000US-0215984P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;
 XX WPI; 2002-154722/20.
 XX
 XX Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
 PT useful for therapeutic purposes, for studying the expression and function
 PT of the polynucleotide, and for expressing the flavoprotein.
 XX
 XX Claim 19; Page 15; 143pp; English.
 XX
 XX The invention comprises DNA, cDNA and protein sequences of the human
 CC electron-transfer flavoprotein, beta polypeptide (ETVF) gene (located on
 CC chromosome 19q13.3-13.4). The invention specifically relates to the
 CC identification of 27 novel polymorphic sites within the ETVF gene.
 CC Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
 CC for nine primary flavoprotein dehydrogenases and is located in the
 CC mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
 CC (ETFB) subunit. Electrons accepted by ETF are transferred to the
 CC mitochondrial respiratory chain by ETF dehydrogenases (ETFDH).
 CC Deficiency of ETF or ETFDH leads to glutaric acidemia type II (GAI1).
 CC Therefore ETVF is a pharmaceutically-important gene in the treatment of
 CC GAI1. The novel ETVF polymorphisms identified in the invention are useful
 CC for genotyping and haplotyping the ETVF gene of an individual. The ETVF
 CC protein and nucleic acids of the invention are useful for studying the
 CC expression and function of ETVF in vivo. The ETVF protein and nucleic
 CC acids are also useful for testing the efficacy of therapeutic agents and
 CC compounds for glutaric acidemia type II. The nucleic acids of the
 CC invention are useful in the production of a transgenic animal expressing
 CC the ETVF gene. Nucleic acids ABL39414-ABL39440 represent claimed ETVF
 CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed

KW UDP glycosyltransferase 1; UGT1A1; human; haplotyping; ss;
 KW drug discovery; Gilbert's syndrome; Crigler-Najjar syndrome;
 KW allele-specific oligonucleotide.
 OS Homo sapiens.
 XX WO200179230-A2.
 XX 25-OCT-2001.
 XX 13-APR-2001; 2001WO-US012273.
 XX 18-APR-2000; 2000US-0197514P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Choi JY, Koshiy B, Rounds E;
 XX WPI; 2002-075063/10.
 XX Genotyping a human UDP glycosyltransferase 1 gene of an individual for
 PT determining the haplotype of an individual, involves determining the
 PT identity of a nucleotide pair at specific polymorphic sites for two
 PT copies of the gene.
 XX Claim 18; Page 14; 81pp; English.
 XX The invention relates to genotyping a human UDP glycosyltransferase
 CC (UGT1A1) gene of an individual, involving determining for the two copies
 CC of the UGT1A1 gene present in the individual, the identity of the
 CC nucleotide pair at one or more polymorphic sites. The new method is
 CC useful for determining whether an individual has a haplotype or haplotype
 CC pairs, given in the specification. It is useful for improving the
 CC efficacy and reliability of several steps in the discovery and
 CC development of drugs for treating diseases associated with UGT1A1
 CC activity, e.g., Gilbert's syndrome and Crigler-Najjar syndrome, to
 CC validate UGT1A1 as a candidate agent for treating a specific condition or
 CC disease predicted to be associated with UGT1A1 activity, and in the
 CC design of clinical trials of candidate drugs for treating a specific
 CC condition or disease predicted to be associated with UGT1A1 activity. The
 CC method is useful to screen for compounds targeting UGT1A1 to treat a
 CC specific condition or disease associated with UGT1A1 activity. A nucleic
 CC acid (I) comprising a polymorphic variant of a reference sequence for the
 CC UGT1A1 gene or cDNA (II) or its fragment is useful in studying the
 CC expression and function of UGT1A1, and in expressing UGT1A1 protein for
 CC use in screening for candidate drugs to treat diseases related to UGT1A1
 CC activity. (I) or (II) is useful for therapeutic purposes. (II) or a
 CC recombinant organism comprising (II) is useful for studying expression of
 CC the UGT1A1 isogenes in vivo, for in vivo screening and testing of drugs
 CC targeted against UGT1A1 protein, and for testing the efficacy of
 CC therapeutic agents and compounds for Gilbert's syndrome and Crigler-
 CC Najjar syndrome, in a biological system. AAS99134-AAS99203 represent UDP
 CC glycosyltransferase 1 gene allele-specific oligonucleotides used in the
 CC method of the invention
 XX Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
 SQ Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTCCGCGCTG 10
 |||||
 DB 10 GTCCGCTG 2
 RESULT 251
 ABV84886
 ID ABV84886 standard; cDNA; 10 BP.
 XX
 AC ABV84886;
 XX
 DT 12-DEC-2002 (first entry)

XX Human thymosin beta-4 SAGE tag #696.
 XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; ss.
 XX Homo sapiens.
 XX JP2002209591-A.
 XX 30-JUL-2002.
 XX 19-JAN-2001; 2001JP-00012328.
 XX 19-JAN-2001; 2001JP-00012328.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2002-631294/68.
 XX Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.
 XX Claim 55; Page 29; 139pp; Japanese.
 XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly
 CC expressed in chronic hepatitis C liver tissue
 XX Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGCGCAAGG 19
 |||||
 DB 2 TGCTGAAGG 10
 RESULT 252
 ABV84695
 ID ABV84695 standard; cDNA; 10 BP.
 XX
 AC ABV84695;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Chronic hepatitis C/HCC differentially expressed gene SAGE tag #505.
 KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX Homo sapiens.
 XX

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PN JP2002209591-A.
XX
PD
XX
XX 30-JUL-2002.
XX
PF 19-JAN-2001; 2001JP-00012328.
XX
PR 19-JAN-2001; 2001JP-00012328.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-631294/68.
XX
XX Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes.
XX
XX Claim 46; Page 25; 139pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve
XX to uniquely identify each transcript and can thus be used to analyse the
XX pattern of gene expression in particular cell types. The invention also
XX relates to proteins encoded by the genes expressed in chronic hepatitis C
XX liver tissue or HCC, antibodies against these proteins, and inhibitors of
XX the expression of groups of genes that are overexpressed in chronic
XX hepatitis C liver tissue or HCC. Groups of genes differentially expressed
XX in chronic hepatitis C tissue or HCC may be used for the diagnosis and
XX treatment of these diseases. Such genes, inhibitors of their expression
XX or activity, and antibodies against the gene products may be used in the
XX development of drugs to treat chronic hepatitis C and/or HCC. Sequences
XX ABV84691-ABV84790 are SAGE tags representing the 100 least highly
XX expressed genes out of those genes which are underexpressed in
XX hepatocellular carcinoma compared with chronic hepatitis C liver tissue
XX
XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGGCT 9
Db || |||||
2 GGACGCGCT 10

RESULT 253
ABV84505
ID ABV84505 standard; cDNA; 10 BP.
XX
XX AC ABV84505;
XX
XX DT 12-DEC-2002 (first entry)
XX
XX DE Human apolipoprotein A-I SAGE tag #315.
XX
XX KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XX CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
XX expression pattern; differential expression; ss.
XX
XX OS Homo sapiens.
XX
XX PN JP2002209591-A.
XX
XX XX 30-JUL-2002.
XX
XX PF 19-JAN-2001; 2001JP-00012328.
XX
XX PR 19-JAN-2001; 2001JP-00012328.
XX
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-631294/68.
XX
XX Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes.
XX
XX Claim 46; Page 25; 139pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve
XX to uniquely identify each transcript and can thus be used to analyse the
XX pattern of gene expression in particular cell types. The invention also
XX relates to proteins encoded by the genes expressed in chronic hepatitis C
XX liver tissue or HCC, antibodies against these proteins, and inhibitors of
XX the expression of groups of genes that are overexpressed in chronic
XX hepatitis C liver tissue or HCC. Groups of genes differentially expressed
XX in chronic hepatitis C tissue or HCC may be used for the diagnosis and
XX treatment of these diseases. Such genes, inhibitors of their expression
XX or activity, and antibodies against the gene products may be used in the
XX development of drugs to treat chronic hepatitis C and/or HCC. Sequences
XX ABV84691-ABV84790 are SAGE tags representing the 100 least highly
XX expressed genes out of those genes which are underexpressed in
XX hepatocellular carcinoma compared with chronic hepatitis C liver tissue
XX
XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGGCT 9
Db || |||||
2 GGACGCGCT 10

RESULT 254
ABV84523
ID ABV84523 standard; cDNA; 10 BP.
XX
XX AC ABV84523;
XX
XX DT 12-DEC-2002 (first entry)
XX
XX DE Human HCC underexpressed gene SAGE tag #333.
XX
XX KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XX CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
XX expression pattern; differential expression; ss.
XX
XX OS Homo sapiens.
XX
XX PN JP2002209591-A.
XX
XX XX 30-JUL-2002.
XX
XX PF 19-JAN-2001; 2001JP-00012328.
XX
XX PR 19-JAN-2001; 2001JP-00012328.
XX
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-631294/68.
XX
XX Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes.
XX
XX Claim 28; Page 19; 139pp; Japanese.

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XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84491-ABV84590 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in
 CC hepatocellular carcinoma compared with normal liver tissue
 XX
 SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTCTGGCGCT 9
 DB 2 GGACGGCGT 10
 ||| |||||

RESULT 255
 ABV84710
 ID ABV84710 standard; cDNA; 10 BP.
 XX
 AC ABV84710;
 XX
 DT 12-DRC-2002 (first entry)
 XX
 DE Human apolipoprotein A-I SAGE tag #520.
 XX

KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX
 OS Homo sapiens.

XX JP2002209591-A.
 XX 30-JUL-2002.
 XX
 PF 19-JAN-2001; 2001JP-00012328.
 XX
 PR 19-JAN-2001; 2001JP-00012328.
 XX

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2002-631294/68.
 XX
 PT Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.
 XX
 PS Claim 46; Page 25; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve

CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in
 CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTCTGGCGCT 9
 DB 2 GGACGGCGT 10
 ||| |||||

RESULT 256
 ABV84764
 ID ABV84764 standard; cDNA; 10 BP.
 XX
 AC ABV84764;
 XX

DT 12-DEC-2002 (first entry)

XX Chronic hepatitis C/HCC differentially expressed gene SAGE tag #574.

KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX
 OS Homo sapiens.

XX JP2002209591-A.
 XX 30-JUL-2002.
 XX
 PF 19-JAN-2001; 2001JP-00012328.
 XX
 PR 19-JAN-2001; 2001JP-00012328.
 XX

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2002-631294/68.
 XX
 PT Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.
 XX
 PS Claim 46; Page 26; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression

CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly
CC expressed genes out of those genes which are underexpressed in
CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTG 10
|| |||||
DB 2 GACGCGCTG 10

RESULT 257
ABV84791
ID ABV84791 standard; cDNA; 10 BP.
XX
XX AC ABV84791;
XX
XX DT 12-DEC-2002 (first entry)
XX
XX DE Human apolipoprotein A-I SAGE tag #601.
XX

KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; ss.
XX
XX OS Homo sapiens.

XX JP2002209591-A.
XX
XX PN 30-JUL-2002.
XX
XX PD
XX PF 19-JAN-2001; 2001JP-00012328.
XX
XX PR 19-JAN-2001; 2001JP-00012328.
XX

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX DR WPI; 2002-631294/68.
XX
XX

XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve
XX to uniquely identify each transcript and can thus be used to analyse the
XX pattern of gene expression in particular cell types. The invention also
XX relates to proteins encoded by the genes expressed in chronic hepatitis C
XX liver tissue or HCC, antibodies against these proteins, and inhibitors of
XX the expression of groups of genes that are overexpressed in chronic
XX hepatitis C liver tissue or HCC. Groups of genes differentially expressed
XX in chronic hepatitis C tissue or HCC may be used for the diagnosis and
XX treatment of these diseases. Such genes, inhibitors of their expression
XX or activity, and antibodies against the gene products may be used in the
XX development of drugs to treat chronic hepatitis C and/or HCC. Sequences
XX ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly
XX expressed in chronic hepatitis C liver tissue

SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGCGCTG 9
|| |||||
DB 2 GGACGCGCT 10

RESULT 258
ABV84741
ID ABV84741 standard; cDNA; 10 BP.
XX
XX AC ABV84741;
XX
XX DT 12-DEC-2002 (first entry)
XX
XX DE Chronic hepatitis C/HCC differentially expressed gene SAGE tag #551.
XX

KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; differential expression; ss.
XX
XX OS Homo sapiens.

XX JP2002209591-A.
XX
XX PN 30-JUL-2002.
XX
XX PD
XX PF 19-JAN-2001; 2001JP-00012328.
XX
XX PR 19-JAN-2001; 2001JP-00012328.
XX

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX DR WPI; 2002-631294/68.
XX
XX

XX Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes.
XX
XX PS Claim 46; Page 26; 139pp; Japanese.
XX

XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve
XX to uniquely identify each transcript and can thus be used to analyse the
XX pattern of gene expression in particular cell types. The invention also
XX relates to proteins encoded by the genes expressed in chronic hepatitis C
XX liver tissue or HCC, antibodies against these proteins, and inhibitors of
XX the expression of groups of genes that are overexpressed in chronic
XX hepatitis C liver tissue or HCC. Groups of genes differentially expressed
XX in chronic hepatitis C tissue or HCC may be used for the diagnosis and
XX treatment of these diseases. Such genes, inhibitors of their expression
XX or activity, and antibodies against the gene products may be used in the
XX development of drugs to treat chronic hepatitis C and/or HCC. Sequences
XX ABV84691-ABV84790 are SAGE tags representing the 100 least highly
XX expressed genes out of those genes which are underexpressed in
XX hepatocellular carcinoma compared with chronic hepatitis C liver tissue

SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGCGCTG 9
|| |||||
DB 2 GGACGCGCT 10


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RESULT 259
ABV84919
ID ABV84919 standard; cDNA; 10 BP.
XX AC
XX ABV84919;
XX 12-DEC-2002 (first entry)
XX DT
XX DE
XX DE Human apolipoprotein A-I SAGE tag #729.
XX
XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XX KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
XX KW expression pattern; ss.
XX
XX OS Homo sapiens.
XX
XX JP2002209591-A.
XX PN
XX 30-JUL-2002.
XX PD
XX PF 19-JAN-2001; 2001JP-00012328.
XX
XX PR 19-JAN-2001; 2001JP-00012328.
XX
XX PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-631294/68.
XX DR
XX Human chronic hepatitis C tissue expression exasperating gene group
XX PT comprises 100 high-ranking genes.
XX
XX PS Claim 64; Page 30; 139pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve
XX to uniquely identify each transcript and can thus be used to analyse the
XX pattern of gene expression in particular cell types. The invention also
XX relates to proteins encoded by the genes expressed in chronic hepatitis C
XX liver tissue or HCC, antibodies against these proteins, and inhibitors of
XX the expression of groups of genes that are overexpressed in chronic
XX hepatitis C liver tissue or HCC. Groups of genes differentially expressed
XX in chronic hepatitis C tissue or HCC may be used for the diagnosis and
XX treatment of these diseases. Such genes, inhibitors of their expression
XX or activity, and antibodies against the gene products may be used in the
XX development of drugs to treat chronic hepatitis C and/or HCC. Sequences
XX ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
XX expressed in hepatocellular carcinoma
XX
XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGGCT 9
DB 2 GGACGCGCT 10

RESULT 260
ABV84967
ID ABV84967 standard; cDNA; 10 BP.
XX AC
XX ABV84967;
XX 12-DEC-2002 (first entry)
XX DT
XX DE Human thymosin beta-4 SAGE tag #777.
XX

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```

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XX KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
XX KW expression pattern; ss.
XX
XX OS Homo sapiens.
XX
XX JP2002209591-A.
XX PN
XX 30-JUL-2002.
XX PD
XX PF 19-JAN-2001; 2001JP-00012328.
XX
XX PR 19-JAN-2001; 2001JP-00012328.
XX
XX PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-631294/68.
XX DR
XX Human chronic hepatitis C tissue expression exasperating gene group
XX PT comprises 100 high-ranking genes.
XX
XX PS Claim 64; Page 31; 139pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve
XX to uniquely identify each transcript and can thus be used to analyse the
XX pattern of gene expression in particular cell types. The invention also
XX relates to proteins encoded by the genes expressed in chronic hepatitis C
XX liver tissue or HCC, antibodies against these proteins, and inhibitors of
XX the expression of groups of genes that are overexpressed in chronic
XX hepatitis C liver tissue or HCC. Groups of genes differentially expressed
XX in chronic hepatitis C tissue or HCC may be used for the diagnosis and
XX treatment of these diseases. Such genes, inhibitors of their expression
XX or activity, and antibodies against the gene products may be used in the
XX development of drugs to treat chronic hepatitis C and/or HCC. Sequences
XX ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
XX expressed in hepatocellular carcinoma
XX
XX Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
DB 2 TGGTGAAGG 10

RESULT 261
ABK23578/c
ID ABK23578 standard; DNA; 10 BP.
XX
XX ABK23578;
XX 09-APR-2002 (first entry)
XX DT
XX DE Transcript tag DNA sequence #167 induced or suppressed by N-myc.
XX
XX Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
XX KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;
XX KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
XX OS Homo sapiens.
XX
XX WO200185941-A2.
XX PN

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PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-NL000361.
XX
PR 11-MAY-2000; 2000EP-00201698.
PR 29-JUN-2000; 2000EP-00202284.
XX
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI Versteeg R, Caron HN;
XX
DR WPI; 2002-066603/09.
XX
PT A new nucleic acid library of myc-dependent downstream genes capable of
PT supporting a neoplastic characteristic of cancer is useful to find new
PT therapies and diagnoses for cancer.
XX
PS Disclosure; Page 53; 69pp; English.
XX
CC The present invention relates to a nucleic acid library comprising myc-
CC dependent downstream genes or their functional fragments essentially
CC capable of supporting a neoplastic character of cancer such as growth,
CC invasion or spread. These myc target or tag sequences are identified by
CC SAGE (serial analysis of gene expression). The library is useful to find
CC new diagnoses and treatments for cancer. The invention is also useful to
CC enhance production of recombinant proteins in a production system with
CC high expression of endogenous or transfected myc oncogenes. ABK23412-
CC ABK23828 represent transcript tag DNA sequences that are activated or
CC repressed by N-myc in human neuroblastoma
XX
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCCGCGCT 9
Db |||||
10 GGTCCGCGCT 2

RESULT 262
ABA96213/c
ID ABA96213 standard; DNA; 10 BP.
XX
AC ABA96213;
XX
DT 13-MAR-2002 (first entry)
XX
DE Half-site oligonucleotide ON-10.
XX
KW Multidimensional library; MDL; industrial; pharmaceutical; biomedicine;
KW bioregulation; multidimensional peptide; MDP; vaccine; ss.
XX
OS Synthetic.
XX
PN WO200186293-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-IB000810.
XX
PR 12-MAY-2000; 2000US-00570477.
XX
PA (SUPR-) SUPRATEK PHARMA INC.
PA (BIOP-) BIOPHAGE INC.
XX
PI Popkov M, Mandeville R, Romar O, Alakhov V;
XX
DR WPI; 2002-089806/12.
XX
PT New multidimensional library useful for screening molecules that
PT potentially interact with a target molecule, e.g. multidimensional

PT peptides useful in any industrial or pharmaceutical application.
XX
XX Example 1; Page 57; 77pp; English.
XX
CC The invention relates to a multidimensional library (MDL) for screening
CC molecules that potentially interact with a target molecule. A MDL may be
CC represented by various natural or artificial polymeric compounds
CC including oligonucleotides, proteins, polypeptides, peptides,
CC polycarbohydrates etc., where the library comprises at least one molecule
CC comprising a general formula (Xyn)m, where: (Xyn) is a repeating unit of
CC the at least one molecule; x = a functional unit that interacts with the
CC target molecule; y = a structural unit; n = the number of the structural
CC units in the repeating unit; and m = a number of repeating units in the
CC at least one molecule. The MDL is useful for screening molecules that
CC potentially interact with a target molecule, particularly for screening
CC proteins, polypeptides or peptides for binding specificity and desired
CC affinity for target molecule. The multidimensional peptide products can
CC be used in any industrial or pharmaceutical application that uses a
CC peptide binding moiety specific for any given target. These are also
CC useful in a wide variety of in vivo applications in the fields of
CC biomedicine, bioregulation and control. Other in vivo uses include
CC administration of multidimensional peptides (MDP) and MDP compositions as
CC immunogens for vaccines, which useful for active immunisation procedures.
CC The present sequence is that of an oligonucleotide useful in the
CC construction of the MDL
XX
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCCGCGCT 9
Db |||||
10 GGTCCGCGCT 2

RESULT 263
AAS19821
ID AAS19821 standard; DNA; 10 BP.
XX
AC AAS19821;
XX
DT 08-MAY-2002 (first entry)
XX
DE Oligonucleotide #1 to detect human RANGAP1 gene polymorphisms.
XX
KW Human; single nucleotide polymorphism; SNP; RANGAP1;
KW haplotyping chromosome 22q13.2-q13.31; Ran GTPase activating protein 1;
KW genotyping; cancer; irregular cell cycle associated disorder; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200179240-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US012455.
XX
PR 17-APR-2000; 2000US-0198072P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-075068/10.
XX
PT Genotyping human Ran GTPase activating protein 1 gene of individual for
PT determining haplotype of individual, involves determining identity of
PT nucleotide pair at specific polymorphic sites for two copies of the gene.
XX
PS Claim 17; Page 15; 148pp; English.
XX

```

CC The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
 CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
 CC genotyping the RANGAP1 gene. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the RANGAP1 gene
 CC polymorphisms. The polynucleotides and screened compounds are useful for
 CC treatment of diseases associated with RANGAP1 activity, such as cancer
 CC and other disorders associated with an irregular cell cycle. AAS19821-
 CC AAS19898 represent primer-extension oligonucleotides for detecting human
 CC RANGAP1 gene polymorphisms
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCGCTGTG 12
 |||||
 DB 2 CGCGCGGTG 10

RESULT 264

ABA933366
 ID ABA93366 standard; DNA; 10 BP.

XX ABA93366;

XX ABA93366;

XX 22-APR-2002 (first entry)

XX Human ACAA1 gene polymorphism detection primer SEQ ID NO:81.

XX Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22;

XX peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype;

XX single nucleotide polymorphism; polymorphic variant; enzyme; probe;

XX primer; allele specific oligonucleotide; ss.

XX Homo sapiens.

XX WO200187903-A2.

XX 22-NOV-2001.

XX 03-MAY-2001; 2001WO-US014330.

XX 18-MAY-2000; 2000US-0205022P.

XX (GENA-) GENAISSANCE PHARM INC.

XX (DUDA/) DUDA A E.

XX Chew A, Koshiy B;

XX WPI; 2002-164134/21.

XX Isolated polynucleotide, comprising a polymorphic variant of the acetyl-

XX Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)

XX gene useful for providing haplotype information and in therapy for

XX treating related disorders.

XX Claim 17; Page 14; 93pp; English.

XX The present invention describes a polypeptide (I) which is a polymorphic

XX variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal 3-

XX oxoacyl-Coenzyme A thiolase) ACAA1 protein (AB00516). ACAA1 is located

XX on chromosome 3p23-p22. (I) can be encoded by ABA93286 (or ABA93288)

XX where the sequence comprises one of the haplotypes shown in Table 4 or

XX one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are

XX given in the specification. The polynucleotide encoding ACAA1 can be used

XX for providing haplotype and genotype information of an individual.

XX Furthermore, the polynucleotide is useful for the treatment of disorders

XX related to its abnormal expression or function. ABA93289 to ABA93383

XX represent allele specific oligonucleotides (ASOs) which are used in the

CC detection of polymorphisms in the human ACAA1 gene

XX

SQ Sequence 10 BP; 4 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

|||||

DB 1 TGGAGAAGG 9

|||||

1 TGGAGAAGG 9

RESULT 265

AAS19954/c

ID AAS19954 standard; DNA; 10 BP.

XX AAS19954;

XX AAS19954;

XX 26-MAR-2002 (first entry)

XX Primer-extension oligonucleotide #6 to detect human DNAL4 polymorphisms.

XX Human; single nucleotide polymorphism; SNP; DNAL4; chromosome 22q13.1;

XX dynein axonemal light polypeptide chain 4; haplotyping; genotyping;

XX neuroprotective; neurological disorder; primer; ss.

XX Homo sapiens.

XX WO200179235-A2.

XX 25-OCT-2001.

XX 16-APR-2001; 2001WO-US012304.

XX 17-APR-2000; 2000US-0197460P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bentivegna SC, Chew A, Choi JY, Koshiy B;

XX WPI; 2002-075065/10.

XX Genotyping human dynein, axonemal light polypeptide chain 4 gene of

XX individual, useful for determining haplotype of individual, comprises

XX determining identity of nucleotide pair at specific polymorphic sites for

XX two copies of gene.

XX Claim 18; Page 13; 79pp; English.

XX The present invention relates to novel single nucleotide polymorphisms

XX (SNPs) in the human dynein, axonemal light polypeptide chain 4 (DNAL4)

XX gene located on chromosome 22q13.1, and methods for haplotyping and/or

XX genotyping the DNAL4 gene. The methods of the invention make use of

XX allele-specific oligonucleotides (ASOs) as probes and primers and/or

XX primer-extension oligonucleotides for detecting the DNAL4 gene

XX polymorphisms. The polynucleotides and screened compounds are useful for

XX the treatment of diseases associated with DNAL4 activity, such as

XX neurological disorders. AAS19949-AAS19976 represent primer-extension

XX oligonucleotides for detecting human DNAL4 gene polymorphisms

XX

SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18

|||||

DB 10 GTGGCTAAG 2

|||||

10 GTGGCTAAG 2

|||||

10 GTGGCTAAG 2

RESULT 266

XX 11-OCT-2001; 2001WO-US042637.
 XX
 PR 11-OCT-2000; 2000US-0239740P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Bentivegna SC, Kazemi A, Koshy B, Parks KE, Rounds E, Sausker EA;
 XX WPI; 2002-519230/55.
 DR
 XX Novel genetic variants of Cytochrome P450, Subfamily I (Aromatic Compound
 PT -Inducible) isogenes, useful for improving efficiency and reliability in
 PT drug development for treating cancers.
 XX
 PS Claim 16; Page 15; 93pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising a first
 CC nucleotide sequence which comprises cytochrome P450, subfamily I
 CC (aromatic compound-inducible) (CYP1A2), selected from isoforms 1-8 and 10
 CC -16 given in the specification, where the isogenes comprise the regions
 CC of a CYP1A2 gene sequence (ABK87391) or the cDNA (ABK87392). Also
 CC included are haplotyping or genotyping CYP1A2 gene of an individual,
 CC predicting a haplotype pair for CYP1A2 gene of an individual,
 CC an association between a trait and at least one haplotype or haplotype
 CC pair of CYP1A2 gene, primers and probes for performing the
 CC genotyping/haplotyping, a recombinant non-human organism transformed or
 CC transfected with the CYP1A2 polynucleotide, where the organism expresses
 CC a CYP1A2 protein or variant, a fragment of a CYP1A2 isogene comprising at
 CC least 10 nucleotides and a polymorphism selected from the 18 identified
 CC polymorphisms, polymorphic variants of the CYP1A2 polypeptide, an anti-
 CC CYP1A2 monoclonal antibody, a computer system for storing and analyzing
 CC polymorphism data for the CYP1A2 gene, and a genome anthology for CYP1A2
 CC gene. The polymorphic variants, haplotyping/genotyping methods and
 CC antibodies are useful in diagnostic, prognostic and therapeutic methods
 CC and in screening for drugs that are useful for treating cancers, tardive
 CC dyskinesia (TD) and porphyria cutanea tarda (PCT). The gene for CYP1A2 is
 CC located on chromosome 15q22-qter. The present sequence is the 3' end of
 CC an allele specific primer extension PCR primer used to detect the
 CC polymorphisms
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 CGCGCTGTG 12
 DB | | | | | | |
 9 CGCGCTGTG 1
 RESULT 269
 AAS94665/C
 ID AAS94665 standard; DNA; 10 BP.
 XX
 AC AAS94665;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human PLTP gene allele-specific oligonucleotide PCR primer #24.
 XX
 KW Human; phospholipid transfer protein; PLTP; haplotyping; haplotype pair;
 KW single nucleotide polymorphism; genotyping; gene therapy; drug screening;
 KW binding affinity; atherosclerosis; ss; sequencing primer; PCR primer;
 KW probe.
 XX
 OS Homo sapiens.
 XX
 PN WO200172966-A2.
 XX
 PD 04-OCT-2001.
 XX

PF 26-MAR-2001; 2001WO-US009776.
 XX
 PR 24-MAR-2000; 2000US-0192127P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Choi JY, Koshy B;
 XX WPI; 2002-010724/01.
 DR
 XX New isolated polynucleotide which is polymorphic variant of phospholipid
 PT transfer protein (PLTP) gene, having any one of polymorphic sites PS1-
 PT PS25, for studying function of PLTP, and expressing PLTP protein.
 XX
 PS Claim 17; Page 85; 99pp; English.
 XX
 CC The invention relates to single nucleotide polymorphisms in the gene
 CC encoding the human phospholipid transfer protein (PLTP). A method for
 CC haplotyping the PLTP gene in an individual comprises identifying the
 CC nucleotide at one or more polymorphic sites and determining whether one
 CC of the copies of the gene is defined by one of the PLTP haplotypes given
 CC in the specification or whether both copies are defined by a haplotype
 CC pair. This method is useful in genotyping, whereby all possible haplotype
 CC pairs can be assigned to specific genotypes. An association between a
 CC trait and a haplotype or haplotype pair of the PLTP gene can be
 CC identified by comparing the frequency of the haplotype or haplotype pair
 CC in a population exhibiting the trait with the frequency of the haplotype
 CC or haplotype pair in a reference population, where a higher haplotype
 CC frequency in the trait population indicates the trait is associated with
 CC the haplotype or haplotype pair. PLTP and its corresponding DNA are used
 CC for studying the expression and function of PLTP, for use in screening
 CC for candidate drugs to treat diseases related to PLTP activity. The
 CC sequences are also useful for studying the effect of variation on the
 CC biological activity of PLTP as well as on the binding affinity of
 CC candidate drugs targeting PLTP for treating atherosclerosis. Sequences
 CC AAS94566-AAS94691 represent allele-specific oligonucleotide probes,
 CC sequencing primers and PCR primers used for detecting PLTP gene
 CC polymorphisms
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GTGGCGAAG 18
 DB | | | | | | |
 10 GTGGCGAAG 2
 RESULT 270
 AAD25031/C
 ID AAD25031 standard; DNA; 10 BP.
 XX
 AC AAD25031;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human AANAT gene polymorphism detecting primer #21.
 XX
 KW Human; genetic variant; arylalkylamine N-acetyltransferase; AANAT gene;
 KW haplotyping; genotyping; pineal gland disorder; melatonin synthesis;
 KW gene therapy; antisense therapy; primer; polymorphism; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200187909-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US016279.
 XX
 PR 18-MAY-2000; 2000US-0205068P.
 XX

XX (GENA-) GENAISSANCE PHARM INC.
 XX Choi JY, Kazemi A, Nandabalan K;
 XX WPI; 2002-055682/07.
 XX New genetic variants of human arylalkylamine N-acetyltransferase (ANAT)
 PT gene for studying expression, function of the gene and expressing ANAT
 PT protein for use in screening for drugs to treat disorders of pineal
 PT gland.
 XX
 XX Claim 18; Page 13; 67pp; English.
 XX
 CC The patent discloses novel genetic variants of the arylalkylamine N-
 CC acetyltransferase (ANAT) gene. The invention also relates to
 CC compositions and methods for genotyping and/or genotyping the ANAT
 CC gene. Polymorphic variants of ANAT protein are useful for screening for
 CC drugs targeting the polypeptide. ANAT polynucleotides are useful for
 CC studying the expression and function of ANAT and for expressing ANAT
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to ANAT activity. The methods are used to develop diagnostic
 CC tests and therapeutic treatment for disorders of pineal gland that derive
 CC from defects in melatonin synthesis. It is useful for determining whether
 CC an individual has one of the haplotypes 1-4 or the haplotype pairs. The
 CC haplotyping method is useful to validate ANAT as a candidate target for
 CC treating a specific condition or disease predicted to be associated with
 CC ANAT activity. ANAT sequences of the invention are also used in gene
 CC therapy and antisense therapy. The present DNA sequence is a primer which
 CC is used for detecting human ANAT gene polymorphisms
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCGGAGG 19
 Db 9 TGGCGCAGG 1
 RESULT 271
 ABK30052
 ID ABK30052 standard; DNA; 10 BP.
 AC ABK30052;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Vancomycin-resistant enterococci, VanH promoter mutant M10.
 XX
 CC Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
 KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
 KW vanH promoter; androgen receptor promoter; AR promoter;
 KW human epidermal growth factor receptor 2 promoter; her2 promoter;
 KW beta lactamase promoter; B1a promoter; transgene; cancer; breast cancer;
 KW colon cancer; immunological disorder; prostate cancer; cytostatic;
 KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
 KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
 KW gene expression modulator; multiple sclerosis; MS;
 KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
 KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
 KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
 KW mutant; transgenic; ds.
 XX
 OS Enterococcus sp.
 XX
 XX WO200194600-A2.
 FN
 XX
 PD 13-DEC-2001.
 XX
 XX 06-JUN-2001; 2001WO-US018343.

XX 06-JUN-2000; 2000US-0209549P.
 PR (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PA Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
 PI Velligan WD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
 PI Lim MY, Bruce TW;
 XX WPI; 2002-130595/17.
 DR
 XX New nucleic acid regulatory sequences, which are able to regulate
 PT expression of a gene operably linked to a promoter, useful for regulating
 PT the expression of transgenes and for treating e.g., cancer and
 PT immunological diseases.
 PT
 XX Example 4; Page 50; 95pp; English.
 XX
 CC The invention describes an isolated nucleic acid regulatory sequence for
 CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
 CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
 CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
 CC (Bla) promoter. Transcription regulatory sequences may be used to
 CC regulate expression of the endogenous, autologous or heterologous genes
 CC operably linked to the promoter, and may be incorporated into
 CC heterologous nucleic acid constructs for use in regulated expression of
 CC transgenes. Regulated expression of cyclin D1 can be used in cancer
 CC therapies, such as breast, colon or pancreatic cancers and familial
 CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
 CC may be used in the treatment of immunological disorders, such as
 CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
 CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
 CC arthritis. Regulated expression of genes under the control of the HBV
 CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
 CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
 CC hepatocellular carcinoma, and in the regulated expression of liver cell-
 CC specific genes. Regulated expression of the vanH gene promoter can be
 CC used in treatment of Enterococcus infection, while regulated expression
 CC of the androgen receptor gene can be used in the treatment of prostate
 CC cancer. This sequence represents a mutated promoter region used in the
 CC invention to determine the regulatory regions involved in gene
 CC expression, described in the method of the invention
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTCCGCGCTG 10
 Db 1 GGCGCGCTG 9
 RESULT 272
 ABL36392
 ID ABL36392 standard; DNA; 10 BP.
 XX
 AC ABL36392;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Human lysosomal acid phosphatase 2 primer-extension oligonucleotide 28.
 XX
 KW Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;
 KW lysosome-specific enzyme; orthophosphoric monoester hydrolysis;
 KW Hodgkin's disease; HD; acid phosphatase deficiency;
 KW novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;
 KW transgenic animal; primer; probe; primer-extension oligonucleotide; SNP;
 KW single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX

PN WO200194362-A2.
 XX 13-DEC-2001.
 XX 07-JUN-2001; 2001WO-US018457.
 XX 07-JUN-2000; 2000US-0210047P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Kliehm SE, Messer C, Tanguay DA;
 XX WPI; 2002-154563/20.
 XX Novel genetic variants of acid phosphatase 2, lysosomal polypeptide gene
 PT useful in studying expression and function of the protein, and for
 PT screening drugs to treat diseases e.g. Hodgkin's disease.
 XX
 XX Claim 19; Page 15; 109pp; English.
 XX The invention comprises the human lysosomal acid phosphatase 2 (ACP2)
 CC nucleic acid and protein sequences. Specifically, the invention relates
 CC to the discovery of 22 novel polymorphic sites within the APC2 gene. The
 CC invention also comprises methods for haplotyping and genotyping the ACP2
 CC gene in an individual. The ACP2 gene (located on chromosome 11) encodes a
 CC lysosomal-specific enzyme that catalyses the hydrolysis of
 CC orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and
 CC protein are pharmaceutically important in the treatment of Hodgkin's
 CC disease (HD) and acid phosphatase deficiency. The novel ACP2 gene
 CC polymorphisms of the invention are useful in haplotyping the ACP2 gene.
 CC ACP2 haplotyping is useful in validating ACP2 as a target (and designing
 CC drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's
 CC disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are
 CC useful for ACP2 genotyping, which can also be used to develop diagnostic
 CC tests and therapeutic treatments. The ACP2 protein and nucleic acids of
 CC the invention are useful in the production of a transgenic animal which
 CC expresses ACP2 protein. The ACP2 nucleic acids of the invention are
 CC useful in the production of allele-specific oligonucleotides designed to
 CC genotype each of the ACP2 polymorphisms. Nucleic acids ABL36299-ABL36320
 CC represent claimed ACP2 allele-specific probes. Nucleic acids ABL36321-
 CC ABL36364 represent claimed ACP2 allele-specific PCR primers. Nucleic
 CC acids ABL36365-ABL36408 represent claimed ACP2 primer-extension
 CC oligonucleotides
 XX
 XX Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTGCGGCTG 10
 Db ||||| |||||
 2 GTGCGGCTG 10
 RESULT 273
 AAL48136
 ID AAL48136 standard; DNA; 10 BP.
 XX
 XX AAL48136;
 XX
 XX 27-SEP-2002 (first entry)
 XX Human neurotrophin Y primer extension oligo SEQ ID NO: 60.
 XX Human; neurotrophin Y; NPY; isogene; SNP; atherosclerosis; obesity;
 KW psychological disorder; single nucleotide polymorphism; alcoholism;
 KW antiarteriosclerotic; anorectic; PCR; primer extension oligonucleotide;
 KW ss.
 XX Homo sapiens.
 OS
 XX WO200251857-A1.

XX 04-JUL-2002.
 XX 21-DEC-2000; 2000WO-US034758.
 XX 21-DEC-2000; 2000WO-US034758.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Denton RR, Lanz EM, Nandabalan K, Stephens JC;
 XX WPI; 2002-566671/60.
 XX New genetic variants of the human Neurotrophin Y (NPY) gene useful for
 PT treating disorders affected by abnormal expression or function of NPY
 PT isogene e.g., atherosclerosis or obesity.
 XX
 XX Disclosure; Page 17; 80pp; English.
 XX The present invention provides the human neurotrophin Y (NPY) gene and
 CC single nucleotide polymorphisms (SNPs) identified therein. The sequence
 CC can be used in the treatment of disorders associated with NPY, including
 CC atherosclerosis, obesity, psychological disorders and alcoholism. The
 CC present sequence is an allele specific primer extension oligonucleotide
 CC used to isolate the human NPY coding sequence
 XX
 XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCGCTGTGG 13
 Db ||||| |||||
 1 GCTCTGTGG 9
 RESULT 274
 AAS95999/c
 ID AAS95999 standard; DNA; 10 BP.
 XX
 XX AAS95999;
 XX
 XX 26-FEB-2002 (first entry)
 XX Human CALM1 gene allele-specific oligonucleotide #108.
 DE Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;
 KW haplotyping; SCVA3; Alzheimer's disease; drug screening;
 KW calcium-dependent signal transduction; PCR primer; ss.
 XX Homo sapiens.
 OS
 XX WO200179218-A2.
 XX
 XX 25-OCT-2001.
 XX 09-APR-2001; 2001WO-US011509.
 XX 12-APR-2000; 2000US-0196340P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
 XX WPI; 2002-049190/06.
 XX New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in
 PT expressing CALM1 protein for use in screening for candidate drugs to
 PT treat diseases related to CALM1 activity such as Alzheimer's disease.
 XX
 XX Claim 17; Page 14; 82pp; English.

CC The invention relates to an isolated polynucleotide comprising a sequence
 CC selected from a polymorphic variant of calmodulin 1 (CALM1). The
 CC polymorphic variant comprises an CALM1 isogene defined by a haplotype
 CC selected from haplotypes 1-21 given in the specification. The
 CC polymorphisms are useful for studying the biological function of CALM1 as
 CC well as in identifying drugs targeting this protein for the treatment of
 CC a disorder related to its abnormal expression or function. The
 CC polymorphic variants may also be used in screening for compounds
 CC targeting CALM1 to treat a specific condition or disease predicted to be
 CC associated with CALM1 activity. Establishing CALM1 haplotype or haplotype
 CC pair of an individual is useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with SCVA3 activity, e.g. Alzheimer's
 CC disease and diseases involving defects in calcium-dependent signal
 CC transduction. Haplotyping the CALM1 gene in an individual is also useful
 CC in the design of clinical trials of candidate drugs for treating a
 CC specific condition or disease predicted to be associated with CALM1
 CC activity. AAS95892-AAS96018 represent human CALM1 allele- specific
 CC oligonucleotides and PCR primers of the invention
 XX
 SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
 DB 10 CGCTGCGC 2

RESULT 275
 AAS96001/C
 ID AAS96001 standard; DNA; 10 BP.

XX AAS96001;
 AC AAS96001;
 DT 26-FEB-2002 (first entry)
 XX Human CALM1 gene allele-specific oligonucleotide #110.
 DE Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;
 KW haplotyping; SCVA3; Alzheimer's disease; drug screening;
 KW calcium-dependent signal transduction; PCR primer; ss.
 XX Homo sapiens.
 OS
 XX WO200179218-A2.
 PN
 XX 25-OCT-2001.
 PD
 XX 09-APR-2001; 2001WO-US011509.
 PF
 XX 12-APR-2000; 2000US-0196340P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
 PI WPI; 2002-049190/06.
 DR
 XX
 XX New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in
 PT expressing CALM1 protein for use in screening for candidate drugs to
 PT treat diseases related to CALM1 activity such as Alzheimer's disease.
 XX
 PS Claim 17; Page 14; 82pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising a sequence
 CC selected from a polymorphic variant of calmodulin 1 (CALM1). The
 CC polymorphic variant comprises an CALM1 isogene defined by a haplotype
 CC selected from haplotypes 1-21 given in the specification. The
 CC polymorphisms are useful for studying the biological function of CALM1 as
 CC well as in identifying drugs targeting this protein for the treatment of

CC a disorder related to its abnormal expression or function. The
 CC polymorphic variants may also be used in screening for compounds
 CC targeting CALM1 to treat a specific condition or disease predicted to be
 CC associated with CALM1 activity. Establishing CALM1 haplotype or haplotype
 CC pair of an individual is useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with SCVA3 activity, e.g. Alzheimer's
 CC disease and diseases involving defects in calcium-dependent signal
 CC transduction. Haplotyping the CALM1 gene in an individual is also useful
 CC in the design of clinical trials of candidate drugs for treating a
 CC specific condition or disease predicted to be associated with CALM1
 CC activity. AAS95892-AAS96018 represent human CALM1 allele- specific
 CC oligonucleotides and PCR primers of the invention
 XX

SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
 DB 9 GCGCTGCGG 1

RESULT 276

ID ABK81811 standard; DNA; 10 BP.
 XX
 AC ABK81811;

DT 13-AUG-2002 (first entry)

XX Human CHRM5 gene polymorphism detection oligonucleotide primer #17.

XX Human; cholinergic receptor muscarinic 5; CHRM5; genotyping; haplotyping;
 KW single nucleotide polymorphism; SNP; primer; ss.

XX Homo sapiens.

XX WO200232924-A2.

XX 25-APR-2002.

XX 11-OCT-2001; 2001WO-US032022.

XX 19-OCT-2000; 2000WO-US029071.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bieglecki KM, Chew A, Choi JY, Denton RR, Nandabalan K;

XX Sausker EA, Stephens JC;

XX WPI; 2002-435523/46.

XX Novel cholinergic receptor, muscarinic 5 polynucleotide useful
 PT therapeutically and in screening for candidate drug to treat diseases
 PT related to the receptor activity.

XX Claim 16; Page 14; 72pp; English.

XX The present invention relates to a new cholinergic receptor, muscarinic 5
 CC (CHRM5) polynucleotide comprising a sequence which is a polymorphic
 CC variant for a reference sequence for the CHRM5 gene or its fragment, or a
 CC polymorphic variant of a reference sequence for a CHRM5 cDNA or its
 CC fragment. The invention is useful in drug screening assays. The molecules
 CC of the invention are useful in studying the expression and function of
 CC CHRM5, and in expressing CHRM5 protein for use in screening for candidate
 CC drugs to treat diseases related to CHRM5 activity. The methods of the
 CC invention are useful in developing diagnostic tests and therapeutic
 CC treatments. The method is also useful in the design of clinical trials of
 CC candidate drugs for treating specific condition or disease associated
 CC with CHRM5 activity and is useful in determining whether an individual

CC has one of the haplotypes or one of the haplotype pairs. The invention is
 CC useful in a variety of diagnostic and prognostic formats and therapeutic
 CC methods. The invention is also useful in genotyping and/or haplotyping
 CC the CHRM5 gene in an individual. The present nucleic acid sequence
 CC represents one of a collection of oligonucleotide primers (ABK81795-
 CC ABK81814) that were used in the invention to detect polymorphisms in the
 CC human CHRM5 gene

XX Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
 |||||
 Db 2 GTGGCGAAG 10

RESULT 277

ACA94410
 ID ACA94410 standard; DNA; 10 BP.

XX ACA94410;

DT 18-JUL-2003 (first entry)

XX DNA tag from human transcript repressed in adenomas/cancers #5.

XX Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.

XX Homo sapiens.

XX WO2003022863-A1.

XX 20-MAR-2003.

XX 09-SEP-2002; 2002WO-US028518.

XX 07-SEP-2001; 2001US-0317494P.

XX 30-MAY-2002; 2002US-0383805P.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Buckhaults P, Kinzler KW, Vogelstein B;

XX WPI; 2003-313220/30.

XX Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.

XX Example 1; Page 18; 59pp; English.

XX The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA
 CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
 CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces by
 CC detection of increased reaction product or decreased RDP substrate, and

CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a
 CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or RDP substrate
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC repressed in colorectal cancer or colorectal adenoma

XX
 SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

|||||

Db 2 TGGCGAAGG 10

RESULT 278

ACA94519/C

ID ACA94519 standard; DNA; 10 BP.

XX ACA94519;

DT 18-JUL-2003 (first entry)

XX DNA tag from human transcript repressed in adenomas/cancers #52.

XX Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.

XX Homo sapiens.

XX WO2003022863-A1.

XX 20-MAR-2003.

XX 09-SEP-2002; 2002WO-US028518.

XX 07-SEP-2001; 2001US-0317494P.

XX 30-MAY-2002; 2002US-0383805P.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Buckhaults P, Kinzler KW, Vogelstein B;

XX WPI; 2003-313220/30.

XX Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.

XX Disclosure; Page 27; 59pp; English.

XX The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP

PA (LISS/) LI S.
PA (PIET/) PIETRZYNSKI G.
PA (ALAK/) ALAKHOV V.
XX
PI Tchistiakova L, Li S, Pietrzynski G, Alakhov V;
XX
DR WPI; 2003-719970/68.
XX
XX New peptides capable of crossing the small intestine or blood brain
PT barrier are useful as a ligand to increase bioavailability in the
PT treatment of disease associated with central nervous system pathologies.
XX
XX Example 3; Page 21; 33pp; English.
XX
CC The invention describes a polypeptide capable of crossing the small
CC intestine or blood brain barrier. The polypeptide is used to treat a
CC disease associated with central nervous system pathologies. This sequence
CC represents an oligonucleotide used in the creation of a phage capable of
CC producing peptide that can deliver a biological agent across the small
CC intestine or blood brain barrier.
XX
XX Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
SQ Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTGGCGCT 9
||| |||||
DB 10 GGTGGCGCT 2

RESULT 281
ADJ93954/C
ID ADJ93954 standard; DNA; 10 BP.
XX
AC ADJ93954;
XX
XX 06-MAY-2004 (first entry)
XX
DE Azotobacter bacteria RAPD-PCR primer, Azr4.
XX
XX edaphic; bacterial biomass; aqueous soil suspension; biofilm; fertilizer;
KW bacterisation; soil; agricultural waste; cereal; maize; primer; ss.
XX
XX Azotobacter chroococcum.
XX
XX FR2833016-Al.
XX
XX 06-JUN-2003.
XX
XX 30-NOV-2001; 2001FR-00015542.
XX
XX 30-NOV-2001; 2001FR-00015542.
XX
XX (VALB-) VALBIOS SA.
XX
XX Claude PP;
XX
XX WPI; 2003-560903/53.
XX
XX Production of bacterial biomasses useful for bacterization of soil and
PT agricultural waste comprises contacting soil suspension with substrate,
PT maturing biofilm and recovering and culturing most prolific strains.
XX
XX Disclosure; Page 18; 50pp; French.
XX
CC The invention relates to the novel method for production of edaphic
CC bacterial biomasses. The method comprises contacting an aqueous soil
CC suspension with a substrate to form a biofilm, maturing the biofilm to
CC allow dominant strains to migrate into the supernatant liquid, and
CC recovering and culturing the most prolific strains in liquid media. The
CC biomasses can be used as a fertilizer. The biomasses are useful for

CC bacterisation of the soil and agricultural waste, especially cereal
CC (including maize) waste. This polynucleotide sequence represents a primer
CC used in the exemplification of the invention.
XX
SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CGCGCTGTG 12
|||||||
DB 10 CGCGCTGG 2

RESULT 282
ADG65513/C
ID ADG65513 standard; DNA; 10 BP.
XX
AC ADG65513;
XX
XX 11-MAR-2004 (first entry)
XX
XX UCP2 primer extension primer seq id 109.
DE
XX
XX anorectic; antidiabetic; immunomodulator; gene therapy; haplotyping;
KW uncoupling protein 2; mitochondrial; proton carrier; UCP2;
KW polymorphic site; haplotype; haplotype pair; obesity; diabetes;
KW immunological disorder; body mass defect; thermoregulation defect; human;
KW primer extension; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX US2003207284-Al.
XX
XX 06-NOV-2003.
XX
XX 16-JUL-2002; 2002US-00197019.
XX
XX 25-JAN-2001; 2001WO-US002485.
XX
XX (CHEW/) CHEW A.
XX (DENT/) DENTON R R.
XX (GILS/) GILSON C R.
XX (NAND/) NANDABALAN K.
XX (PARK/) PARKS K E.
XX
XX Chew A, Denton RR, Gilson CR, Nandabalan K, Parks KE;
PI WPI; 2004-051505/05.
XX
XX Haplotyping Uncoupling Protein 2 gene of an individual comprises
PT identifying the phased sequence of nucleotides at polymorphic sites of
PT the gene and assigning a haplotype or haplotype pair consistent with the
PT phased sequence.
XX
XX Disclosure; SEQ ID NO 109; 64pp; English.
XX
XX The invention describes haplotyping the uncoupling protein 2
CC (mitochondrial, proton carrier) (UCP2) gene of an individual comprising
CC identifying the phased sequence of nucleotides at polymorphic sites (PS)1
CC -23 for at least one copy of the individual's UCP2 gene and assigning to
CC the individual a UCP2 haplotype or haplotype pair that is consistent with
CC the phased sequence. The composition and methods are useful in
CC haplotyping and/or genotyping the UCP2 gene in an individual to e.g.
CC screen for drugs targeting the UCP2 protein to treat a condition or
CC disease predicted to be associated with UCP2 activity. The disease or
CC condition may include obesity, diabetes, immunological disorders and
CC other diseases associated with defects in body mass and thermoregulation.
CC This sequence represents a primer extension primer used for detecting
CC human uncoupling protein 2 (UCP2) gene polymorphisms.
XX
XX Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match	38.9%;	Score 7.4;	DB 1;	Length 10;	CC
Best Local Similarity	88.9%;	Pred. No. 1.7e+02;			CC
Matches 8;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	CC
Qy	2	GTCGGCTG 10			CC
Db	9	GTAGCGCTG 1			CC
RESULT 283					CC
ADN89094/c					CC
ID ADN89094		standard; DNA; 10 BP.			CC
XX		ADN89094;			CC
AC					CC
XX					CC
DT		15-JUL-2004 (first entry)			CC
XX		Hyperlipidemia treatment associated human ITGB3 haplotype probe #159.			CC
DE					CC
XX		ss; probe; antilipemic; gene therapy; allele; polymorphic site;			CC
KW		integrin beta 3; ITGB3; statin responsee marker; hyperlipidemia.			CC
KW					CC
XX					CC
OS		Homo sapiens.			CC
XX					CC
PN		WO2004033710-A2.			CC
XX					CC
PD		22-APR-2004.			CC
XX					CC
PF		09-OCT-2003; 2003WO-US032361.			CC
XX					CC
PR		09-OCT-2002; 2002US-0417743P.			CC
XX					CC
PA		(GENA-) GENAISSANCE PHARM INC.			CC
XX					CC
PI		Bentivegna SC, Bieglecki KM, Brain CD, Dain BJ, Cappola G;			CC
PI		Judson RS, Lachowicz M, Lee HH, Litvyn L, Messer C, Petersen N;			CC
PI		Reed CR, Rounds EM, Russo DP, Windemuth AK;			CC
XX		WPI; 2004-340942/31.			CC
DR					CC
XX					CC
XX		New kit comprising a set of oligonucleotides, useful for determining			CC
PT		whether an individual has a statin response marker I or II for preparing			CC
PT		a composition for treating hyperlipidemia.			CC
XX					CC
XX		Disclosure; SEQ ID NO 162; 202pp; English.			CC
PS					CC
XX		A kit comprising a set of oligonucleotides designed for identifying at			CC
CC		least one of the alleles at each polymorphic site (PS) in a set of 129			CC
CC		polymorphic sites (PSs) given in the specification, is new. The kit			CC
CC		identifies at least one of the alleles at each polymorphic site (PS) in a			CC
CC		set of 129 polymorphic sites (PSs) given in the specification, for			CC
CC		example: PS1 and PS42; PS19 and PS42; PS3, PS12, and PS42; a set of			CC
CC		polymorphic sites comprising a linked haplotype to any one of haplotypes			CC
CC		101-194, 201-463 or 501-515 given in the specification; or a set of			CC
CC		polymorphic sites comprising a substitute haplotype for any one of			CC
CC		haplotypes 101-194, 201-463 or haplotypes 501-515 given in the			CC
CC		specification; where the nucleotide position of each polymorphic site			CC
CC		corresponds to the following nucleotide position in the 32577-bp			CC
CC		sequence: 1118 (PS1), 1773 (PS3), 1875 (PS4), 1911 (PS5), 1957 (PS6),			CC
CC		2087 (PS10), 2157 (PS12), 13384 (PS15), 13405 (PS16), 16200 (PS19), 17194			CC
CC		(PS20), 17273 (PS21), 20035 (PS26), 20047 (PS28), 20615 (PS30), 21944			CC
CC		(PS33), 22155 (PS35), 25705 (PS37), 25921 (PS38), 27882 (PS39), and 30618			CC
CC		(PS42). INDEPENDENT CLAIMS are also included for: determining whether an			CC
CC		individual has a statin response marker I or a statin response marker II;			CC
CC		selecting a statin therapy to provide an optimal High Density Lipoprotein			CC
CC		Cholesterol (HDL) response in an individual; predicting an individual's			CC
CC		High Density Lipoprotein Cholesterol (HDL) response to treatment with a			CC
CC		statin; predicting an individual's High Density Lipoprotein Cholesterol			CC
CC		(HDL) response to treatment with a statin; manufacturing a drug product;			CC
CC		seeking regulatory approval for marketing a pharmaceutical formulation			CC
CC		for treating a disease or condition in a population partially or wholly			CC
CC		defined by having a statin response marker I; marketing a drug product			CC

comprising a statin as at least one active ingredient for treating a disease or condition in a population partially or wholly defined by having a statin response marker I; an isolated polynucleotide comprising a first nucleotide sequence which comprises an integrin, beta 3(ITGB3) isogene encoding a ITGB3 polypeptide, where the ITGB3 isogene consisting of isogenes 1-38 and 40-98 defined by a correspondingly numbered haplotype, where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 1317913723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 25559-26029, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence, except where substituted by the sequence of alleles for the nucleotide positions in the 32577-bp sequence and a second nucleotide sequence which is complementary to the first nucleotide sequence; a recombinant nonhuman organism transformed or transfected with the isolated polynucleotide, where the organism expresses an ITGB3 polypeptide encoded by the selected ITGB3 isogene; an isolated fragment of an integrin, beta 3(ITGB3) isogene, where the fragment comprises one or mom polymorphisms consisting of thymine at PS 1, guanine at PS2, cytosine at PS3, thymine at PS4, cytosine at PS5, adenine at PS6, thymine at PS7, thymine at PS8, guanine at PS9, adenine at PS10, adenine at PS11, thymine at PS12, adenine at PS13, guanine at PS 16, adenine at PS 18, thymine at PS 19, guanine at PS2 1, guanine at PS22, cytosine at PS23, cytosine at PS24, thymine at PS25: adenine at PS26, adenine at PS27, thymine at PS29, adenine at PS30, cytosine at PS31, guanine at PS32, adenine at PS33, adenine at PS35, cytosine at PS37, thymine at PS38, cytosine at PS39, adenine at PS40, thymine at PS41, thymine at PS42, guanine at PS43 and guanine at PS44; a genome anthology for the integrin, beta 3(ITGB3) gene which comprises two or more ITGB3 isogenes consisting of isogenes 1-98, where each of the selected isogenes is defined by a correspondingly numbered haplotype given in the specification, and where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 13179-13723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 2555926029, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence except where substituted by the sequence of alleles for the correspondingly numbered haplotype at each of file polymorphic sites; haplotyping the integrin, beta 3 (ITGB3) gene of an individual; assigning a haplotype pair for the integrin, beta 3 (ITGB3) gene to an individual; reducing the potential for bias in a clinical trial of a candidate drug for treating a disease or condition predicted to be associated with ITGB3 activity; an isolated polypeptide comprising a ITGB3 protein variant consisting of protein variants A, B, C, D, E, F and G and comprising 788-amino acid sequence, except where substituted by the corresponding sequence of amino acids whose positions and alleles are given in the specification; an isolated monoclonal antibody specific for and immunoreactive with the selected ITGB3 protein variant comprising the isolated polypeptide; screening for drugs targeting the selected ITGB3 protein variant comprising the isolated polypeptide; an isolated fragment of an ITGB3 protein variant, where the fragment is at least 6 amino acids in length and comprises one or more variant amino acids consisting of methionine at a position corresponding to amino acid position 14, arginine at a position corresponding to amino acid position 66, methionine at a position corresponding to amino acid position 445, and glutamine at a position corresponding to amino acid position 515 the 788-amino acid sequence; screening for drugs targeting the selected ITGB3 protein variant comprising the isolated polypeptide; screening for compounds targeting the ITGB3 protein to treat a condition or disease predicted to be associated with ITGB3 activity; validating the ITGB3 protein as a candidate target for treating a medical condition predicted to be associated with ITGB3 activity; and an isolated oligonucleotide designed for detecting a polymorphism in the integrin, beta 3 (ITGB3) gene at a polymorphic site (PS) consisting of PS1-PS44, where the oligonucleotide contains or is located one to several nucleotides downstream of the selected PS, where the oligonucleotide has a length of about 15 to about 100 nucleotides. Preferred Kit: The kit further comprises a manual with instructions for performing one or more reactions on a human nucleic acid sample to identify the allele(s) present in the individual at each polymorphic site in the set of polymorphic sites and determining if the individual has a statin response marker I or a statin response marker II based on the identified allele(s). The set of oligonucleotides is designated for identifying both alleles at each polymorphic site of the selected set of polymorphic sites. The set of PSs comprises PS3, PS12 and PS42; PS 1, PS12 and PS42;

PS3 and PS42: PS1 and PS42; PS1, PS3, PS12 and PS42; or PS39. The set of PS is PS3, PS12 or PS42. The individual is Caucasian. The linkage disequilibrium between the linked haplotype and any one of haplotypes 101-194, 201-463 or 501-515 has ΔG_r^2 consisting of at least 0.75, at least 0.80, at least 0.85, at least 0.90, at least 0.95 or 1.0. At least one of the oligonucleotides in the set of oligonucleotides is an allele-specific oligonucleotide comprising a nucleotide sequence consisting of 10-15 bp. The set of polymorphic sites is PS3, PS12, and PS42 and the set of oligonucleotides comprises first, second and third allele-specific oligonucleotide (ASO) probes, where the first ASO probe comprises 15-bp sequence, or its complement, and S in the 15-bp sequence is guanine; the second ASO probe comprises 15-bp sequence, or its complement, and Y in the 15-bp sequence is cytosine, and the third ASO probe comprises 15 bp, or its complement, and Y in the 15-bp sequence is cytosine. Preferred Article: The article of manufacture comprises a pharmaceutical formulation and at least one indicium identifying a population for whom the pharmaceutical formulation is indicated, where the pharmaceutical formulation comprises a statin as at least one active ingredient and the identified population is partially or wholly defined by having a statin response marker I, where a trial population having the statin response marker I exhibits a better HDLC response to the pharmaceutical formulation than to treatment with atorvastatin or salt of atorvastatin acid. It also comprises packaging material and a pharmaceutical formulation contained within the packaging material, where the pharmaceutical formulation comprises a statin as at least one separate active ingredient, and the packaging material comprises an approved label which states that the pharmaceutical formulation is indicated for a population partly or wholly defined by having a statin response marker I, where a trial population having the statin response marker exhibits a better HDLC response to the pharmaceutical formulation than to treatment with atorvastatin or a salt of atorvastatin acid. Preferred Oligonucleotide: The isolated oligonucleotide is an allele-specific oligonucleotide that specifically hybridizes to an allele of the ITGB3 gene at a region containing the polymorphic site. The isolated oligonucleotide is a primer-extension oligonucleotide. The kit is for haplotyping the integrin, beta 3 (ITGB3) gene of all individual, comprises a set of oligonucleotides designed for identifying at least one of the alleles at each polymorphic site (PS) in a set of two or more polymorphic sites. Preferred Method: Determining whether an individual has a statin response marker I or a statin response marker II comprises determining the copy number in the individual of the haplotype, where if the selected haplotype is one of haplotypes given in the specification, then the individual has a statin response marker I if the individual has at least one copy of the selected haplotype and a statin response marker II if the individual has zero copy of the selected haplotype; and the individual has a statin response marker I if the individual has zero or one copy of the selected haplotype and a statin response marker II if the individual has two copies of the selected haplotype. The individual is a candidate for treatment with a statin. The determining step comprises genotyping each polymorphic site in a set of polymorphic sites comprising the selected haplotype and using the results of the genotyping step to identify, for the set of polymorphic sites the haplotype pair present in the individual. The determining step comprises consulting a data repository, that provides information on the copy number present in the individual for the selected haplotype. The data repository is the individual's medical records or a medical data card. Assigning an individual to a first or second statin response marker group comprises determining the copy number in the individual or a haplotype and assigning the individual to the first statin response marker group if the individual has at least one copy of the selected haplotype and to the second statin response marker group if the individual has zero copy of the selected haplotype; and assigning the individual to the first statin response marker group if the individual has zero or one copy of the selected haplotype and to the second statin response marker group if the individual has two copies of the selected haplotype. The determining step comprises genotyping each polymorphic site in a set of polymorphic sites

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 8 CTGTGCGCA 16
 || |||||

Db 10 CTATGCGCA 2
 RESULT 284
 ADN89098
 ID ADN89098 standard; DNA; 10 BP.
 XX
 AC ADN89098;
 XX
 15-JUL-2004 (first entry)
 XX
 Hyperlipidemia treatment associated human ITGB3 haplotype probe #163.
 DE ss; probe; antilipemic; gene therapy; allele; polymorphic site;
 KW integrin beta 3; ITGB3; statin response marker; hyperlipidemia.
 XX
 OS Homo sapiens.
 XX
 WO2004033710-A2.
 XX
 22-APR-2004.
 XX
 09-OCT-2003; 2003WO-US032361.
 XX
 09-OCT-2002; 2002US-0417743P.
 XX
 (GENA-) GENAISANCE PHARM INC.
 XX
 Bentivegna SC, Bieglecki KM, Brain CD, Dain BJ, Cappola G;
 Judson RS, Lachowicz M, Lee HH, Litvyn L, Messer C, Petersen N;
 Reed CR, Rounds EM, Russo DP, Windemuth AK;
 WPI; 2004-340942/31.
 XX
 New kit comprising a set of oligonucleotides, useful for determining whether an individual has a statin response marker I or II for preparing a composition for treating hyperlipidemia.
 PT
 Claim 13; SEQ ID NO 166; 202pp; English.
 PS
 A kit comprising a set of oligonucleotides designed for identifying at least one of the alleles at each polymorphic site (PS) in a set of 129 polymorphic sites (PSs) given in the specification, is new. The kit identifies at least one of the alleles at each polymorphic site (PS) in a set of 129 polymorphic sites (PSs) given in the specification, for example: PS1 and PS42; PS19 and PS42; PS3, PS12, and PS42; a set of polymorphic sites comprising a linked haplotype to any one of haplotypes 101-194, 201-463 or 501-515 given in the specification; or a set of polymorphic sites comprising a substitute haplotype for any one of haplotypes 101-194, 201-463 or haplotypes 501-515 given in the specification; where the nucleotide position of each polymorphic site corresponds to the following nucleotide position in the 32577-bp sequence: 1118 (PS1), 1773 (PS3), 1875 (PS4), 1911 (PS5), 1957 (PS6), 2087 (PS10), 2157 (PS12), 13384 (PS15), 13405 (PS16), 16200 (PS19), 17194 (PS20), 17273 (PS21), 20035 (PS26), 20047 (PS28), 20615 (PS30), 21944 (PS33), 22155 (PS35), 25705 (PS37), 25921 (PS38), 27882 (PS39), and 30618 (PS42). INDEPENDENT CLAIMS are also included for: determining whether an individual has a statin response marker I or a statin response marker II; selecting a statin therapy to provide an optimal High Density Lipoprotein Cholesterol (HDL) response in an individual; predicting an individual's High Density Lipoprotein Cholesterol (HDL) response to treatment with a statin; predicting an individual's High Density Lipoprotein Cholesterol (HDL) response to treatment with a statin; manufacturing a drug product; seeking regulatory approval for marketing a pharmaceutical formulation for treating a disease or condition in a population partially or wholly defined by having a statin response marker I; marketing a drug product comprising a statin as at least one active ingredient for treating a disease or condition in a population partially or wholly defined by having a statin response marker I; an isolated polynucleotide comprising a first nucleotide sequence which comprises an integrin, beta 3 (ITGB3) isogene encoding a ITGB3 polypeptide, where the ITGB3 isogene consisting of isogenes 1-38 and 40-98 defined by a correspondingly numbered haplotype, where each of the isogenes comprises nucleotides 1000-2235,

4256-4716, 1317913723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 20537221009, 21731-22412, 24385-24930, 25559-26029, 27822-28255, 30263-30754, and 31300-31718 of the 32577-bp sequence, except where substituted by the sequence of alleles for the correspondingly numbered haplotype at the polymorphic sites whose nucleotide positions in the 32577-bp sequence and a second nucleotide sequence which is complementary to the first nucleotide sequence; a recombinant nonhuman organism transformed or transfected with the isolated polynucleotide, where the organism expresses an ITGB3 polypeptide encoded by the selected ITGB3 isogene; an isolated fragment of an integrin, beta 3 (ITGB3) isogene, where the fragment comprises one or more polymorphisms consisting of thymine at PS 1, guanine at PS2, cytosine at PS3, thymine at PS4, cytosine at PS5, adenine at PS6, thymine at PS7, thymine at PS8, guanine at PS9, adenine at PS10, adenine at PS11, thymine at PS12, adenine at PS13, guanine at PS16, adenine at PS 18, thymine at PS 19, guanine at PS21, guanine at PS22, cytosine at PS23, cytosine at PS24, thymine at PS25, adenine at PS26, adenine at PS27, thymine at PS28, adenine at PS30, cytosine at PS31, guanine at PS32, adenine at PS33, adenine at PS35, cytosine at PS37, thymine at PS38, cytosine at PS39, adenine at PS40, thymine at PS41, thymine at PS42, guanine at PS43 and guanine at PS44; a genome anthology for the integrin, beta 3 (ITGB3) gene which comprises two or more ITGB3 isogenes consisting of isogenes 1-98, where each of the selected isogenes is defined by a correspondingly numbered haplotype given in the specification, and where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 13179-13723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 20537221009, 21731-22412, 24385-24930, 2555926029, 27822-28255, 30263-30754, and 31300-31718 of the 32577-bp sequence except where substituted by the sequence of alleles for the correspondingly numbered haplotype at each of file polymorphic sites; haplotyping the integrin, beta 3 (ITGB3) gene of an individual, assigning a haplotype pair for the integrin, beta 3 (ITGB3) gene to an individual; reducing the potential for bias in a clinical trial of a candidate drug for treating a disease or condition predicted to be associated with ITGB3 activity; an isolated polypeptide comprising a ITGB3 protein variant consisting of protein variants A, B, C, D, E, F and G and comprising 788-amino acid sequence, except where substituted by the corresponding sequence of amino acids whose positions and alleles are given in the specification; an isolated monoclonal antibody specific for and immunoreactive with the selected ITGB3 protein variant comprising the isolated polypeptide; screening for drugs targeting the selected ITGB3 protein variant comprising the isolated polypeptide; an isolated fragment of an ITGB3 protein variant, where the fragment is at least 6 amino acids in length and comprises one or more variant amino acids consisting of methionine at a position corresponding to amino acid position 14, arginine at a position corresponding to amino acid position 66, methionine at a position corresponding to amino acid position 445, and glutamine at a position corresponding to amino acid position 515 the 788-amino acid sequence; screening for drugs targeting the selected ITGB3 protein variant comprising the isolated polypeptide; screening for compounds targeting the ITGB3 protein to treat a condition or disease predicted to be associated with ITGB3 activity; validating the ITGB3 protein as a candidate target for treating a medical condition predicted to be associated with ITGB3 activity; and an isolated oligonucleotide designed for detecting a polymorphism in the integrin, beta 3 (ITGB3) gene at a polymorphic site (PS) consisting of PS1-PS44, where the oligonucleotide contains or is located one to several nucleotides downstream of the selected PS, where the oligonucleotide has a length of about 15 to about 100 nucleotides. Preferred Kit: The kit further comprises a manual with instructions for performing one or more reactions on a human nucleic acid sample to identify the allele(s) present in the individual at each polymorphic site in the set of polymorphic sites and determining if the individual has a statin response marker I or a statin response marker II based on the identified allele(s). The set of oligonucleotides is designated for identifying both alleles at each polymorphic site of the selected set of polymorphic sites. The set of PSs comprises PS3, PS12 and PS42; PS 1, PS12 and PS42; PS3 and PS42; PS1 and PS42; PS1, PS3, PS12 and PS42; or PS39. The set of PS is PS3, PS12 or PS42. The individual is Caucasian. The linkage disequilibrium between the linked haplotype and any one of haplotypes 101-194, 201-463 or 501-515 has $\Delta G_r/2$ consisting of at least 0.75, at least 0.80, at least 0.85, at least 0.90, at least 0.95 or 1.0. At least one of the oligonucleotides in the set of oligonucleotides is an allele-specific oligonucleotide comprising a nucleotide sequence consisting of 10-15 bp.

The set of polymorphic sites is PS3, PS12, and PS42 and the set of oligonucleotides comprises first, second and third allele-specific oligonucleotide (ASO) probes, where the first ASO probe comprises 15-bp sequence, or its complement, and S in the 15-bp sequence is guanine; the second ASO probe comprises 15-bp sequence, or its complement, and Y in the 15-bp sequence is cytosine, and the third ASO probe comprises 15 bp, or its complement, and Y in the 15-bp sequence is cytosine. Preferred Article: The article of manufacture comprises a pharmaceutical formulation and at least one indicium identifying a population for whom the pharmaceutical formulation is indicated, where the pharmaceutical formulation comprises a statin as at least one active ingredient and the identified population is partially or wholly defined by having a statin response marker I, where a trial population having the statin response marker I exhibits a better HDLC response to the pharmaceutical formulation than to treatment with atorvastatin or salt of atorvastatin acid. It also comprises packaging material and a pharmaceutical formulation contained within the packaging material, where the pharmaceutical formulation comprises a statin as at least one separate active ingredient, and the packaging material comprises an approved label which states that the pharmaceutical formulation is indicated for a population partly or wholly defined by having a statin response marker I, where a trial population having the statin response marker exhibits a better HDLC response to the pharmaceutical formulation than to treatment with atorvastatin or a salt of atorvastatin acid. Preferred Oligonucleotide: The isolated oligonucleotide is an allele-specific oligonucleotide that specifically hybridizes to an allele of the ITGB3 gene at a region containing the polymorphic site. The isolated oligonucleotide is a primer-extension oligonucleotide. The kit is for haplotyping the integrin, beta 3 (ITGB3) gene of all individual, comprises a set of oligonucleotides designed for identifying at least one of the alleles at each polymorphic site (PS) in a set of two or more polymorphic sites. Preferred Method: Determining whether an individual has a statin response marker I or a statin response marker II comprises determining the copy number in the individual of the haplotype, where if the selected haplotype is one of haplotypes given in the specification, then the individual has a statin response marker I if the individual has at least one copy of the selected haplotype and a statin response marker II if the individual has zero copy of the selected haplotype; and the individual has a statin response marker I if the individual has zero or one copy of the selected haplotype and a statin response marker II if the individual has two copies of the selected haplotype. The individual is a candidate for treatment with a statin. The determining step comprises genotyping each polymorphic site in a set of polymorphic sites comprising the selected haplotype and using the results of the genotyping step to identify, for the set of polymorphic sites the haplotype pair present in the individual. The determining step comprises consulting a data repository, that provides information on the copy number present in the individual for the selected haplotype. The data repository is the individual's medical records or a medical data card. Assigning an individual to a first or second statin response marker group comprises determining the copy number in the individual or a haplotype and assigning the individual to the first statin response marker group if the individual has at least one copy of the selected haplotype and to the second statin response marker group if the individual has zero copy of the selected haplotype; and assigning the individual to the first statin response marker group if the individual has zero or one copy of the selected haplotype and to the second statin response marker group if the individual has two copies of the selected haplotype. The determining step comprises genotyping each polymorphic site in a set of polymorphic sites

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02; Mismatches 1; Indels 0; Gaps 0; Matches 8; Conservative 0;

QY 6 CGCTGTGGC 14

|||||||

Db 1 CGCTGTGAC 9

RESULT 285

ADQ82166

ID ADQ82166 standard; DNA; 10 BP.

XX

AC ADO82166;
 XX DT 21-OCT-2004 (first entry)
 XX XX Human Short stature homeobox-containing DNA binding site #3.
 XX DE
 XX XX cardiovascular; endocrine; SHOX; PCR; binding site; ds;
 KW natriuretic peptide; short stature; growth protein;
 KW cardiovascular disease; short stature homeobox-containing gene.
 XX OS Homo sapiens.
 XX XX WO2004062555-A2.
 PN XX
 PD XX 29-JUL-2004.
 XX XX 12-JAN-2004; 2004WO-EP000134.
 XX PF
 XX XX 13-JAN-2003; 2003EP-00000728.
 PR XX (RAPP/) RAPPOLD-HOERBRAND G.
 XX PA
 XX XX Rappold-Hoerbrand G, Haecker B;
 PI XX
 XX XX WPI; 2004-544028/52.
 DR XX
 XX XX Use of natriuretic peptide in combination with a growth protein, e.g.
 XX PT Short stature Homeobox-containing gene (SHOX) protein for preparing
 PT pharmaceutical compositions for treating short stature in a subject or
 PT cardiovascular diseases.
 XX XX Disclosure; Fig 2B; 36pp; English.
 PS XX
 XX XX The present invention relates to the use of a natriuretic peptide (atrial
 CC natriuretic peptide, ANP or brain natriuretic peptide, BNP) in
 CC combination with a growth protein, e.g. Short stature Homeobox-containing
 CC gene (SHOX) protein for the preparation of pharmaceutical compositions
 CC for the treatment of short stature in a subject being suspected of having
 CC a genetic defect in the SHOX gene or for treatment of patients with
 CC cardiovascular diseases. The natriuretic peptide (ANP or BNP) in
 CC combination with a growth protein, e.g. SHOX protein is useful for the
 CC preparation of pharmaceutical compositions for the treatment of short
 CC stature in a subject being suspected of having a genetic defect in the
 CC SHOX gene or for treatment of patients with cardiovascular diseases. It
 CC is also useful for the preparation of pharmaceutical compositions for
 CC stimulating or increasing human growth or for treating patients with
 CC idiopathic short stature, patients with Turner syndrome, or patients with
 CC Leri-Weill syndrome. The present sequence is a SHOX DNA binding site used
 CC in the exemplification of the invention.
 XX XX
 XX Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCGAAGG 19
 |||||
 Db 1 TGGCGAAGG 9
 RESULT 286
 ADR27907/c
 ID ADR27907 standard; DNA; 10 BP.
 XX AC ADR27907;
 XX XX
 XX 04-NOV-2004 (first entry)
 DT XX
 XX Human VE-statin exon 2 3' oligonucleotide.
 DE XX
 XX Cytostatic; Ophthalmological; Vasotropic; Antiarteriosclerotic;
 KW VE-statin; endothelium; perivascular smooth muscle cell; angiogenesis;
 KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; mouse;
 ds.

KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; human;
 KW ds.
 XX Homo sapiens.
 OS
 XX FR2851249-A1.
 PN
 XX 20-AUG-2004.
 PD
 XX 17-FEB-2003; 2003FR-00001875.
 PP
 XX 17-FEB-2003; 2003FR-00001875.
 PR
 XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 XX PA
 XX Soncin F, Mattot V;
 PI
 XX WPI; 2004-618122/60.
 DR
 XX Using VE-statins to inhibit recruitment of perivascular smooth muscle
 PT cells, for treating e.g. cancer and retinopathy, also new VE-statins,
 PT related nucleic acids and antibodies.
 XX XX
 XX Example 3; Page 11; 63pp; French.
 PS
 XX The present invention relates to a method for preparing a composition for
 CC inhibiting recruitment of perivascular cells of smooth muscle type using
 CC a VE-statin protein (1; ADR27861-ADR27863 and ADR27902). VE-statins,
 CC soluble factors secreted by endothelial cells of the blood vessels, block
 CC recruitment of perivascular smooth muscle cells (but do not affect their
 CC proliferation), so inhibit angiogenesis. VE-statins, also their peptide
 CC fragments, nucleic acids encoding them and vectors containing this
 CC nucleic acid, are used for treating cancer, retinopathy, atherosclerosis
 CC and restenosis, including in gene therapy. The VE-statin nucleic acids
 CC can also be used to produce transgenic animals (for studying the VE-
 CC statin proteins and genes); the VE-statins are used to screen for
 CC specific (ant)agonists, and antibodies specific for VE-statins can be
 CC used to determine expression profiles, particularly for diagnosis of
 CC diseases associated with VE-statins. The present sequence was used to
 CC illustrate the structure of the human VE-statin gene.
 XX XX
 XX Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCGAAGG 19
 |||||
 Db 9 TGGCGGAGG 1
 RESULT 287
 ADR27977/c
 ID ADR27977 standard; DNA; 10 BP.
 XX AC ADR27977;
 XX XX
 XX 04-NOV-2004 (first entry)
 DT XX
 XX Murine VE-statin intron acceptor site.
 DE XX
 XX Cytostatic; Ophthalmological; Vasotropic; Antiarteriosclerotic;
 KW VE-statin; endothelium; perivascular smooth muscle cell; angiogenesis;
 KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; mouse;
 KW ds.
 XX OS Mus musculus.
 XX XX
 XX FR2851249-A1.
 PN
 XX 20-AUG-2004.
 PD
 XX

PF 17-FEB-2003; 2003FR-00001875.
 XX
 PR 17-FEB-2003; 2003FR-00001875.
 XX
 PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 XX Soncin F, Mattot V;
 XX
 PI WPI; 2004-618122/60.
 XX
 DR Using VE-statins to inhibit recruitment of perivascular smooth muscle
 PT cells, for treating e.g. cancer and retinopathy, also new VE-statins,
 PT related nucleic acids and antibodies.
 XX
 XX Example 3; Page 11; 63pp; French.
 XX
 XX The present invention relates to a method for preparing a composition for
 CC inhibiting recruitment of perivascular cells of smooth muscle type using
 CC a VE-statin protein (I; ADR27861-ADR27863 and ADR27902). VE-statins,
 CC soluble factors secreted by endothelial cells of the blood vessels, block
 CC recruitment of perivascular smooth muscle cells (but do not affect their
 CC proliferation), so inhibit angiogenesis. VE-statins, also their peptide
 CC fragments, nucleic acids encoding them and vectors containing this
 CC nucleic acid, are used for treating cancer, retinopathy, atherosclerosis
 CC and restenosis, including in gene therapy. The VE-statin nucleic acids
 CC can also be used to produce transgenic animals (for studying the VE-
 CC statin proteins and genes); the VE-statins are used to screen for
 CC specific (ant)agonists, and antibodies specific for VE-statins can be
 CC used to determine expression profiles, particularly for diagnosis of
 CC diseases associated with VE-statins. The present sequence was used to
 CC illustrate the structure of the murine VE-statin gene.
 XX
 SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
 XX

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CTGTGGCGA 16
 Db 10 CTGTGGTGA 2
 ||||| ||

RESULT 288
 ADR88561/c
 ID ADR88561 standard; DNA; 10 BP.
 XX
 AC ADR88561;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 XX Alpha 7 nicotinic ACh receptor exon-intron boundary DNA seqid 92.
 DE
 XX schizophrenia; alpha7 allele; polymorphism;
 KW alpha 7 nicotinic ACh receptor; human; CHRNA7; intron-exon boundary; ds.
 KW
 XX Homo sapiens.
 OS
 XX US2004185468-A1.
 PN
 XX 23-SEP-2004.
 PD
 XX 26-NOV-2003; 2003US-00723940.
 PF
 XX 23-OCT-1997; 97US-00956518.
 PR
 XX (USGO) USA DEPT VETERANS AFFAIRS.
 PA
 XX Leonard S, Freedman R;
 PI WPI; 2004-689185/67.
 XX
 XX Identifying individuals predisposed to schizophrenia, by providing

PT nucleic acid comprising alpha7 allele from subject, detecting
 PT polymorphism within alpha7 allele, and correlating polymorphism with
 XX predisposition to schizophrenia.
 XX
 PS Example 3; SEQ ID NO 92; 105pp; English.
 XX
 XX The invention describes a method of identifying (MI) individuals
 CC predisposed to schizophrenia, involving providing a nucleic acid from a
 CC human subject, where the nucleic acid comprises an alpha7 allele,
 CC detecting the presence of a polymorphism within the alpha7 allele, and
 CC correlating the presence of the polymorphism with a predisposition to
 CC schizophrenia. Also described are: a kit for determining if a subject is
 CC predisposed to schizophrenia, comprising a reagent suitable for use in
 CC specifically detecting a polymorphism in an alpha7 allele, and
 CC instructions for determining whether a subject is predisposed to
 CC schizophrenia; and screening (M2) compounds, involving providing a cell
 CC comprising an alpha7 allele with the polymorphism, and one or more test
 CC compounds, contacting the cell with the test compound, and detecting a
 CC change in alpha7 expression in the cell in the presence of the test
 CC compound relative to the absence of the test compound. (MI) is useful for
 CC identifying individuals predisposed to schizophrenia. This sequence
 CC represents an exon-intron boundary sequence of the human alpha 7
 CC nicotinic ACh receptor (CHRNA7) DNA.
 XX
 SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
 XX

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CTGTGGCGA 16
 Db 10 CTGTGGAGA 2
 ||||| ||

RESULT 289
 ADS76954/c
 ID ADS76954 standard; DNA; 10 BP.
 XX
 AC ADS76954;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 XX Breast cancer detection oligonucleotide #736.
 DE
 XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
 KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
 KW cathepsin L inhibitor; cathepsin F inhibitor;
 KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
 KW collagen antagonist; diagnosis; breast tissue; cancer.
 XX
 XX Homo sapiens.
 OS
 XX WO2004085621-A2.
 PN
 XX 07-OCT-2004.
 PD
 XX 22-MAR-2004; 2004WO-US008866.
 PF
 XX 20-MAR-2003; 2003US-0456735P.
 PR
 XX (DAND) DANA FARBER CANCER INST INC.
 PA
 XX Polyak K, Porter D, Allinen M;
 PI WPI; 2004-728732/71.
 XX
 XX Diagnosing breast cancer comprises determining expression levels of a
 PT gene selected from those differentially expressed in normal or cancerous
 PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
 PT and cystatin C.
 XX
 PS Example 2; SEQ ID NO 736; 149pp; English.


```

AC ADS76564;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #346.
XX
ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX
WPI; 2004-728732/71.
XX
Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
PS Example 2; SEQ ID NO 346; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 11 TGGCGAAGG 19
Db 2 TGGTGAAGG 10
|||||
|||||

RESULT 293
ADS76953/c
ID ADS76953 standard; DNA; 10 BP.
XX
AC ADS76953;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #735.
XX
ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.

```

```

XX WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX
WPI; 2004-728732/71.
XX
Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
PS Example 2; SEQ ID NO 735; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 6 CGCTGTGGC 14
Db 10 CGCGTGGC 2
|||||
|||||

RESULT 294
ADS77055
ID ADS77055 standard; DNA; 10 BP.
XX
AC ADS77055;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #837.
XX
ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX

```

DR WPI; 2004-728732/71.
 PT Diagnosing breast cancer comprises determining expression levels of a
 PT gene selected from those differentially expressed in normal or cancerous
 PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
 PT and cystatin C.
 XX
 XX
 PS Example 2; SEQ ID NO 837; 149pp; English.
 CC
 CC The invention relates to a method of diagnosis (M1) comprising: (a)
 CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
 CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GCTGTGGCG 15
 DB 1 GCTGTGGCG 9
 RESULT 295
 ADS78162/c
 ID ADS78162 standard; DNA; 10 BP.
 AC
 AC ADS78162;
 XX
 XX 30-DEC-2004 (first entry)
 XX
 DE Breast cancer detection oligonucleotide #1944.
 XX
 XX ss; primer; cytostatic; RNA interference; RNai; gene silencing;
 KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
 KW cathepsin L inhibitor; cathepsin F inhibitor;
 KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
 KW collagen antagonist; diagnosis; breast tissue; cancer.
 XX
 OS Homo sapiens.
 XX
 XX WO2004085621-A2.
 XX
 XX 07-OCT-2004.
 XX
 XX 22-MAR-2004; 2004WO-US008866.
 XX
 XX 20-MAR-2003; 2003US-0456735P.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 PA Polyak K, Porter D, Allinen M;
 PI
 PI WPI; 2004-728732/71.
 DR
 DR Diagnosing breast cancer comprises determining expression levels of a
 PT gene selected from those differentially expressed in normal or cancerous
 PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
 PT and cystatin C.
 XX
 XX
 PS Example 6; SEQ ID NO 1944; 149pp; English.
 CC
 CC The invention relates to a method of diagnosis (M1) comprising: (a)
 CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the

CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.
 XX
 SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CGCTGTGGC 14
 DB 10 CGCGGTGGC 2
 RESULT 296
 ADS76565
 ID ADS76565 standard; DNA; 10 BP.
 AC
 AC ADS76565;
 XX
 XX 30-DEC-2004 (first entry)
 XX
 DE Breast cancer detection oligonucleotide #347.
 XX
 XX ss; primer; cytostatic; RNA interference; RNai; gene silencing;
 KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
 KW cathepsin L inhibitor; cathepsin F inhibitor;
 KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
 KW collagen antagonist; diagnosis; breast tissue; cancer.
 XX
 OS Homo sapiens.
 XX
 XX WO2004085621-A2.
 XX
 XX 07-OCT-2004.
 XX
 XX 22-MAR-2004; 2004WO-US008866.
 XX
 XX 20-MAR-2003; 2003US-0456735P.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 PA Polyak K, Porter D, Allinen M;
 PI
 PI WPI; 2004-728732/71.
 DR
 DR Diagnosing breast cancer comprises determining expression levels of a
 PT gene selected from those differentially expressed in normal or cancerous
 PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
 PT and cystatin C.
 XX
 XX
 PS Example 2; SEQ ID NO 347; 149pp; English.
 CC
 CC The invention relates to a method of diagnosis (M1) comprising: (a)
 CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
 CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.
 XX
 SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCGAAGG 19

```

Db      ||| ||| |||
        2 TGGTGAAGG 10

RESULT 297
ADS77022/c
ID ADS77022 standard; DNA; 10 BP.
XX
XX
AC ADS77022;
XX
XX 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #804.
XX
KW ss; primer; cytostatic; RNA interference; RNai; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX
XX 22-MAR-2004; 2004WO-US008866.
XX
XX 20-MAR-2003; 2003US-0456735P.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Polyak K, Porter D, Allinen M;
XX
XX WPI; 2004-728732/71.
XX
XX Diagnosing breast cancer comprises determining expression levels of a
XX gene selected from those differentially expressed in normal or cancerous
XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
XX and cystatin C.
XX
XX Example 2; SEQ ID NO 804; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
XX providing a test sample of breast tissue; (b) determining the level of
XX expression in the test sample of a gene (e.g. interleukin-8, superoxide
XX dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
XX specification, and (c) if the gene is expressed in the test sample at a
XX lower level than in a control normal breast tissue sample, diagnosing the
XX test sample as containing cancer cells. The method is used for diagnosing
XX breast cancer. This sequence corresponds to an oligonucleotide primer
XX used in the method of the invention.
XX
XX Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
Db ||| ||| |||
10 CGCAGTGGC 2

RESULT 298
ADU19103/c
ID ADU19103 standard; DNA; 10 BP.
XX
XX ADU19103;
XX
XX 13-JAN-2005 (first entry)
XX
DE Hypoxia-related tumorigenesis-related SAGE tag #894.

```

```

XX screening; hypoxia-related tumorigenesis;
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX
XX Unidentified.
XX
XX WO2004092198-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US011087.
XX
XX 09-APR-2003; 2003US-0461712P.
XX
XX (GENZ ) GENZYME CORP.
XX
XX Nacht M;
XX
XX WPI; 2004-758333/74.
XX
XX Identifying agents that alter biological activity of a polypeptide
XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis
XX comprises contacting an agent with a target cell and monitoring activity
XX of expressed product.
XX
XX Disclosure; Page 73; 100pp; English.
XX
XX The invention comprises a method of screening for candidate agents
XX capable of altering the biological activity of a protein encoded by a
XX nucleotide involved in hypoxia-related tumorigenesis. The method of the
XX invention involves: contacting a test agent with a target cell expressing
XX the nucleotide, and monitoring the activity of the expressed protein
XX product; if the test agent modifies the activity of the expressed protein
XX then this is a candidate agent. The method of the invention is useful for
XX modifying hypoxia-induced gene regulation and for diagnosing, prognosing
XX or treating tumours. The present DNA sequence represents a SAGE tag that
XX was used in the exemplification of the invention.
XX
XX Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
Db ||| ||| |||
9 GCGCAGTGG 1

RESULT 299
ADU18946
ID ADU18946 standard; DNA; 10 BP.
XX
XX ADU18946;
XX
XX 13-JAN-2005 (first entry)
XX
XX Hypoxia-related tumorigenesis-related SAGE tag #737.
XX
XX screening; hypoxia-related tumorigenesis;
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX
XX Unidentified.
XX
XX WO2004092198-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US011087.
XX
XX 09-APR-2003; 2003US-0461712P.
XX
XX (GENZ ) GENZYME CORP.

```

XX PI Nacht M;
 XX XX WPI; 2004-758333/74.
 XX XX Identifying agents that alter biological activity of a polypeptide
 PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis
 PT comprises contacting an agent with a target cell and monitoring activity
 PT of expressed product.
 XX XX Disclosure; Page 70; 100pp; English.
 PS PS The invention comprises a method of screening for candidate agents
 XX capable of altering the biological activity of a protein encoded by a
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the
 CC invention involves: contacting a test agent with a target cell expressing
 CC the nucleotide, and monitoring the activity of the expressed protein
 CC product; if the test agent modifies the activity of the expressed protein
 CC then this is a candidate agent. The method of the invention is useful for
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
 CC or treating tumours. The present DNA sequence represents a SAGE tag that
 CC was used in the exemplification of the invention.
 XX XX Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCCTGTGG 13
 Db | | | | |
 2 GCCTGTGG 10
 RESULT 300
 ADU18864
 ID ADU18864 standard; DNA; 10 BP.
 XX AC ADU18864;
 XX 13-JAN-2005 (first entry)
 XX Hypoxia-related tumorigenesis-related SAGE tag #655.
 DE screening; hypoxia-related tumorigenesis;
 XX hypoxia-induced gene regulation; tumour; SAGE tag; ds.
 XX Unidentified.
 OS WO2004092198-A2.
 PN 28-OCT-2004.
 PD 09-APR-2004; 2004WO-US011087.
 PF 09-APR-2003; 2003US-0461712P.
 PR (GENZ) GENZYME CORP.
 PA Nacht M;
 XX WPI; 2004-758333/74.
 XX Identifying agents that alter biological activity of a polypeptide
 PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis
 PT comprises contacting an agent with a target cell and monitoring activity
 PT of expressed product.
 XX XX Disclosure; Page 68; 100pp; English.
 PS The invention comprises a method of screening for candidate agents
 CC capable of altering the biological activity of a protein encoded by a
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the

CC invention involves: contacting a test agent with a target cell expressing
 CC the nucleotide, and monitoring the activity of the expressed protein
 CC product; if the test agent modifies the activity of the expressed protein
 CC then this is a candidate agent. The method of the invention is useful for
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
 CC or treating tumours. The present DNA sequence represents a SAGE tag that
 CC was used in the exemplification of the invention.
 XX XX Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 TGTGGCGAA 17
 Db | | | | |
 1 TGTGGCGTA 9
 RESULT 301
 ADZ24419
 ID ADZ24419 standard; DNA; 10 BP.
 XX AC ADZ24419;
 XX 16-JUN-2005 (first entry)
 XX Human SNP detection related oligonucleotide #1386.
 DE ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;
 XX immune disorder; cardiovascular disease; metabolic disorder;
 KW respiratory disease; musculoskeletal disease; renal disease;
 KW nephrotropic; endocrine disease; genitourinary disease.
 XX Homo sapiens.
 OS WO2005030952-A1.
 PN 07-APR-2005.
 PD 30-SEP-2004; 2004WO-JP014784.
 PF 30-SEP-2003; 2003JP-00342519.
 PR 28-MAY-2004; 2004JP-00158717.
 XX (RIKE) RIKEN KK.
 PA (STAG-) STAGEN CO LTD.
 PA (SEKI/) SEKINE A.
 PA (IIDA/) IIDA A.
 PA (SAIT/) SAITO S.
 XX Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;
 PI WPI; 2005-305936/31.
 DR Analyzing haplotype, by detecting polymorphism in drug-related genes,
 XX electing common polymorphism (CP), building haplotype block using CP,
 PT specifying CP within block, specifying tag polymorphism from CP within
 PT block.
 XX Disclosure; SEQ ID NO 1386; 1290pp; Japanese.
 PS The invention relates to a method of analyzing haplotype, by detecting
 CC gene polymorphism in drug-related genes such as aryl acetylamine
 CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
 CC sub-family A (ABCI), member 1. The method is useful for analyzing
 CC haplotype. The method is useful for estimating the sensitivity or disease
 CC of a medicine or a foreign material, for selecting medicine for
 CC preventing or treating diseases, for determining appropriate dosage of
 CC medicine for preventing or treating a disease, for analyzing a drug
 CC interaction, and for determining the related polymorphism relative to the
 CC sensitivity of the medicine, foreign material or disease. The diseases
 CC include malignant tumor, immune disorder circulatory disease, metabolic

CC disease, kidney disease, respiratory disease and muscle associated
 CC disease. The method enables analysis of the individual differences
 CC related to the sensitivity of a medicine, using a haplotype, without
 CC using each single nucleotide polymorphism. The present sequence
 CC represents a human SNP detection related oligonucleotide.
 XX
 SQ Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
 ||| |||||
 Db 1 GCGATGTGG 9

RESULT 302
 ADZ24430
 ID ADZ24430 standard; DNA; 10 BP.
 XX
 AC ADZ24430;
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE Human SNP detection related oligonucleotide #1397.
 XX
 KW ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;
 KW immune disorder; cardiovascular disease; metabolic disorder;
 KW respiratory disease; musculoskeletal disease; renal disease;
 KW nephrotropic; endocrine disease; genitourinary disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2005030952-A1.
 XX
 PD 07-APR-2005.
 XX
 PF 30-SEP-2004; 2004WO-JP014784.
 XX
 PR 30-SEP-2003; 2003JP-00342519.
 PR 28-MAY-2004; 2004JP-00158717.
 XX
 PA (RIKE) RIKEN KK.
 PA (STAG-) STAGEN CO LTD.
 PA (SEKI/) SEKINE A.
 PA (IIDA/) IIDA A.
 PA (SAIT/) SAITO S.
 XX
 PI Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;
 XX
 DR WPI; 2005-305936/31.
 XX
 XX Analyzing haplotype, by detecting polymorphism in drug-related genes,
 PT electing common polymorphism (CP), building haplotype block using CP,
 PT specifying CP within block, specifying tag polymorphism from CP within
 PT block.
 XX
 PS Disclosure; SEQ ID NO 1397; 1290pp; Japanese.
 XX
 XX The invention relates to a method of analyzing haplotype, by detecting
 CC gene polymorphism in drug-related genes such as aryl acetylammide
 CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
 CC sub-family A (ABC1), member 1. The method is useful for analyzing
 CC haplotype. The method is useful for estimating the sensitivity or
 CC of a medicine or a foreign material, for selecting medicine for
 CC preventing or treating diseases, for determining appropriate dosage of
 CC medicine for preventing or treating a disease, for analyzing a drug
 CC interaction, and for determining the related polymorphism relative to the
 CC sensitivity of the medicine, foreign material or disease. The diseases
 CC include malignant tumor, immune disorder circulatory disease, metabolic
 CC disease, kidney disease, respiratory disease and muscle associated
 CC disease. The method enables analysis of the individual differences

CC related to the sensitivity of a medicine, using a haplotype, without
 CC using each single nucleotide polymorphism. The present sequence
 CC represents a human SNP detection related oligonucleotide.
 XX
 SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
 ||| |||||
 Db 1 GCGATGTGG 9

RESULT 303
 AEA37223
 ID AEA37223 standard; DNA; 10 BP.
 XX
 AC AEA37223;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE MoMLV derived vector associated polynucleotide #2.
 XX
 KW expression; drug screening; diagnosis; protein purification;
 KW protein interaction; gene tagging; ds.
 XX
 OS Unidentified.
 XX
 PN WO2005054476-A1.
 XX
 PD 16-JUN-2005.
 XX
 PF 13-SEP-2004; 2004WO-US029658.
 XX
 PR 12-SEP-2003; 2003US-00660893.
 XX
 PA (NEWL-) NEWLINK GENETICS INC.
 XX
 PI Link CJ, Seregina T, Vahanian NN, Higginbotham JN, Ramsey WJ;
 PI Powers BJ, Shukla SA, Young WB, Dicolandrea T, Mautino MR;
 XX
 DR WPI; 2005-425418/43.
 XX
 XX Elucidating protein expression profile of test cell line, by randomly
 PT introducing promoterless polynucleotide construct into genome of cells,
 PT identifying cells expressing marker peptide fused to protein and
 PT determining proteins.
 XX
 PS Disclosure; Fig 2K; 141pp; English.
 XX
 XX The invention describes a method of elucidating (M1) a protein expression
 CC profile of a test cell line or group of cells. The method involves
 CC randomly introducing into the genome of a cell or group of cells a
 CC promoterless polynucleotide construct (I), comprising in a 5'-3'
 CC orientation: a splice acceptor consensus sequence, a complementary
 CC sequence of a first type IIS restriction enzyme recognition sequence, an
 CC oligonucleotide sequence encoding an assayable marker peptide, a splice
 CC of a second type IIS restriction enzyme recognition sequence, a sequence
 CC donor consensus sequence, where the promoterless polynucleotide construct
 CC when introduced into an actively expressed gene results in the generation
 CC of a fusion protein, containing the assayable marker peptide inserted at
 CC a random position within two exons coding for the cellular protein
 CC encoded by the gene, identifying those cells expressing the marker
 CC peptide fused to the cellular protein, and determining the identity of
 CC the proteins to which the marker peptide is fused in each group of cells.
 CC Also described are: identifying (M2) differentially expressed proteins in
 CC two different populations of cells; and identifying (M3) protein/protein
 CC interactions. (M1) is useful for elucidating a protein expression profile
 CC of a test cell line or group of cells and for identifying differentially
 CC expressed proteins in two different populations of cells. (M1) and (M2)
 CC are useful for screening small molecule drugs, which involves generating

CC cells using (M1) or (M2), selecting cells which have integrated the
 CC marker peptide into a locus coding a protein for which a small molecule
 CC drug is to be identified, establishing a monoclonal cell line from the
 CC cells, and screening the cell line against libraries of drug compounds to
 CC identify compounds which decrease expression of the marker polypeptide by
 CC inhibiting expression of the protein to which the marker polypeptide is
 CC fused, where the screening is performed in cells generated by (M1) or
 CC (M3). This sequence represents a polynucleotide associated with the
 CC creation of a MoMuV derived vector associated with determining the
 CC protein expression profile of a cell line.

XX
 SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9
 |||||
 Db 2 GGTCGCGCT 10

RESULT 304

AAT29313
 ID AAT29313 standard; DNA; 10 BP.

AC AAT29313;

XX
 DT 25-MAR-2003 (revised)
 DT 28-JUN-1996 (first entry)

XX 5'-primer for mammalian G-protein coupled receptor coding sequences.

XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
 KW characterisation; biological samples; PCR amplification; indexing;
 KW identification; cloning; analysis; genes; genome mapping;
 KW disease diagnosis; ss.

XX Synthetic.

XX WO9531574-A1.

XX 23-NOV-1995.

XX 12-MAY-1995; 95WO-US006032.

XX 16-MAY-1994; 94US-00242887.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX Lopeznieto CE, Nigam SK;

XX WPI; 1996-010958/01.

XX Characterisation of nucleotide sequences using primer pairs - by PCR
 PT amplification and indexing of amplification prods. w.r.t. primers used
 PT for genome mapping and disease diagnosis.

XX Claim 46; Page 55; 72pp; English.

XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
 CC from them, which target mammalian G-protein coupled receptor coding
 CC sequences, together comprise a PCR primer kit. The kit is used in a new
 CC method for the characterisation of nucleic acid sequences obtd. from
 CC mammalian biological samples, which comprises PCR amplification and
 CC indexing of the prods. w.r.t. the primer pair that hybridised to its
 CC delineating subsequences. The method may be used in the identification,
 CC cloning and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
 |||||
 Db 4 GCTGTGG 10

RESULT 305

AAV09238/c
 ID AAV09238 standard; DNA; 10 BP.

XX AAV09238;

XX 07-JUL-1998 (first entry)

XX Degenerate RT-PCR primer 2.

XX Degenerate peptide; RT-PCR; amplification; cytochrome P450 gene;
 KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.

XX Synthetic.

XX WO9749832-A2.

XX 31-DEC-1997.

XX 23-JUN-1997; 97WO-CA000488.

XX 21-JUN-1996; 96US-00667546.

XX 01-OCT-1996; 96US-00724466.

XX (TOOH) UNIV QUEENS KINGSTON.

XX Petkovich PM;

XX WPI; 1998-077193/07.

XX Identifying DNA encoding inducible or suppressible cytochrome P450 - by
 PT screening for drugs which reduce the catabolism of retinoic acid, useful
 PT in cancer chemotherapy and the treatment of acne and psoriasis.

XX Example 1; Page 52; 113pp; English.

XX This is a degenerate RT-PCR primer used in combination with a 3' poly(T)
 CC primer (AAV09225-V09236) for the amplification of the inducible
 CC cytochrome P450RAI gene which specifically metabolises a derivative of
 CC the retinoic acid (RA). The cytochrome P450 gene in general produces
 CC enzymes involved in the oxidative metabolism of endogenous and exogenous
 CC compounds. The cytochrome P450 nucleotide sequence can be used to induce
 CC or suppress the expression of its protein. P450RAI is highly induced by
 CC RA in cell lines and tissues. This allows for development of a drug
 CC screen using promoters and nucleotide sequences to identify drugs which
 CC are useful for reducing the catabolism of RA

XX Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGCGCAA 17
 |||||
 Db 9 TGCGCAA 3

RESULT 306

AAV12230/c
 ID AAV12230 standard; DNA; 10 BP.

XX AAV12230;

XX 22-JUN-1998 (first entry)

XX DE Differential display 5' PCR primer.
 XX KW Retinoid metabolising protein; P45ORAI; retinoid oxidase; retinoic acid;
 KW zebrafish; inhibitor; antisense; cancer; actinic keratosis;
 KW oral leukoplakia; head tumour; neck tumour;
 KW non-small cell lung carcinoma; basal cell carcinoma;
 KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis;
 KW therapy; diagnosis; screening; differential display; PCR; primer; ss.
 XX OS Synthetic.
 XX PN WO9749815-A1.
 XX PD 31-DEC-1997.
 XX PF 23-JUN-1997; 97WO-CA000440.
 XX PR 21-JUN-1996; 96US-00667546.
 XX PR 01-OCT-1996; 96US-00724466.
 XX PA (TOOH) UNIV QUEENS KINGSTON.
 XX PI Petkovich PM, White JA, Beckett BR, Jones G;
 XX WPI; 1998-077178/07.
 XX Retinoid metabolising protein - useful to develop products to treat, e.g.
 XX cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
 XX ichthyosis.
 XX PS Disclosure; Page 14; 110pp; English.
 XX CC 5' PCR primers (see AAV12229-33) were used in various combinations with
 CC polyT primers (see AAV12217-28) in a differential display PCR of cDNA
 CC derived from mRNA of control or retinoic acid-treated zebrafish (Danio
 CC rerio). Bands demonstrating reproducible differential amplifications were
 CC found using the primers given in AAV12221 and AAV12231. This PCR product
 CC was reamplified (see AAV12234-35). A differential display product (see
 CC AAV12213) which exhibited a dependence on the presence of retinoic acid
 CC for its expression was isolated, and was used to isolate a full-length
 CC clone (see AAV12203) coding for a novel retinoid metabolising protein
 CC (see AAV44159), designated zP45ORAI
 XX SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TGGCGAA 17
 Db 9 TGGCGAA 3
 RESULT 307
 AAV34959
 ID AAV34959 standard; DNA; 10 BP.
 AC AAV34959;
 XX 13-OCT-1998 (first entry)
 XX Synthetic Agaricus bisporus RAPD primer.
 XX Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.
 XX OS Synthetic.
 XX PN WO9821975-A1.
 XX PD 28-MAY-1998.
 PF 19-NOV-1996; 96WO-US018686.
 PR 19-NOV-1996; 96WO-US018686.
 PA (AMYC-) AMYCEL INC.
 XX Loftus MG, Lodder SC, Legg EJ;
 XX WPI; 1998-312054/27.
 XX New strains of Agaricus bisporus with improved cap whiteness - compared
 XX with the U1 strain but retaining other desirable features of this strain.
 XX Disclosure; Page 10; 26pp; English.
 XX CC The sequence is that of an RAPD (random amplified DNA) primer which was
 CC used in the isolation of an Agaricus bisporus mushroom strain which has
 CC whiter caps, less scaling than known strains, particularly for mushrooms
 CC produced in the first break, so it is more valuable (suitable for
 CC marketing fresh rather than canning). It also retains the desirable
 CC characteristics (good cap shape and shelf life, thick stem and veil) of
 CC the U1 strain
 XX SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCGAAGG 19
 Db 4 GCGAAGG 10
 RESULT 308
 AAV50187
 ID AAV50187 standard; DNA; 10 BP.
 XX AAV50187;
 DT 21-OCT-1998 (first entry)
 XX Yeast tag for additional NORF chromosome 5 tag position 118089.
 KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
 KW eukaryotic cell; antifungal; SAGE tag; gene expression;
 XX serial analysis of gene expression; probe; ss.
 OS Saccharomyces cerevisiae.
 OS Synthetic.
 XX PN WO9832847-A2.
 XX PD 30-JUL-1998.
 XX PF 22-JAN-1998; 98WO-US001216.
 XX PR 23-JAN-1997; 97US-0035917P.
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX Velculescu VE, Vogelstein B, Kinzler KW;
 XX WPI; 1998-427943/36.
 XX Yeast transcriptome - useful for modulating eukaryotic cell, for
 XX screening antifungal agents, and for identifying genes in cell cycle
 XX progression.
 XX Claim 1; Page 24; 44pp; English.
 XX Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
 XX involved in cell cycle progression selected from the group of

PF 19-NOV-1996; 96WO-US018686.
 PR 19-NOV-1996; 96WO-US018686.
 PA (AMYC-) AMYCEL INC.
 XX Loftus MG, Lodder SC, Legg EJ;
 XX WPI; 1998-312054/27.
 XX New strains of Agaricus bisporus with improved cap whiteness - compared
 XX with the U1 strain but retaining other desirable features of this strain.
 XX Disclosure; Page 10; 26pp; English.
 XX CC The sequence is that of an RAPD (random amplified DNA) primer which was
 CC used in the isolation of an Agaricus bisporus mushroom strain which has
 CC whiter caps, less scaling than known strains, particularly for mushrooms
 CC produced in the first break, so it is more valuable (suitable for
 CC marketing fresh rather than canning). It also retains the desirable
 CC characteristics (good cap shape and shelf life, thick stem and veil) of
 CC the U1 strain
 XX SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCGAAGG 19
 Db 4 GCGAAGG 10
 RESULT 308
 AAV50187
 ID AAV50187 standard; DNA; 10 BP.
 XX AAV50187;
 DT 21-OCT-1998 (first entry)
 XX Yeast tag for additional NORF chromosome 5 tag position 118089.
 KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
 KW eukaryotic cell; antifungal; SAGE tag; gene expression;
 XX serial analysis of gene expression; probe; ss.
 OS Saccharomyces cerevisiae.
 OS Synthetic.
 XX PN WO9832847-A2.
 XX PD 30-JUL-1998.
 XX PF 22-JAN-1998; 98WO-US001216.
 XX PR 23-JAN-1997; 97US-0035917P.
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX Velculescu VE, Vogelstein B, Kinzler KW;
 XX WPI; 1998-427943/36.
 XX Yeast transcriptome - useful for modulating eukaryotic cell, for
 XX screening antifungal agents, and for identifying genes in cell cycle
 XX progression.
 XX Claim 1; Page 24; 44pp; English.
 XX Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
 XX involved in cell cycle progression selected from the group of

CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression) tags for highly expressed genes and NORF genes are given in AAV50051 to AAV50345. The present invention describes: (1) a method of using yeast genes to modulate the cell cycle which comprises administering to a cell an isolated DNA molecule comprising a yeast gene which is involved in cell cycle progression selected from differentially expressed genes (SAGE tags given in AAV50051 to AAV50345); (2) a method for screening candidate antifungal drugs which comprises contacting a test substance with a yeast cell and monitoring expression of a yeast gene which is involved in cell cycle progression; (3) a method of identifying human genes which are involved in cell cycle progression which comprises hybridizing a probe comprising at least 10 contiguous nucleotides of a yeast gene which is differentially expressed between at least 2 phases selected from the log phase, the S phase and the G2/M phase; and (4) a probe for ascertaining the phase in the cell cycle, where the probe comprises at least 14 contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to AAV50345), or as an array of probes on a solid support.

XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12
DB 4 CGCTGTG 10

RESULT 309
AAV35966
ID AAV35966 standard; DNA; 10 BP.
XX
AC AAV35966;
XX
XX 26-AUG-1998 (first entry)
DE
XX
XX Primer used in RAPD assay of the invention.
XX
XX Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
XX Synthetic.
OS
Sus sp.
XX
PN W09815837-Al.
XX
XX 16-APR-1998.
XX
XX 07-OCT-1997; 97WO-GB002741.
XX
XX 07-OCT-1996; 96GB-00020904.
PR 18-FEB-1997; 97GB-00003350.
PR 20-MAR-1997; 97GB-00005796.
PR 09-SEP-1997; 97GB-00019002.
XX
XX (MEAT-) MEAT & LIVESTOCK COMMISSION.
XX
XX Maltin CA, Steven J, Warkup CC;
XX
XX WPI; 1998-240968/21.
DR
XX
XX Assay for alleles or muscle fibre composition characteristic of Duroc type pigs - comprises determination of genotype or muscle fibre properties, used to identify animals for breeding programs and to assess meat quality.
PT
PT
XX
XX Example 3; Page 33; 56pp; English.
PS
XX
XX PCR primers AAV35877-996 were used in a rapid amplification of polymorphic DNA (RAPD) reaction in the assay of the invention. This assay is used to determine if an animal has an allele for, or muscle fibre composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce

CC meat of superior quality (particularly tenderness) but are normally less efficient feed converters and fatter than other types. The assay comprises analysing a tissue sample to determine if the genotype comprises the allele, and genetic features typical of animals with Duroc-type MFC are present. The method is used to select animals that have Duroc characteristics for use in breeding programmes (to develop the CC animals with Duroc pig characteristics), and to assess meat quality XX

SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGG 7
DB 4 GGTGCGG 10

RESULT 310
AAV77467/c
ID AAV77467 standard; DNA; 10 BP.
XX
XX AAV77467;
AC
XX
XX 05-AUG-1999 (first entry)
DT
XX
XX US5912147 primer 11.
DE
XX
XX Primer; quantitation; genetic instability; tumour cell; detection;
KW neoplastic transformation; carcinogenesis; ss.
XX
XX Synthetic.
XX
XX US5912147-A.
PN
XX
XX 15-JUN-1999.
PD
XX
XX 22-OCT-1996; 96US-00734973.
PF
XX
XX 22-OCT-1996; 96US-00734973.
PR
XX
XX (HEAL-) HEALTH RES INC.
PA
XX
XX Anderson G, Stoler D, Basik M;
PI
XX
XX WPI; 1999-357197/30.
DR
XX
XX Quantitating genetic instability.
PT
XX
XX Claim 4; Col 19-20; 27pp; English.
PS
XX
XX This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from (i) a nucleotide sequence (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CG)XY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR, where R is a purine selected from adenine and guanine and x = 6-16, (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple

```

XX
SQ      Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTGCGGC 8
DB      10 GTGCGGC 4
      |||||
      |||||

RESULT 311
AAZ28347/c
ID      AAZ28347 standard; cDNA; 10 BP.
XX
AC      AAZ28347;
XX
DT      20-DEC-1999 (first entry)
XX
DE      Lung cancer indicator polynucleotide #27.
XX
KW      Lung cancer; tumour; primary squamous cell; gene expression pattern; ss;
KW      antibody; detect; diagnosis; transgenic animal; expressed sequence tag.
XX
OS      Homo sapiens.
XX
XX      WO950278-A1.
XX
XX      07-OCT-1999.
XX
PF      10-MAR-1999; 99WO-US006938.
XX
PR      31-MAR-1998; 98US-0080037P.
XX
PA      (GENZ ) GENZYME CORP.
XX
PI      Beaudry GA, Madden SL, Bertelsen AH;
XX
DR      WPI; 1999-591271/50.
XX
PT      Polynucleotides which are differentially expressed in lung cancer, used
PT      for diagnosis and screening for therapeutic agents.
XX
PS      Claim 1; Page 51; 69pp; English.
XX
XX      Sequences Z28321-Z28360 are polynucleotides isolated from primary
XX      squamous cell lung cancers of two patients. These sequences represent a
XX      profile of gene expression patterns in lung cancer. Sequences Z28321-
XX      Z28360 correspond to previously characterised genes. Sequences Z28341-
XX      Z28360 do not correspond to known genes, although some do correspond to
XX      reported Expressed Sequence Tags (ESTs). This sequence does correspond to
XX      an EST (Genbank Accession No. AAl142). The presence of these
XX      polynucleotide sequences in lung cells is indicative of lung cancer. The
XX      sequences can be used to generate antibodies for the detection of tumour
XX      cells. Detection of the overexpression of the polynucleotides and their
XX      gene products can be used in the diagnosis of lung cancer or the
XX      susceptibility to the disease. The sequences can also be used to screen
XX      for agents potentially useful for treating lung cancer and to generate
XX      transgenic animals (for studying gene function and for drug screening)
XX
SQ      Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
DB      9 CTGTGGC 3
      |||||
      |||||

RESULT 312

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AAZ61441/c
ID      AAZ61441 standard; DNA; 10 BP.
XX
AC      AAZ61441;
XX
DT      19-JUN-2000 (first entry)
XX
DE      Primer SP4A5 for genetic mapping and cloning of the Pi-ta region.
XX
KW      Disease resistance protein; rice; Pi-ta gene; resistance gene;
KW      Pi-ta resistance gene-mediated defence response; fungal pathogen;
KW      rice blast fungus; PCR primer; ss.
XX
OS      Oryza sativa.
XX
XX      WO200008162-A1.
XX
XX      17-FEB-2000.
XX
PF      03-AUG-1999; 99WO-US017706.
XX
PR      04-AUG-1998; 98US-0095229P.
PR      21-JUN-1999; 99US-00336946.
XX
PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      Valent BS, Bryan GT;
XX
XX      WPI; 2000-205715/18.
XX
PT      Novel nucleic acid fragments conferring Pi-ta resistance gene-mediated
PT      defense response for producing transgenic plants resistant to fungal
PT      pathogens, especially rice blast fungus.
XX
PS      Example 3; Page 29; 96pp; English.
XX
XX      AAZ61437-52 represent random amplified polymorphic DNA (RAPD) primers
XX      which were used for genetic mapping and cloning of the Pa-ti disease
XX      resistance region of rice. The rice Pi-ta gene was cloned by a map-based
XX      cloning strategy. The Pi-ta protein has a novel structure, compared to
XX      all known classes of resistance gene products. The polynucleotide
XX      sequence confers a Pi-ta resistance gene-mediated defence response
XX      against diseases caused by fungal pathogens, particularly the rice blast
XX      fungus. Introduction of the cloned Pi-ta gene into susceptible rice
XX      confers resistance to pathogen strains
XX
SQ      Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCGCTGT 11
DB      7 GCGCTGT 1
      |||||
      |||||

RESULT 313
AAZ79591
ID      AAZ79591 standard; DNA; 10 BP.
XX
AC      AAZ79591;
XX
DT      10-APR-2000 (first entry)
XX
DE      Human dendritic cell SAGE tag, SEQ ID NO:2019.
XX
KW      SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW      APC; monocyte-derived dendritic cell; differential gene expression;
KW      immunostimulatory cofactor; costimulatory factor; CTL;
KW      cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX      Homo sapiens.

```

XX WO9965924-A2.
 XX PD 23-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US013800.
 XX PR 19-JUN-1998; 98US-0089833P.
 XX PR 19-JUN-1998; 98US-0089844P.
 XX PR 19-JUN-1998; 98US-0089853P.
 XX PR 19-JUN-1998; 98US-0089878P.
 XX PR 19-JUN-1998; 98US-0089991P.
 XX PR 19-JUN-1998; 98US-0089992P.
 XX PR 19-JUN-1998; 98US-0089993P.
 XX PR 19-JUN-1998; 98US-0089994P.
 XX PR 19-JUN-1998; 98US-0089997P.
 XX PR 19-JUN-1998; 98US-0089999P.
 XX PR 19-JUN-1998; 98US-0090000P.
 XX PR 19-JUN-1998; 98US-0090035P.
 XX PR 19-JUN-1998; 98US-0090036P.
 XX PR 19-JUN-1998; 98US-0090039P.
 XX PR 19-JUN-1998; 98US-0090040P.
 XX PR 19-JUN-1998; 98US-0090041P.
 XX PR 19-JUN-1998; 98US-0090042P.
 XX PR 19-JUN-1998; 98US-0090043P.
 XX PR 19-JUN-1998; 98US-0090044P.
 XX PR 19-JUN-1998; 98US-0090045P.
 XX PR 19-JUN-1998; 98US-0090047P.
 XX PR 19-JUN-1998; 98US-0090048P.
 XX PR 19-JUN-1998; 98US-0090072P.
 XX PR 19-JUN-1998; 98US-0090076P.
 XX PR 19-JUN-1998; 98US-0090077P.
 XX PR 19-JUN-1998; 98US-0090078P.
 XX PR 19-JUN-1998; 98US-0090079P.
 XX PR 08-DEC-1998; 98US-0090080P.
 XX PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 XX (ROBE/) ROBERTS B L.
 XX (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 XX cells, useful in gene vaccines against cancer.
 XX Claim 1; Page 122; 130pp; English.
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 XX expression) tags used to identify mRNA transcripts encoding
 XX immunostimulatory cofactor proteins which are preferentially or
 XX differentially expressed in monocyte-derived dendritic cells compared
 XX with monocytes. Some of the transcripts correspond to known genes or ESTs
 XX (expressed sequence tags) which were previously unknown to be
 XX preferentially or differentially expressed in dendritic cells, while
 XX other transcripts correspond to novel genes. Antigen-presenting cell
 XX (APC)-associated costimulatory factors play an important role in the
 XX activation of the cytotoxic immune response, particularly against tumour
 XX cells. Tumour antigen presentation via the MHC (major histocompatibility
 XX complex) and subsequent recognition by T-cell receptors is alone
 XX insufficient to activate a robust cytotoxic immune response that can lyse
 XX the tumour cells, immunostimulatory cofactors also being required for
 XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 XX sequences identified using the SAGE tags have several potential uses.
 XX They may be used in vaccines to induce an immune response, particularly
 XX against a tumour antigen; to modulate the immune response, particularly
 XX for agents that modulate expression of differentially expressed genes in
 XX an APC; and as hybridisation probes/amplification primers for the
 XX diagnosis, prognosis and monitoring of diseases related to abnormal
 XX expression of these genes. Detection of the dendritic cell differentially
 XX expressed genes, or of their encoded proteins, can be used to identify

CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
 Db 1 GCTGTGG 7
 |||||

RESULT 314

AAZ77871

ID AAZ77871 standard; DNA; 10 BP.

XX AC AAZ77871;

DT 10-APR-2000 (first entry)

DE Human dendritic cell SAGE tag, SEQ ID NO:299.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN WO9965924-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013800.

XX PR 19-JUN-1998; 98US-0089833P.
 XX PR 19-JUN-1998; 98US-0089844P.
 XX PR 19-JUN-1998; 98US-0089853P.
 XX PR 19-JUN-1998; 98US-0089878P.
 XX PR 19-JUN-1998; 98US-0089991P.
 XX PR 19-JUN-1998; 98US-0089992P.
 XX PR 19-JUN-1998; 98US-0089993P.
 XX PR 19-JUN-1998; 98US-0089994P.
 XX PR 19-JUN-1998; 98US-0089997P.
 XX PR 19-JUN-1998; 98US-0089999P.
 XX PR 19-JUN-1998; 98US-0090000P.
 XX PR 19-JUN-1998; 98US-0090035P.
 XX PR 19-JUN-1998; 98US-0090036P.
 XX PR 19-JUN-1998; 98US-0090039P.
 XX PR 19-JUN-1998; 98US-0090040P.
 XX PR 19-JUN-1998; 98US-0090041P.
 XX PR 19-JUN-1998; 98US-0090042P.
 XX PR 19-JUN-1998; 98US-0090043P.
 XX PR 19-JUN-1998; 98US-0090044P.
 XX PR 19-JUN-1998; 98US-0090045P.
 XX PR 19-JUN-1998; 98US-0090047P.
 XX PR 19-JUN-1998; 98US-0090048P.
 XX PR 19-JUN-1998; 98US-0090072P.
 XX PR 19-JUN-1998; 98US-0090076P.
 XX PR 19-JUN-1998; 98US-0090077P.
 XX PR 19-JUN-1998; 98US-0090078P.
 XX PR 19-JUN-1998; 98US-0090079P.
 XX PR 19-JUN-1998; 98US-0090080P.
 XX PR 08-DEC-1998; 98US-0111715P.

XX	(GENZ) GENZYME CORP.
PA	(ROBE/) ROBERTS B L.
PA	(SHAN/) SHANKARA S.
XX	
PI	Roberts BL, Shankara S;
XX	
DR	WPI; 2000-106077/09.
XX	
PT	Isolated polynucleotides differentially expressed in antigen-presenting
PT	cells, useful in gene vaccines against cancer.
XX	
PS	Claim 1; Page 72; 130pp; English.
XX	
CC	Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC	expression) tags used to identify mRNA transcripts encoding
CC	immunostimulatory cofactor proteins which are preferentially or
CC	differentially expressed in monocyte-derived dendritic cells compared
CC	with monocytes. Some of the transcripts correspond to known genes or ESTs
CC	(expressed sequence tags) which were previously unknown to be
CC	preferentially or differentially expressed in dendritic cells, while
CC	other transcripts correspond to novel genes. Antigen-presenting cell
CC	(APC)-associated costimulatory factors play an important role in the
CC	activation of the cytotoxic immune response, particularly against tumour
CC	cells. Tumour antigen presentation via the MHC (major histocompatibility
CC	complex) and subsequent recognition by T-cell receptors is alone
CC	insufficient to activate a robust cytotoxic immune response that can lyse
CC	the tumour cells, immunostimulatory cofactors also being required for
CC	efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC	sequences identified using the SAGE tags have several potential uses.
CC	They may be used in vaccines to induce an immune response, particularly
CC	against a tumour antigen; to modulate the genotype of an APC; to screen
CC	for agents that modulate expression of differentially expressed genes in
CC	an APC; and as hybridisation probes/amplification primers for the
CC	diagnosis, prognosis and monitoring of diseases related to abnormal
CC	expression of these genes. Detection of the dendritic cell differentially
CC	expressed genes, or of their encoded proteins, can be used to identify
CC	cells as belonging to the monocyte lineage. Cells containing these genes
CC	can be used in active immunotherapy (or to stimulate production of a
CC	population of antigen-specific effector cells) and vectors containing
CC	them are used in gene therapy. Co-administration of tumour antigens and
CC	APC-associated costimulatory factors ensures adequate antigen
CC	presentation to endogenous APCs and upregulates the APCs for the
CC	secretion of co-stimulatory signals, migration to T cell-rich sites,
CC	recruitment of T cell growth factors and secretion of chemokines for
CC	recruitment of immune effector cells
XX	
SQ	Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
	Query Match 36.8%; Score 7; DB 1; Length 10;
	Best Local Similarity 100.0%; Pred. No. 2.1e+02;
	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	6 CGCTGTG 12
Db	1 CGCTGTG 7
RESULT 315	
AZ79427/c	
ID AAZ79427 standard; DNA; 10 BP.	
XX	
AC	AZ79427;
XX	
DT	10-APR-2000 (first entry)
DE	Human dendritic cell SAGE tag, SEQ ID NO:1855.
XX	
KW	SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW	APC; monocyte-derived dendritic cell; differential gene expression;
KW	immunostimulatory cofactor; costimulatory factor; CTL;
KW	cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9965924-A2.
XX	
PD	23-DEC-1999.
XX	
PF	18-JUN-1999; 99WO-US013800.
XX	
PR	19-JUN-1998; 98US-0089833P.
PR	19-JUN-1998; 98US-0089844P.
PR	19-JUN-1998; 98US-0089853P.
PR	19-JUN-1998; 98US-0089878P.
PR	19-JUN-1998; 98US-0089919P.
PR	19-JUN-1998; 98US-0089922P.
PR	19-JUN-1998; 98US-0089933P.
PR	19-JUN-1998; 98US-0089944P.
PR	19-JUN-1998; 98US-0089977P.
PR	19-JUN-1998; 98US-0089999P.
PR	19-JUN-1998; 98US-0090000P.
PR	19-JUN-1998; 98US-0090035P.
PR	19-JUN-1998; 98US-0090036P.
PR	19-JUN-1998; 98US-0090039P.
PR	19-JUN-1998; 98US-0090040P.
PR	19-JUN-1998; 98US-0090041P.
PR	19-JUN-1998; 98US-0090042P.
PR	19-JUN-1998; 98US-0090043P.
PR	19-JUN-1998; 98US-0090044P.
PR	19-JUN-1998; 98US-0090045P.
PR	19-JUN-1998; 98US-0090047P.
PR	19-JUN-1998; 98US-0090048P.
PR	19-JUN-1998; 98US-0090072P.
PR	19-JUN-1998; 98US-0090076P.
PR	19-JUN-1998; 98US-0090077P.
PR	19-JUN-1998; 98US-0090078P.
PR	19-JUN-1998; 98US-0090079P.
PR	19-JUN-1998; 98US-0090080P.
PR	08-DEC-1998; 98US-0111715P.
XX	
PA	(GENZ) GENZYME CORP.
PA	(ROBE/) ROBERTS B L.
PA	(SHAN/) SHANKARA S.
XX	
PI	Roberts BL, Shankara S;
XX	
DR	WPI; 2000-106077/09.
XX	
PT	Isolated polynucleotides differentially expressed in antigen-presenting
PT	cells, useful in gene vaccines against cancer.
XX	
PS	Claim 1; Page 118; 130pp; English.
XX	
PS	Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC	expression) tags used to identify mRNA transcripts encoding
CC	immunostimulatory cofactor proteins which are preferentially or
CC	differentially expressed in monocyte-derived dendritic cells compared
CC	with monocytes. Some of the transcripts correspond to known genes or ESTs
CC	(expressed sequence tags) which were previously unknown to be
CC	preferentially or differentially expressed in dendritic cells, while
CC	other transcripts correspond to novel genes. Antigen-presenting cell
CC	(APC)-associated costimulatory factors play an important role in the
CC	activation of the cytotoxic immune response, particularly against tumour
CC	cells. Tumour antigen presentation via the MHC (major histocompatibility
CC	complex) and subsequent recognition by T-cell receptors is alone
CC	insufficient to activate a robust cytotoxic immune response that can lyse
CC	the tumour cells, immunostimulatory cofactors also being required for
CC	efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC	sequences identified using the SAGE tags have several potential uses.
CC	They may be used in vaccines to induce an immune response, particularly
CC	against a tumour antigen; to modulate the genotype of an APC; to screen
CC	for agents that modulate expression of differentially expressed genes in
CC	an APC; and as hybridisation probes/amplification primers for the
CC	diagnosis, prognosis and monitoring of diseases related to abnormal
CC	expression of these genes. Detection of the dendritic cell differentially
CC	expressed genes, or of their encoded proteins, can be used to identify
CC	

CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
 DB 9 GCTGTGG 3

RESULT 316
 AAZ78099/C
 ID AAZ78099 standard; DNA; 10 BP.
 XX
 AC AAZ78099;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:527.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

XX 19-JUN-1998; 98US-0089833P.

XX 19-JUN-1998; 98US-0089844P.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089878P.

XX 19-JUN-1998; 98US-0089911P.

XX 19-JUN-1998; 98US-0089922P.

XX 19-JUN-1998; 98US-0089933P.

XX 19-JUN-1998; 98US-0089944P.

XX 19-JUN-1998; 98US-0089977P.

XX 19-JUN-1998; 98US-0089999P.

XX 19-JUN-1998; 98US-0090000P.

XX 19-JUN-1998; 98US-0090035P.

XX 19-JUN-1998; 98US-0090036P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX 19-JUN-1998; 98US-0090042P.

XX 19-JUN-1998; 98US-0090043P.

XX 19-JUN-1998; 98US-0090044P.

XX 19-JUN-1998; 98US-0090045P.

XX 19-JUN-1998; 98US-0090047P.

XX 19-JUN-1998; 98US-0090048P.

XX 19-JUN-1998; 98US-0090072P.

XX 19-JUN-1998; 98US-0090076P.

XX 19-JUN-1998; 98US-0090077P.

XX 19-JUN-1998; 98US-0090078P.

XX 19-JUN-1998; 98US-0090079P.

XX 19-JUN-1998; 98US-0090080P.

PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B.L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106077/09.
 DR
 XX

PT Isolated polynucleotides differentially expressed in antigen-presenting
 cells, useful in gene vaccines against cancer.

XX Claim 1; Page 80; 130pp; English.

CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX

SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
 DB 9 CTGTGGC 3

RESULT 317

AAZ82030

ID AAZ82030 standard; DNA; 10 BP.

XX AAZ82030;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #1264.

XX Human; metastatic breast tumour tissue; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 XX antimetastatic; vaccine; diagnosis; ss.

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OS Homo sapiens.
XX WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX
XX PI Roberts BL, Shankara S;
XX
XX DR WPI; 2000-106079/09.
XX
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX
XX PS Claim 1; Page 92; 219pp; English.
XX
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines, for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX
XX SQ Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 U; 0 Other;
    Query Match 36.8%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 2.1e+02;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CGCGCTG 10
    |||||
Db 3 CGCGCTG 9
RESULT 318
AAZ83360/C
ID AAZ83360 standard; DNA; 10 BP.
XX
XX AC AAZ83360;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell upregulated transcript tag #2594.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
KW

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KW antimetastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX
XX PI Roberts BL, Shankara S;
XX
XX DR WPI; 2000-106079/09.
XX
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX
XX PS Claim 1; Page 129; 219pp; English.
XX
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines, for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX
XX SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
    Query Match 36.8%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 2.1e+02;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CTGTGGC 14
    |||||
Db 9 CTGTGGC 3
RESULT 319
AAZ84570/C
ID AAZ84570 standard; DNA; 10 BP.
XX
XX AC AAZ84570;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell downregulated transcript tag #3804.
XX

```

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 XX antimetastatic; vaccine; diagnosis; ss.
 OS Homo sapiens.
 XX WO9965928-A2.
 PN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 160; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
 SQ Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GCTGTGG 13
 |||||
 Db 7 GCTGTGG 1
 RESULT 320
 AAZ82784
 ID AAZ82784 standard; DNA; 10 BP.
 XX AAZ82784;
 AC AAZ82784;
 XX 07-APR-2000 (first entry)
 XX

DE Metastatic breast tumour cell upregulated transcript tag #2018.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 XX WO9965928-A2.
 PN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 113; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
 SQ Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCGAAGG 19
 |||||
 Db 1 GCGAAGG 7
 RESULT 321
 AAZ84917
 ID AAZ84917 standard; DNA; 10 BP.
 XX AAZ84917;
 AC AAZ84917;
 XX

DT 07-APR-2000 (first entry)
 XX Metastatic breast tumour cell downregulated transcript tag #4151.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 QS Homo sapiens.
 XX WO9965928-A2.
 PN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI1; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 DR non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 169; 219pp; English.
 PS AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 SQ Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 CGCTGTG 12
 |||||
 Db 1 CGCTGTG 7
 RESULT 322
 AAZ86247/c
 ID AAZ86247 standard; DNA; 10 BP.
 XX

AC AAZ86247;
 XX 07-APR-2000 (first entry)
 XX Metastatic breast tumour cell downregulated transcript tag #5481.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS WO9965928-A2.
 PN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI1; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 DR non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 203; 219pp; English.
 PS AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 5 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
 SQ Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GCTGTGG 13
 |||||
 Db 8 GCTGTGG 2
 RESULT 323
 AAZ81792

ID AAZ81792 standard; DNA; 10 BP.
 AC AAZ81792;
 XX
 DT 07-APR-2000 (first entry)
 XX
 XX Metastatic breast tumour cell upregulated transcript tag #1026.
 DE
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.
 XX
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 86; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 324
 AAZ81334
 ID AAZ81334 standard; DNA; 10 BP.
 XX
 AC AAZ81334;
 XX
 DT 07-APR-2000 (first entry)
 XX
 XX Metastatic breast tumour cell upregulated transcript tag #568.
 DE
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.
 XX
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 73; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGAAGG 19
 Db 1 GCGAAGG 7

RESULT 325
AAZ85903
ID AAZ85903 standard; DNA; 10 BP.
XX AC AAZ85903;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #5137.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN W09965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 195; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GTGGCGA 16

Db 1 GTGGCGA 7
RESULT 326
AAZ82560
ID AAZ82560 standard; DNA; 10 BP.
XX AC AAZ82560;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #1794.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN W09965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 106; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      8 CTGTGGC 14
Db      4 CTGTGGC 10

RESULT 327
AAZ82992/c
ID  AAZ82992 standard; DNA; 10 BP.
XX  AC  AAZ82992;
XX  DT  07-APR-2000 (first entry)
XX  DE  Metastatic breast tumour cell upregulated transcript tag #2226.
XX  KW  Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX  KW  non-metastatic breast tumour tissue; gene therapy; anticancer;
XX  KW  antimetastatic; vaccine; diagnosis; ss.
XX  OS  Homo sapiens.
XX  PN  WO9965928-A2.
XX  PD  23-DEC-1999.
XX  PF  18-JUN-1999; 99WO-US013647.
XX  PR  19-JUN-1998; 98US-0089853P.
XX  PR  19-JUN-1998; 98US-0089997P.
XX  PR  19-JUN-1998; 98US-0090039P.
XX  PR  19-JUN-1998; 98US-0090040P.
XX  PR  19-JUN-1998; 98US-0090041P.
XX  PA  (GENZ ) GENZYME CORP.
XX  PA  (ROBE/) ROBERTS B.L.
XX  PA  (SHAN/) SHANKARA S.
XX  PI  Roberts BL, Shankara S;
XX  WPI; 2000-106079/09.
XX  Isolated polynucleotides differentially expressed between metastatic and
XX  non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX  treatment of cancer.
XX  Claim 1; Page 119; 219pp; English.
XX  AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX  that are preferentially transcribed in the metastatic breast tumour
XX  tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX  to AAZ86677 represent tags corresponding to distinct transcripts that are
XX  preferentially transcribed in the primary or non-metastatic breast tumour
XX  tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX  transcripts can be used for diagnosis, prognosis, monitoring and
XX  treatment of breast cancer, particularly where metastatic. Diagnosis is
XX  by standard immunoassays or hybridisation/amplification reactions.
XX  Compounds that modulate expression of the transcripts are potentially
XX  useful for treatment of (metastatic) breast cancer, while promoters from
XX  the transcripts are used to direct expression, in selected cell types, of
XX  e.g. therapeutic genes (also ribozymes or antisense sequences),
XX  particularly an antigen-encoding sequence for use in gene or cell-based
XX  vaccines. Polypeptides encoded by the transcripts are also useful in
XX  vaccines; for diagnosing breast cancer and for raising specific
XX  antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX  agents. Host cells that produce the polypeptides can be used to expand
XX  and isolate populations of educated, antigen-specific immune effector
XX  cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX  immunotherapy.
XX  Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
XX  Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CTGTGGC 14
Db      4 CTGTGGC 10

RESULT 328
AAZ99863
ID  AAA99863 standard; DNA; 10 BP.
XX  AC  AAA99863;
XX  DT  06-AUG-2003 (revised)
XX  DT  26-JAN-2001 (first entry)
XX  DE  Prokaryote RT-PCR primer PCRS.
XX  KW  Prokaryote; gene identification; environmental stimulus; gene regulation;
XX  KW  bioprocess fermentation; PCR primer; ss.
XX  OS  Bacteria.
XX  PN  WO200056936-A1.
XX  PD  28-SEP-2000.
XX  PF  24-MAR-2000; 2000WO-US007912.
XX  PR  25-MAR-1999; 99US-0126038P.
XX  PA  (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX  PI  Bentley WE, Gill RT;
XX  WPI; 2000-587669/55.
XX  Performing differential display of prokaryotic mRNA by a RT (reverse
XX  transcriptase)/RAP (random arbitrary-primed) PCR based technique comprises
XX  using a unique combination of random primers in a single amplification
XX  step.
XX  Claim 1; Page 19; 63pp; English.
XX  The present invention is concerned with a method of differential display
XX  of prokaryotic mRNA by RT-PCR. This involves the amplification of the
XX  mRNA once, and the further amplification of the cDNA, rather than the
XX  repeated amplification of the mRNA sample. It also eliminates the need
XX  for sequencing gels, using Northern and total RNA dot blots to confirm
XX  differentially displayed transcript levels. The primers AAA99849-A99868
XX  were used in a reverse transcription PCR amplification, and primers
XX  AAA99869-A99876 were used to prepare probes for a Northern blot analysis.
XX  The method can be used to rapidly identify genes with increased or
XX  decreased transcription following environmental stimuli, in bioprocess
XX  fermentations, and to analyse gene regulation. (Updated on 06-AUG-2003 to
XX  correct OS field.)
XX  Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
XX  Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 TGGCGAA 17
Db      4 TGGCGAA 10

RESULT 329
AAZ73648/c
ID  AAA73648 standard; DNA; 10 BP.
XX  XX

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AC AAA73648;
 XX
 DT 30-JAN-2001 (first entry)
 XX
 DE Probe #17 for sequencing by hybridisation.
 DE
 KW Nucleic acid sequencing; sequencing by hybridisation; SBH; probe; ss.
 XX
 XX Synthetic.
 OS
 XX WO200040758-A2.
 XX
 PD 13-JUL-2000.
 XX
 XX 06-JAN-2000; 2000WO-US000458.
 PF
 XX 06-JAN-1999; 99US-0115284P.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac R, Drmanac S, Kita D, Cooke C, Xu C;
 PI
 XX WPI; 2000-475839/41.
 DR
 XX Identifying one or more sequences of a target nucleic acid (NA), useful
 PT for parallel analyses, comprises contacting the NA with a set of pools of
 PT probes comprising mixture of probes with different information regions.
 XX
 PS Disclosure; Page 53; 196pp; English.
 XX
 CC The present sequence is a probe used to demonstrate the method of the
 CC invention, which is concerned with the use of pools of probes to enable
 CC sequencing by hybridisation, a process known as SBH. Overlapping probes
 CC are used which allows the identification of sequences longer than the
 CC probe length, and either the target nucleic acid or the probe is
 CC labelled. The method of the invention is useful for assembling sequences
 CC and in parallel analyses
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 8 CTGTGGC 14
 DB |||||
 7 CTGTGGC 1
 XX
 RESULT 330
 AAA73647/C
 ID AAA73647 standard; DNA; 10 BP.
 XX
 AC AAA73647;
 XX
 DT 30-JAN-2001 (first entry)
 XX
 DE Probe #16 for sequencing by hybridisation.
 DE
 KW Nucleic acid sequencing; sequencing by hybridisation; SBH; probe; ss.
 XX
 XX Synthetic.
 OS
 XX WO200040758-A2.
 XX
 PD 13-JUL-2000.
 XX
 XX 06-JAN-2000; 2000WO-US000458.
 PF
 XX 06-JAN-1999; 99US-0115284P.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac R, Drmanac S, Kita D, Cooke C, Xu C;
 PI
 XX WPI; 2000-475839/41.
 DR
 XX Identifying one or more sequences of a target nucleic acid (NA), useful
 PT for parallel analyses, comprises contacting the NA with a set of pools of
 PT probes comprising mixture of probes with different information regions.
 XX
 PS Disclosure; Page 53; 196pp; English.
 XX
 CC The present sequence is a probe used to demonstrate the method of the
 CC invention, which is concerned with the use of pools of probes to enable
 CC sequencing by hybridisation, a process known as SBH. Overlapping probes
 CC are used which allows the identification of sequences longer than the
 CC probe length, and either the target nucleic acid or the probe is
 CC labelled. The method of the invention is useful for assembling sequences
 CC and in parallel analyses
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 8 CTGTGGC 14
 DB |||||
 7 CTGTGGC 1
 XX
 RESULT 330
 AAA73647/C
 ID AAA73647 standard; DNA; 10 BP.
 XX
 AC AAA73647;
 XX
 DT 30-JAN-2001 (first entry)
 XX
 DE Probe #16 for sequencing by hybridisation.
 DE
 KW Nucleic acid sequencing; sequencing by hybridisation; SBH; probe; ss.
 XX
 XX Synthetic.
 OS
 XX WO200040758-A2.
 XX
 PD 13-JUL-2000.
 XX
 XX 06-JAN-2000; 2000WO-US000458.
 PF
 XX 06-JAN-1999; 99US-0115284P.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac R, Drmanac S, Kita D, Cooke C, Xu C;
 PI
 XX WPI; 2000-475839/41.
 DR
 XX Identifying one or more sequences of a target nucleic acid (NA), useful
 PT for parallel analyses, comprises contacting the NA with a set of pools of
 PT probes comprising mixture of probes with different information regions.
 XX
 PS Disclosure; Page 53; 196pp; English.
 XX
 CC The present sequence is a probe used to demonstrate the method of the
 CC invention, which is concerned with the use of pools of probes to enable
 CC sequencing by hybridisation, a process known as SBH. Overlapping probes
 CC are used which allows the identification of sequences longer than the
 CC probe length, and either the target nucleic acid or the probe is
 CC labelled. The method of the invention is useful for assembling sequences
 CC and in parallel analyses
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 8 CTGTGGC 14
 DB |||||
 7 CTGTGGC 1
 XX
 RESULT 331
 AAA70761/C
 ID AAA70761 standard; DNA; 10 BP.
 XX
 AC AAA70761;
 XX
 DT 17-JAN-2001 (first entry)
 DT
 XX PCR primer #7 for B. pumilus strain B3 DNA amplification.
 DE
 XX PCR primer; amplification; Bacillus pumilus B3; CECT 5105; plant growth;
 KW Bacillus licheniformis B12; CECT 5106; gibberellin; plant hormone;
 KW woody plant; herbaceous plant; disease resistance; ss.
 XX
 OS Bacillus pumilus.
 XX
 XX WO200043497-A1.
 PN
 XX 27-JUL-2000.
 PD
 XX 18-JAN-2000; 2000WO-ES000017.
 PF
 XX 20-JAN-1999; 99ES-00000106.
 PR
 XX (UYSA-) UNIV SAN PABLO CEU.
 PA
 XX Gutierrez Manero J, Probanza Lobo A;
 PI
 XX WPI; 2000-499226/44.
 DR
 XX New strains of Bacillus, useful for promoting growth of herbaceous and
 PT woody plants, produce gibberellin plant hormones.
 PT
 XX Disclosure; Page 15; 28pp; Spanish.
 PS
 XX The invention relates to the isolation of novel strains of bacteria
 CC (Bacillus pumilus B3 (CECT 5105) and B. licheniformis B12 (CECT 5106))
 CC which produce gibberellin plant hormones that regulate plant growth. The
 CC plant growth hormones are produced at level of 0.0029-0.148 mg/l by B3
 CC and at 0.0017-0.123 mg/l by B12, after 24 hour culture at 28 deg. C in
 CC liquid medium. The new strains are used to treat cultured plants (both
 CC woody and herbaceous) to increase their growth, vigour and disease
 CC resistance. Primers AAA70755-A70762 were used to PCR amplify DNA from the
 CC B. pumilus strain B3

PI Drmanac R, Drmanac S, Kita D, Cooke C, Xu C;
 XX
 DR WPI; 2000-475839/41.
 XX
 PT Identifying one or more sequences of a target nucleic acid (NA), useful
 PT for parallel analyses, comprises contacting the NA with a set of pools of
 PT probes comprising mixture of probes with different information regions.
 XX
 XX Disclosure; Page 53; 196pp; English.
 XX
 CC The present sequence is a probe used to demonstrate the method of the
 CC invention, which is concerned with the use of pools of probes to enable
 CC sequencing by hybridisation, a process known as SBH. Overlapping probes
 CC are used which allows the identification of sequences longer than the
 CC probe length, and either the target nucleic acid or the probe is
 CC labelled. The method of the invention is useful for assembling sequences
 CC and in parallel analyses
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 8 CTGTGGC 14
 DB |||||
 8 CTGTGGC 2
 XX
 RESULT 331
 AAA70761/C
 ID AAA70761 standard; DNA; 10 BP.
 XX
 AC AAA70761;
 XX
 DT 17-JAN-2001 (first entry)
 DT
 XX PCR primer #7 for B. pumilus strain B3 DNA amplification.
 DE
 XX PCR primer; amplification; Bacillus pumilus B3; CECT 5105; plant growth;
 KW Bacillus licheniformis B12; CECT 5106; gibberellin; plant hormone;
 KW woody plant; herbaceous plant; disease resistance; ss.
 XX
 OS Bacillus pumilus.
 XX
 XX WO200043497-A1.
 PN
 XX 27-JUL-2000.
 PD
 XX 18-JAN-2000; 2000WO-ES000017.
 PF
 XX 20-JAN-1999; 99ES-00000106.
 PR
 XX (UYSA-) UNIV SAN PABLO CEU.
 PA
 XX Gutierrez Manero J, Probanza Lobo A;
 PI
 XX WPI; 2000-499226/44.
 DR
 XX New strains of Bacillus, useful for promoting growth of herbaceous and
 PT woody plants, produce gibberellin plant hormones.
 PT
 XX Disclosure; Page 15; 28pp; Spanish.
 PS
 XX The invention relates to the isolation of novel strains of bacteria
 CC (Bacillus pumilus B3 (CECT 5105) and B. licheniformis B12 (CECT 5106))
 CC which produce gibberellin plant hormones that regulate plant growth. The
 CC plant growth hormones are produced at level of 0.0029-0.148 mg/l by B3
 CC and at 0.0017-0.123 mg/l by B12, after 24 hour culture at 28 deg. C in
 CC liquid medium. The new strains are used to treat cultured plants (both
 CC woody and herbaceous) to increase their growth, vigour and disease
 CC resistance. Primers AAA70755-A70762 were used to PCR amplify DNA from the
 CC B. pumilus strain B3

```
XX SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
Db 10 GCTGTGG 4

RESULT 332
AAS04437/C
ID AAS04437 standard; DNA; 10 BP.
XX AC AAS04437;
XX DT 07-SEP-2001 (first entry)
XX DE Human DAXX DNA primer-extension oligonucleotide #24.
XX KW Death-associated protein 6; DAXX; polymorphism; haplotype pair; human;
KW immune disorder; autoimmune disease; population diversity; ss;
KW paternity testing; anthropological lineage; forensic application;
KW primer-extension oligonucleotide.
XX OS Homo sapiens.
XX PN WO200125245-A2.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US027487.
XX PR 06-OCT-1999; 99US-0157909P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;
XX WPI; 2001-308220/32.
XX PT New human death-associated protein 6 (DAXX) gene variants comprising 19
XX polymorphic sites useful in studying the effect of variation on the
XX biological activity of DAXX and in developing drugs targeting the
XX protein.
XX PS Disclosure; Page 21; 97pp; English.
XX CC Sequences AAS04414-AAS04451 represent primer-extension oligonucleotides
XX specific for a DNA encoding human death-associated protein 6 (DAXX). This
XX DNA may comprise one or more polymorphisms at specific nucleotide
XX positions to form one of nineteen possible polymorphic variants.
XX CC Associations between a trait and a genotype or a haplotype of the DAXX
XX gene can be identified by comparing the frequency of the genotype or
XX haplotype in a population exhibiting the trait with that of a reference
XX population. A higher frequency in the trait population indicates an
XX association. Methods involving genotyping or haplotyping of the DAXX gene
XX of an individual can lead to prediction of haplotype pairs for the DAXX
XX gene of related individuals, and may be useful in studying the expression
XX and biological function of DAXX, as well as in developing drugs targeting
XX this protein. Polymorphic variants of DAXX are useful in studying the
XX effect of the variation on the biological activity of DAXX as well as on
XX the binding affinity of candidate drugs targeting DAXX for the treatment
XX of autoimmune diseases and other immune disorders. Polymorphism is also
XX useful for studying population diversity, anthropological lineage,
XX paternity testing, forensic applications, and for identifying
XX associations between the DAXX genetic variation and a trait such as level
XX of drug response or susceptibility to disease. DAXX proteins may be used
XX to measure binding affinities of one or more candidate drugs targeting
XX the DAXX protein
XX
```

```
XX SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
Db 10 GCTGTGG 4

RESULT 333
AAH63684
ID AAH63684 standard; cDNA; 10 BP.
XX AC AAH63684;
XX DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 524.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX DR New isolated polynucleotides, useful for identifying specific cell type,
XX PT such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX PS Claim 13; Page 51; 94pp; English.
XX CC The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
Db 4 CTGTGGC 10

RESULT 334
AAS57302
ID AAS57302 standard; DNA; 10 BP.
XX AC AAS57302;
XX DT 16-JAN-2002 (first entry)
XX
```

XX DE Human CHRN2 allele specific oligonucleotide PCR primer terminus #27.
 XX KW Human; cholinergic receptor, nicotinic, beta polypeptide 2; neuronal;
 KW CHRN2; memory disorder; Alzheimer's disease; epilepsy; learning;
 KW chromosome 1q21; schizophrenia; attention deficit/hyperactivity disorder;
 KW ADHD; autosomal dominant nocturnal frontal lobe epilepsy; ADNFLE; ss;
 XX KW allele specific oligonucleotide; ASO; PCR primer.
 XX OS Homo sapiens.
 XX PN WO200174833-A2.
 XX PD 11-OCT-2001.
 XX PF 03-APR-2001; 2001WO-US010666.
 XX PR 03-APR-2000; 2000US-0194155P.
 XX PR 13-JUL-2000; 2000US-0217952P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Choi JY, Kliem SF, Koshy B, Lee HH, Sanchis A;
 XX DR WPI; 2001-626374/72.
 XX KW Genotyping cholinergic receptor, nicotinic, beta-polypeptide 2 gene of an
 PT individual involves determining for two copies of the gene, the identity
 PT of nucleotide pair at polymorphic sites selected from PS1-24.
 XX PS Claim 17; Page 15; 82pp; English.
 XX CC The invention relates to genotyping/haplotyping the cholinergic receptor,
 CC nicotinic, beta-polypeptide 2 (neuronal) (CHRN2) gene of an individual,
 CC comprising determining for the two copies of the CHRN2 gene present in
 CC the individual, the identity of the nucleotide pair at one or more
 CC polymorphic sites selected from PS1-24. Also include are oligonucleotides
 CC for performing the method and the nucleotide sequence of the polymorphic
 CC variants of CHRN2. The method is useful for detecting novel CHRN2
 CC polymorphisms and for determining if an individual has a haplotype or
 CC haplotype pairs defined in the specification and to validate CHRN2 as a
 CC candidate agent for treating a specific condition or disease predicted to
 CC be associated with CHRN2 activity (e.g. a memory disorder, Alzheimer's
 CC disease, epilepsy, a learning disorder, schizophrenia, attention
 CC deficit/hyperactivity disorder, (ADHD) and autosomal dominant nocturnal
 CC frontal lobe epilepsy (ADNFLE)), and in the design of clinical trials of
 CC candidate drugs for treating a specific condition or disease predicted to
 CC be associated with CHRN2 activity. The method is useful to screen for
 CC compounds targeting CHRN2 to treat a specific conditions or disease
 CC associated with CHRN2 activity. The polymorphic nucleic acids are useful
 CC in studying the expression and function of CHRN2, and in expressing
 CC CHRN2 protein for use in screening for candidate drugs to treat diseases
 CC related to CHRN2 activity and are useful for therapeutic purposes. The
 CC CHRN2 gene is located on chromosome 1q21. The present sequence is an
 CC allele specific oligonucleotide (ASO) PCR primer (3' terminus) for
 CC performing the method of the invention
 XX SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GCTGTGG 13
 Db 1 GCTGTGG 7
 RESULT 335
 AAF31259
 ID AAF31259 standard; DNA; 10 BP.
 XX XX
 AC AAF31259;

XX DT 09-APR-2001 (first entry)
 XX DE GC-rich template cycle sequencing mixture related sequence #3.
 XX KW GC-rich template; cycle sequencing; 7-deaza dGTP; dITP;
 KW DNA amplification; ds.
 XX OS Synthetic.
 XX PN WO200102602-A2.
 XX PD 11-JAN-2001.
 XX PF 05-JUL-2000; 2000WO-EP006349.
 XX PR 05-JUL-1999; 99EP-00112943.
 XX PA (LION-) LION BIOSCIENCE AG.
 XX PI Motz M, Voss H;
 XX DR WPI; 2001-138153/14.
 XX KW Use of a mixture comprising 7-deaza dGTP and dITP for direct exponential
 PT amplification and sequencing of nucleic acids, particularly guanosine
 PT cytosine rich templates.
 XX PS Disclosure; Fig 2; 18pp; English.
 XX CC The present invention describes a mixture comprising 7-deaza dGTP and
 CC dITP, which can be used in the cycle sequencing of GC-rich templates. In
 CC addition, the mixture can be used in DNA amplification. Sequences
 CC AAF31257-AAF31267 are examples of compression prone sequences
 XX SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCGAAGG 19
 Db 1 GCGAAGG 7
 RESULT 336
 AAH41713/c
 ID AAH41713 standard; DNA; 10 BP.
 XX AC AAH41713;
 XX DT 28-AUG-2001 (first entry)
 XX DE Anti-PEP gene construction related oligonucleotide S18.
 XX KW Phosphoenopyruvate carboxylase; PEPCase; seed; acetyl-CoA carboxylase;
 KW oilseed; PEP; plant breeding; soya bean; sunflower; rapeseed; peanut;
 KW sesame; crop plant; protein content; fatty acid content; anti-PEP; ss.
 XX OS Synthetic.
 XX PN WO200134812-A1.
 XX PD 17-MAY-2001.
 XX PF 06-NOV-2000; 2000WO-CN000418.
 XX PR 09-NOV-1999; 99CN-00124511.
 XX PA (ZHEJ-) ZHEJIANG AGRIC SCI ACAD.
 XX PI Chen J, Lang C, Huang R, Hu Z, Liu Z;

XX WPI; 2001-335934/35.
 XX
 PT Altering protein/fatty acid composition of seeds, useful for producing
 PT e.g. soya bean or sesame seed with high protein/fatty acid content,
 PT comprises introducing antisense gene.
 XX
 XX
 PS Example 8; Page 9; 25pp; Chinese.
 XX
 CC The present invention describes a method for altering the protein/fatty
 CC acid composition of seeds. The method comprises: (1) cloning
 CC phosphoenolpyruvate carboxylase (PEP) or acetyl-CoA carboxylase (ACC)
 CC genes or their fragments; (2) constructing the corresponding antisense
 CC gene of anti-PEP or anti-ACC; and (3) introducing the antisense gene into
 CC the plant cell of a crop. The method is applicable in plant breeding to
 CC give oilseed crops with high oil or protein content like soya bean,
 CC sunflower, rapeseed, peanut and sesame. The produced crop plants have
 CC high yield of oil or protein. The present sequence represents an
 CC oligonucleotide which is used in the construction of an anti-PEP gene in
 CC an example from the present invention
 XX
 SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GCTGTGG 13
 DB 7 GCTGTGG 1
 RESULT 337
 ABA06097/c
 ID ABA06097 standard; cDNA; 10 BP.
 XX
 AC ABA06097;
 XX
 XX 10-JAN-2002 (first entry)
 XX
 DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 74.
 XX
 XX Human, hepatocyte; gene expression; hepatopathy; ss.
 XX
 OS Homo sapiens.
 XX
 XX JP2001211883-A.
 XX
 PD 07-AUG-2001.
 XX
 PF 31-JAN-2000; 2000JP-00023170.
 XX
 PR 31-JAN-2000; 2000JP-00023170.
 XX
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA
 XX WPI; 2001-629566/73.
 XX
 XX Human normal hepatocyte expression gene group.
 PT
 XX Claim 1; Page 7; 26pp; Japanese.
 PS
 CC The invention relates to a human normal hepatocyte expression gene group
 CC comprising 200 genes in the human normal hepatocyte. The cDNA of each
 CC gene comprises one of 200 fully defined nucleotide sequences as given in
 CC the specification. The gene group and the cDNAs corresponding to each of
 CC the genes in the group are useful in the diagnosis and treatment of human
 CC hepatopathy. The present sequence is a cDNA corresponding to a gene
 CC expressed by normal human hepatocytes
 XX
 SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 TGTGGCG 15
 DB 7 TGTGGCG 1

RESULT 338
 AAF36769/c
 ID AAF36769 standard; DNA; 10 BP.
 XX
 AC AAF36769;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3508.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 XX WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI
 XX WPI; 2001-061874/07.
 DR
 XX
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 125; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX

SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GTGGCGCA 16
Db 7 GTGGCGCA 1
RESULT 339
AAF37041
ID AAF37041 standard; DNA; 10 BP.
XX AAF37041;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3780.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 135; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TGGCGAA 17
Db 4 TGGCGAA 10
RESULT 340
AAF33704
ID AAF33704 standard; DNA; 10 BP.
XX
AC AAF33704;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:443.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 391; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.

CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 CGCTGTG 12
 |||||
 Db 4 CGCTGTG 10

RESULT 341
 AAF36509/C
 ID AAF36509 standard; DNA; 10 BP.
 XX AAF36509;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3248.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 116; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GCGCTGT 11
 |||||
 Db 8 GCGCTGT 2

RESULT 342
 AAF43548/C
 ID AAF43548 standard; DNA; 10 BP.
 XX AAF43548;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11687.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 367; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
Db 10 TGGCGAA 4

RESULT 343
AAF33404
ID AAF33404 standard; DNA; 10 BP.
XX
AC AAF33404;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:143.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 24; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12
Db 4 CGCTGTG 10

RESULT 344
AAF40064/C
ID AAF40064 standard; DNA; 10 BP.
XX
AC AAF40064;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6803.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 243; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression

varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate phases which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGA 16
 Db 8 GTGGCGA 2
 |||||

RESULT 345
 AAF40212

ID AAF40212 standard; DNA; 10 BP.

XX AC AAF40212;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6951.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 248; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate phases which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention.

XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGCGGAA 17
 Db 2 TGCGGAA 8
 |||||

RESULT 346
 AAF34364/C

ID AAF34364 standard; DNA; 10 BP.

XX AC AAF34364;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1103.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 39; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log

described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGGAG 18
Db 9 GCGGAG 3
|||||||

RESULT 347
AAF36295
ID AAF36295 standard; DNA; 10 BP.
AC AAF36295;
XX
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3034.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 108; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a

coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCT 9
Db 2 TCGCGCT 8
|||||||

RESULT 348
AAF42137/c
ID AAF42137 standard; DNA; 10 BP.
XX
AC AAF42137;
XX
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8876.
DE
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

PS Example; Page 317; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGAAGG 19

DB 10 GCGAAGG 4

RESULT 349

AAF37397/C

XX AAF37397 standard; DNA; 10 BP.

XX AAF37397;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4136.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT

PT Gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 147; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10

DB 8 CGCGCTG 2

RESULT 350

AAF43249

ID AAF43249 standard; DNA; 10 BP.

XX AAF43249;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11388.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX

DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 356; 419pp; English.

PS The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17

Db 1 TGGCGAA 7

RESULT 351

AAF40108

ID AAF40108 standard; DNA; 10 BP.

XX AAF40108;

AC AAF40108;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6847.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS Saccharomyces cerevisiae.

XX WO200077214-A2.

PN WO200077214-A2.

XX 21-DEC-2000.

PD 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PR 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

PA (UYJO) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

DR gene expression (SAGE) tags, useful for studying, monitoring and

XX affecting phases of the cell cycle.

XX Example; Page 244; 419pp; English.

PS The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14

Db 3 CTGTGGC 9

RESULT 352

AAF43351

ID AAF43351 standard; DNA; 10 BP.

XX AAF43351;

AC AAF43351;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11490.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS Saccharomyces cerevisiae.

XX WO200077214-A2.

PN WO200077214-A2.

XX 21-DEC-2000.

PD 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 14-JUN-2000; 2000WO-US016223.

XX (UYJO) UNIV JOHNS HOPKINS.

PA (UYJO) UNIV JOHNS HOPKINS.

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PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 360; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate phases of the cell cycle. The
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12
DB |||||
4 CGCTGTG 10

RESULT 353
AAF33705
ID AAF33705 standard; DNA; 10 BP.
XX
AC AAF33705;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:444.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
PN
XX 21-DEC-2000.
XX

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XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Claim 1; Page 391; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate phases of the cell cycle. The
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12
DB |||||
4 CGCTGTG 10

RESULT 354
AAF41416/C
ID AAF41416 standard; DNA; 10 BP.
XX
AC AAF41416;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8155.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX

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PN WO200077214-A2.
XX
XX
PD 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
PF
XX 16-JUN-1999; 99US-00335032.
PR
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 291; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 0 A; 5 C; 1 G; 4 T; 0 U; 0 Other;
SQ
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 GCGGAAG 18
Db 9 GCGGAAG 3
RESULT 355
AAFP41494
ID AAF41494 standard; DNA; 10 BP.
XX
XX AAF41494;
AC
XX
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8233.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

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XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
PN
XX 21-DEC-2000.
PD
XX 14-JUN-2000; 2000WO-US016223.
PF
XX 16-JUN-1999; 99US-00335032.
PR
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 294; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TGGCGAA 17
Db 2 TGGCGAA 8
RESULT 356
AAFP37535
ID AAF37535 standard; DNA; 10 BP.
XX
XX AAF37535;
AC
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4274.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW

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KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 XX WO200077214-A2.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 152; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTCGCG 7
 Db 3 GGTCGCG 9
 RESULT 357
 AAF33686
 ID AAF33686 standard; DNA; 10 BP.
 AC AAF33686;
 XX
 DT 23-MAR-2001 (first entry)
 XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:425.
 XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 XX WO200077214-A2.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Claim 1; Page 390; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTCGCG 7
 Db 3 GGTCGCG 9
 RESULT 358
 AAF36000
 ID AAF36000 standard; DNA; 10 BP.
 XX
 AC AAF36000;

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XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2739.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 97; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 36.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 CGCTGTG 12
XX |||||
XX 4 CGCTGTG 10
XX
XX RESULT 359
XX AAF42020/c

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ID AAF42020 standard; DNA; 10 BP.
XX
XX AAF42020;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8759.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 312; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 36.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 TCGCGCT 9
XX |||||
XX 8 TCGCGCT 2
XX
XX Db

```

RESULT 360
 AAS95650
 ID AAS95650 standard; DNA; 10 BP.
 XX
 AC AAS95650;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human NP1R gene allele-specific oligonucleotide PCR primer #5.
 XX
 KW Human; neuropeptide Y receptor Y1; NP1R; ss; antiarteriosclerotic;
 KW haplotyping; haplotype pair; single nucleotide polymorphism; genotyping;
 KW gene therapy; drug screening; cardiovascular disease; antidepressant;
 KW hypertension; cardiast; depression; probe; sequencing primer; PCR primer;
 KW PCR primer universal tail.
 XX
 OS Homo sapiens.
 XX
 PN W0200185742-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 07-MAY-2001; 2001WO-US014773.
 XX
 PR 05-MAY-2000; 2000US-0201950P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Choi JY, Kliem SE, Koshy B, Lee HH;
 XX
 DR WPI; 2002-055579/07.
 XX
 PT New isolated polynucleotide variant of neuropeptide Y receptor Y1 (NP1R)
 PT for studying the function of NP1R, and expressing NP1R protein for use
 PT in screening candidate drugs to treat NP1R-related diseases.
 XX
 PS Claim 17; Page 12; 48pp; English.
 XX
 CC The invention relates to single nucleotide polymorphisms in the human
 CC neuropeptide Y receptor Y1 (NP1R) gene. A method for haplotyping the
 CC NP1R gene in an individual comprises identifying the nucleotide at one
 CC or more polymorphic sites and determining whether one of the copies of
 CC the gene is defined by one of the NP1R haplotypes given in the
 CC specification or whether both copies are defined by a haplotype pair.
 CC This method is useful in genotyping, whereby all possible haplotype pairs
 CC can be assigned to specific genotypes. An association between a trait and
 CC a haplotype or haplotype pair of the NP1R gene can be identified by
 CC comparing the frequency of the haplotype or haplotype pair in a
 CC population exhibiting the trait with the frequency of the haplotype or
 CC haplotype pair in a reference population, where a higher haplotype
 CC frequency in the trait population indicates the trait is associated with
 CC the haplotype or haplotype pair. NP1R and its corresponding DNA are used
 CC for studying the expression and function of NP1R, for use in screening
 CC for candidate drugs to treat diseases related to NP1R activity, such as
 CC cardiovascular diseases (e.g. hypertension) and depression. The sequences
 CC are also useful for studying the effect of variation on the biological
 CC activity of NP1R as well as on the binding affinity of candidate drugs
 CC targeting NP1R. Sequences AAS95637-AAS95659 represent allele-specific
 CC oligonucleotide probes, sequencing primers, PCR primers and PCR primer
 CC universal tails used to detect NP1R gene polymorphisms
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CTGTGGC 14
 DB 1 CTGTGGC 7

RESULT 361
 AAD25081/c
 ID AAD25081 standard; DNA; 10 BP.
 XX
 AC AAD25081;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Primer #8 used to detect human OSM gene polymorphism.
 XX
 KW Human; oncostatin M; OSM gene; haplotyping; genotyping; cancer; primer;
 KW lung inflammation; polymorphism; rheumatoid arthritis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200187907-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US016157.
 XX
 PR 17-MAY-2000; 2000US-0204868P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Duda AE, Kazemi A, Koshy B;
 XX
 DR WPI; 2002-055680/07.
 XX
 PT New isolated human oncostatin M polynucleotide, useful for therapeutic
 PT purposes, for studying the expression and function of the polynucleotide
 PT and for expressing oncostatin protein.
 XX
 PS Claim 18; Page 13; 71pp; English.
 XX
 CC The invention relates to genetic variants of human oncostatin M (OSM)
 CC gene. The invention also relates to compositions and methods for
 CC haplotyping and/or genotyping OSM gene in an individual. Polynucleotides
 CC of the invention are useful in studying the expression and function of
 CC OSM, and in expressing OSM protein for use in screening candidate drugs
 CC to treat diseases related to OSM activity. They are also useful for
 CC therapeutic purposes. Methods of the invention are useful for determining
 CC whether an individual has a haplotype or haplotype pairs. The method is
 CC also useful for improving the efficacy and reliability of several steps
 CC in the discovery and development of drugs for treating diseases
 CC associated with OSM activity, e.g. cancer, diseases involving lung
 CC inflammation and rheumatoid arthritis. The present sequence is a primer
 CC used for detecting human OSM gene polymorphisms
 XX
 SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
 DB 9 CTGTGGC 3

RESULT 362
 AAD26712
 ID AAD26712 standard; DNA; 10 BP.
 XX
 AC AAD26712;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human GPR31 gene polymorphism detecting primer #13.

Human; G-protein coupled receptor 31; GPR31 protein; haplotyping;
 KW genotyping; gene therapy; cancer; polymorphism; primer; ss.

OS Homo sapiens.
 XX WO200190124-A2.
 XX PD
 XX 29-NOV-2001.
 XX PF
 XX 23-MAY-2001; 2001WO-US016908.
 XX PR
 XX 23-MAY-2000; 2000US-0204572P.
 XX XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX PA
 XX Bieglecki KM, Duda A, Kazemi A, Lee HH, Messer C;
 XX PI
 XX WPI; 2002-089915/12.
 XX DR
 XX Novel genetic variants of G-protein coupled receptor gene useful in
 PT studying expression and function of the protein, and for screening drugs
 PT to treat diseases e.g. cancer.
 XX PT
 XX PS Claim 18; Page 13; 75pp; English.
 XX XX
 CC The invention relates to genetic variants of human G-protein coupled
 CC receptor 31 (GPR31) gene. The invention also relates to compositions and
 CC methods for haplotyping and/or genotyping the GPR31 gene in an
 CC individual. Polynucleotides of the invention are useful in studying the
 CC expression and function of GPR31, and in expressing GPR31 protein for use
 CC in screening candidate drugs to treat diseases related to GPR31 activity
 CC and in studying the effect of the variation on the biological activity of
 CC GPR31 as well as on the binding affinity of candidate drugs targeting
 CC GPR31 for the treatment of cancer. They are also used in gene therapy.
 CC The haplotyping method is useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with GPR31 activity e.g. cancer. This
 CC method is also useful for haplotyping GPR31 gene in an individual, which
 CC can also be used by the pharmaceutical research scientist to validate
 CC GPR31 as a candidate target for, and in design of clinical trials of
 CC candidate drugs, for treating a specific condition or disease
 CC predicted to be associated with GPR31 activity. The present sequence is a
 CC primer used to detect human GPR31 gene polymorphisms
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GCTGTGG 13
 Db 3 GCTGTGG 9
 RESULT 363
 AAS98814
 ID AAS98814 standard; DNA; 10 BP.
 XX AC
 XX AAS98814;
 XX DT
 XX 26-MAR-2002 (first entry)
 XX XX
 DE Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #180.
 XX KW
 KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
 KW cytostatic; gene therapy; malignant histiocytosis; isogene;
 KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
 KW genotype; human; allele specific oligonucleotide; ASO; primer;
 KW primer extension; ss.
 XX KW
 XX Homo sapiens.
 OS
 XX WO200179225-A2.
 XX PN
 XX 25-OCT-2001.

XX 12-APR-2001; 2001WO-US012044.
 PF
 XX 12-APR-2000; 2000US-0196411P.
 XX PR
 XX (GENA-) GENAISSANCE PHARM INC.
 XX PA
 XX Chew A, Choi JY, Koshy B;
 XX PI
 XX WPI; 2002-075058/10.
 XX DR
 XX Novel polymorphic variants of colony stimulating factor 1 receptor useful
 PT in studying expression and function of the protein, useful for screening
 PT candidate drugs to treat diseases e.g. inflammatory disorders.
 XX PT
 XX PS Claim 17; Page 17; 164pp; English.
 XX XX
 CC The invention describes a novel isolated polynucleotide (I) comprising a
 CC sequence which is a polymorphic variant (PV) of a reference sequence for
 CC colony stimulating factor 1 receptor (CSF1R) gene, found on the
 CC polypeptide are useful for improving the discovery and development of
 CC drugs for treating diseases associated with CSF1R activity, e.g.,
 CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
 CC and the haplotypes can be used to validate CSF1R as a candidate target
 CC for treating a specific condition or disease predicted to be associated
 CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
 CC be used in developing diagnostic tests and therapeutic treatments. (I) is
 CC useful in studying the expression and function of CSF1R, and in
 CC expressing CSF1R protein for use in screening for candidate drugs to
 CC treat diseases related to CSF1R activity and in studying the effect of
 CC the variation on the biological activity of CSF1R as well as on the
 CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
 CC useful in a variety of diagnostic and prognostic formats and therapeutic
 CC methods. A transgenic animal is useful in studying expression of the
 CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
 CC targeted against CSF1R protein, and for testing the efficacy of
 CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
 CC are useful as probes and primers, and for assaying a polymorphism in the
 CC target region. Without requiring any a priori knowledge of the phenotypic
 CC effect of any particular CSF1R or haplotype the invention provides a
 CC method for identifying lead compounds that are more likely to show
 CC efficacy in clinical trials. This sequence is a primer used to detect
 CC CSF1R gene polymorphisms by primer extension, described in the method of
 CC the invention
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CTGTGGC 14
 Db 2 CTGTGGC 8
 RESULT 364
 ABQ71544
 ID ABQ71544 standard; DNA; 10 BP.
 XX AC
 XX ABQ71544;
 XX XX
 DT 28-AUG-2002 (first entry)
 XX KW
 KW Zinc finger protein related oligonucleotide target SEQ ID NO:1278.
 XX DE
 XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 XX KW
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX WO200242459-A2.
 XX PN
 XX 25-OCT-2001.

PI Liu Q;
 XX WPI; 2002-500284/53.
 XX
 PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.
 XX
 PS Example 1; Page 38; 8lpp; English.
 XX
 CC The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (I) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determined the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e-02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 GCGGAAG 18
 Db 4 GCGGAAG 10
 |||||
 |||||
 RESULT 367
 ABQ71662
 ID ABQ71662 standard; DNA; 10 BP.
 XX
 AC ABQ71662;
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE Zinc finger protein related oligonucleotide target SEQ ID NO:1654.
 XX
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200242459-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 20-NOV-2001; 2001WO-US043438.
 XX
 PR 20-NOV-2000; 2000US-00716637.
 XX
 PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX
 PI Liu Q;
 XX
 DR WPI; 2002-500284/53.
 XX

PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.
 XX
 PS Example 1; Page 51; 8lpp; English.
 XX
 CC The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determined the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTCCGC 7
 Db 3 GGTCCGC 9
 |||||
 |||||
 RESULT 368
 ABQ71675
 ID ABQ71675 standard; DNA; 10 BP.
 XX
 AC ABQ71675;
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE Zinc finger protein related oligonucleotide target SEQ ID NO:1667.
 XX
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200242459-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 20-NOV-2001; 2001WO-US043438.
 XX
 PR 20-NOV-2000; 2000US-00716637.
 XX
 PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX
 PI Liu Q;
 XX
 DR WPI; 2002-500284/53.
 XX
 PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.
 XX

PS Example 1; Page 51; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such that it
 CC binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention

SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7
 DB 3 GGTCGCG 9

RESULT 369

ABQ71661
 ID ABQ71661 standard; DNA; 10 BP.

AC ABQ71661;

DT 28-AUG-2002 (first entry)

XX Zinc finger protein related oligonucleotide target SEQ ID NO:1653.

DE Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

KW Homo sapiens.

OS Synthetic.

XX WO200242459-A2.

PN 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

PF 20-NOV-2000; 2000US-00716637.

PR (SANG-) SANGAMO BIOSCIENCES INC.

PA Liu Q;

XX WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
 CC gene function and for human therapeutics and plant engineering, comprises
 CC first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 51; 81pp; English.

PS The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)

CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such that it
 CC binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention

SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7
 DB 3 GGTCGCG 9

RESULT 370

ABQ88698
 ID ABQ88698 standard; DNA; 10 BP.

AC ABQ88698;

XX 23-SEP-2002 (first entry)

DE Human CFL1 primer extension oligonucleotide #21.

XX Human; cofillin 1; CFL1; gene therapy; antisense gene therapy;
 KW immunological disorder; primer extension; PCR; primer; probe; ss.

XX Homo sapiens.

XX WO200194376-A1.

PN 13-DEC-2001.

XX 11-JUN-2001; 2001WO-US018815.

XX 09-JUN-2000; 2000US-0210884P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Anastasio AE, Duda A, Kliehm SE, Koshy B, Sausker EA;

XX WPI; 2002-566437/60.

XX Novel genetic variants of human cofillin 1, CFL1 gene for studying
 PT expression, function of the gene and expressing CFL1 protein useful in
 PT identifying drugs to treat immunological disorders.

XX Claim 19; Page 14; 84pp; English.

XX The invention relates to a novel polynucleotide sequence which is a
 CC polymorphic variant of a reference sequence for the cofillin 1 (non-
 CC muscle) (CFL1) gene or its fragment, or a polymorphic variant of a
 CC reference sequence for a CFL1 cDNA or its fragment. The polynucleotide of
 CC the invention may have a use in gene therapy, and in antisense gene
 CC therapy. The polynucleotide is useful for studying the expression and

CC function of CFL1 and expressing CFL1 protein for use in screening for
 CC candidate drugs to treat diseases related to CFL1 activity. The
 CC polymorphism and haplotype data are useful for validating whether CFL1 is
 CC a suitable target for drugs to treat immunological disorders, screening
 CC for such drugs and reducing bias in clinical trials of such drugs. The
 CC present sequence represents one of a set of primer extension
 CC oligonucleotide PCR primers used in the invention to detect polymorphisms
 CC in the CFL1 gene
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
 Db 1 CTGTGGC 7

RESULT 371

ABAO3980
 ID ABAO3980 standard; DNA; 10 BP.

XX AC ABAO3980;

XX DT 19-FEB-2002 (first entry)

XX DE Human STK11 gene polymorphism detection primer SEQ ID NO:47.

XX KW Human; STK11; serine/threonine kinase 11; polymorphism; SNP;
 KW single nucleotide polymorphism; Peutz-Jeghers Syndrome; genotyping;
 KW haplotype; genetic variant; haplotyping; allele-specific oligonucleotide;
 KW primer; primer extension; ss.

XX OS Homo sapiens.

XX PN WO200187906-A2.

XX PD 22-NOV-2001.

XX PF 17-MAY-2001; 2001WO-US016045.

XX PR 17-MAY-2000; 2000US-0204697P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Bieglecki KM, Chew A, Choi JY, Nandabalan K, Sausker EA;

XX WPI; 2002-055679/07.

XX Novel genetic variants of serine/threonine kinase 11 (Peutz-Jeghers
 PT syndrome) useful in studying expression and function of the protein, and
 PT for screening candidate drugs to treat diseases e.g. Peutz-Jeghers
 PT syndrome.

XX Claim 18; Page 14; 86pp; English.

XX The present invention describes a method for haplotyping the
 CC serine/threonine kinase 11 (Peutz-Jeghers syndrome) (STK11) gene of an
 CC individual. STK11 gene sequences can be used in gene therapy. The STK11
 CC gene is useful for screening drug targeting comprising contacting STK11
 CC with a candidate agent and assaying for binding activity. STK11 is useful
 CC for improving the efficiency and reliability of several steps in the
 CC discovery and development of drugs for treating diseases associated with
 CC STK11 activity, e.g. Peutz-Jeghers syndrome. The method is useful for
 CC haplotyping the STK11 gene in an individual, which can also be used in
 CC pharmaceutical research to validate STK11 as a candidate target for, and
 CC in design of clinical trials of candidate drugs for, treating a specific
 CC condition drugs or disease predicted to be associated with STK11
 CC activity. Allele-specific oligonucleotides (ASOs) are useful as probes
 CC and primers for assaying a polymorphism in the target region. The present
 CC sequence represents a primer used for detecting STK11 gene polymorphisms,

CC which is used in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGAAGG 19
 Db 2 GCGAAGG 8

RESULT 372

ABN80659/c
 ID ABN80659 standard; DNA; 10 BP.

XX AC ABN80659;

XX DT 19-JUL-2002 (first entry)

XX DE Human P450 (cytochrome) oxidoreductase ASO primer extension oligo #47.

XX KW Human; P450 (cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;
 KW single nucleotide polymorphism; flavoprotein; enzyme;
 KW primer extension oligonucleotide; ss.

XX OS Homo sapiens.

XX PN WO200226768-A2.

XX PD 04-APR-2002.

XX PF 01-OCT-2001; 2001WO-US030877.

XX PR 29-SEP-2000; 2000US-0236449P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Kazemi A, Kliem SE, Lanz EM, Messer C, Tanguay DA;

XX WPI; 2002-394236/42.

XX New genetic variants comprising haplotypes of the P450 (cytochrome)
 PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug
 PT screening protocols for compounds targeting POR.

XX Claim 16; Page 15; 141pp; English.

XX The present invention provides the protein, gene and cDNA sequences of
 CC human P450 (cytochrome) oxidoreductase POR, and single nucleotide
 CC polymorphisms (SNPs) identified therein. The sequences can be used to
 CC haplotype the POR gene of an individual, and to establish whether POR is
 CC a suitable target for drugs to treat cancer and disorders associated with
 CC impaired protein synthesis in cells. The present sequence is an allele
 CC specific primer extension oligonucleotide for the coding sequences of the
 CC invention

XX SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
 Db 10 CTGTGGC 4

RESULT 373

ABV78586/c
 ID ABV78586 standard; cDNA; 10 BP.

XX

AC ABV78586;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Human Th2 cell preferentially expressed gene SAGE tag, SEQ ID NO:297.
 XX
 KW SAGE tag; serial analysis of gene expression; human; Th2 cell;
 KW activated T cell; T lymphocyte; immune response; expression pattern;
 KW preferential expression; immune disorder; ss.
 XX
 OS Homo sapiens.
 XX
 XX JP2002186482-A.
 PN
 XX
 PD 02-JUL-2002.
 XX
 XX 19-DEC-2000; 2000JP-00385816.
 PF
 XX 19-DEC-2000; 2000JP-00385816.
 PR
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA
 XX WPI; 2002-594261/64.
 XX
 XX Human activated Th1 and Th2 cell expression gene group, useful for the
 PT diagnosis and treatment of Th1 and Th2-related diseases.
 PT
 XX
 XX Claim 28; Page 13; 60pp; Japanese.
 PS
 XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are expressed in activated human Th1
 CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
 CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
 CC lying nearest to the polyA region of cDNAs derived from a variety of
 CC genes. These tags serve to uniquely identify each transcript and can thus
 CC be used to analyse the pattern of gene expression in particular cell
 CC types. The invention also relates to proteins encoded by the genes
 CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
 CC inhibitors of the expression of groups of genes that are expressed in
 CC either or both the two cell types. Groups of genes expressed in Th1
 CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
 CC and Th2-related disorders. Sequences ABV78561-ABV78610 are SAGE tags
 CC representing 50 genes which are more highly expressed in Th2 cells
 CC compared with Th1 cells
 CC
 XX Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 GCTGTGG 13
 DB |||||
 7 GCTGTGG 1
 RESULT 374
 ABV84371/c
 ID ABV84371 standard; cDNA; 10 BP.
 XX
 AC ABV84371;
 XX
 XX 12-DEC-2002 (first entry)
 DT
 XX Human MHC class II DR beta 1 SAGE tag #181.
 DE
 XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX
 OS Homo sapiens.
 XX
 XX JP2002209591-A.
 PN

XX 30-JUL-2002.
 PD
 XX 19-JAN-2001; 2001JP-00012328.
 PF
 XX 19-JAN-2001; 2001JP-00012328.
 PR
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA
 XX WPI; 2002-631294/68.
 DR
 XX Human chronic hepatitis C tissue expression exasperating gene group
 XX comprises 100 high-ranking genes.
 PT
 PT Claim 10; Page 14; 139pp; Japanese.
 XX
 XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84291-ABV84390 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in chronic
 CC hepatitis C liver tissue compared with normal liver tissue
 XX
 XX Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 GCGCTGT 11
 DB |||||
 7 GCGCTGT 1
 RESULT 375
 ABV84863/c
 ID ABV84863 standard; cDNA; 10 BP.
 XX
 AC ABV84863;
 XX
 XX 12-DEC-2002 (first entry)
 DT
 XX Human 3,4-catechol oestrogen UDP glucuronosyltransferase SAGE tag #673.
 DE
 XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; ss.
 XX
 OS Homo sapiens.
 XX
 XX JP2002209591-A.
 PN
 XX 30-JUL-2002.
 PD
 XX 19-JAN-2001; 2001JP-00012328.
 PF
 XX 19-JAN-2001; 2001JP-00012328.
 PR
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA

XX WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group

PT comprises 100 high-ranking genes.

XX

PS Claim 55; Page 29; 139pp; Japanese.

XX

CC The invention relates to SAGE (serial analysis of gene expression) tags

CC representing groups of genes which are differentially expressed in human

CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced

CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.

CC The SAGE tags of this invention consist of a sequence of 10 nucleotides

CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the

CC polyA region of cDNAs derived from a variety of genes. These tags serve

CC to uniquely identify each transcript and can thus be used to analyse the

CC pattern of gene expression in particular cell types. The invention also

CC relates to proteins encoded by the genes expressed in chronic hepatitis C

CC liver tissue or HCC, antibodies against these proteins, and inhibitors of

CC the expression of groups of genes that are overexpressed in chronic

CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed

CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and

CC treatment of these diseases. Such genes, inhibitors of their expression

CC or activity, and antibodies against the gene products may be used in the

CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences

CC ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly

CC expressed in chronic hepatitis C liver tissue

XX

SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCG 15

Db 7 TGTGGCG 1

RESULT 376

ABL52041/C

ID ABL52041 standard; DNA; 10 BP.

XX

AC ABL52041;

XX

XX 11-JUL-2002 (first entry)

XX

DE Human SLC18A2 preferred oligonucleotide primer SEQ ID NO:89.

XX

KW Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;

KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;

KW single nucleotide polymorphism; antiinflammatory; neuroleptic;

KW haplotyping; genotyping; respiratory inflammatory disease;

KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.

XX

OS Homo sapiens.

XX

XX WO20022652-A2.

XX

XX 21-MAR-2002.

XX

PF 17-SEP-2001; 2001WO-US042217.

XX

PR 15-SEP-2000; 2000US-0232895P.

XX

XX (GENA-) GENAISANCE PHARM INC.

PA

XX Anastasio AE, Han J, Kliem SE, Sausker EA;

XX

XX WPI; 2002-393942/42.

XX

XX Novel genetic variants of soluble carrier family 18 (vesicular

PT monoamine), member 2 gene useful for screening drugs to treat diseases

PT e.g. neuropsychiatric disorders involving monoaminergic brain systems.

XX

XX Claim 19; Page 15; 183pp; English.

XX

CC The present invention describes an isolated polynucleotide (I) having a

CC sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),

CC member 2 (SLC18A2) isogene selected from 49 isogenes with regions of a

CC sequence (SS) of 4023 bp (see ABL51954), and defined by a corresponding

CC set of polymorphisms whose locations and identities are given in the

CC specification; or a sequence (S2) complementary to (S1). (I) has

CC antiinflammatory and neuroleptic activities, and can be used in gene

CC therapy. Methods from the present invention can be used for haplotyping

CC and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known

CC as the vesicular monoamine transporter (VMAT2). (I) is useful in studying

CC the expression and function of SLC18A2, and in expressing the SLC18A2

CC protein for use in screening for candidate drugs to treat diseases

CC related to SLC18A2 activity and in studying the effect of the variation

CC on the biological activity of SLC18A2 as well as on the binding affinity

CC of candidate drugs targeting SLC18A2 for the treatment of respiratory

CC inflammatory diseases such as neuropsychiatric disorders involving

CC monoaminergic brain systems. The present sequence represents a preferred

CC oligonucleotide primer for human SLC18A2, which is given in the present

CC invention

XX

SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14

Db 9 CTGTGGC 3

RESULT 377

AAS97348/C

ID AAS97348 standard; DNA; 10 BP.

XX

AC AAS97348;

XX

XX 12-MAR-2002 (first entry)

XX

DE Human CRYBB1 gene ASO primer extension PCR primer 3' end #7.

XX

KW Human; crystallin beta B1; CRYBB1; chromosome 22q12.1; ophthalmological;

KW cataract; allele specific oligonucleotide; ASO; ss; haplotype;

KW genotyping; transgenic animal; PCR primer; primer extension.

XX

OS Homo sapiens.

XX

XX WO200185998-A1.

XX

XX 15-NOV-2001.

XX

XX 07-MAY-2001; 2001WO-US014715.

XX

XX 05-MAY-2000; 2000US-0202253P.

XX

XX (GENA-) GENAISANCE PHARM INC.

PA

XX Choi JY, Kazemi A, Kliem SE, Koshy B, Rounds E;

XX

XX WPI; 2002-062253/08.

XX

XX Novel polymorphic variants of crystallin, beta B1 useful in studying

PT expression and function of the protein, useful for screening candidate

PT drugs to treat diseases e.g. cataract.

XX

XX Claim 17; Page 13; 94pp; English.

XX

XX The invention relates to an isolated polynucleotide comprising a sequence

CC which is a polymorphic variant of a reference sequence for crystallin,

CC	beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their fragment,
CC	where the polymorphic variant comprises a CRYBB1 isoform defined by a
CC	haplotype from haplotypes 1-16 as given in the specification. Also
CC	included are a transgenic non-human animal transformed or transfected
CC	with the polymorphic variant, a computer system for storing and analysing
CC	polymorphism data for CRYBB1 gene, a genome anthology for the CRYBB1 gene
CC	which comprises the defined CRYBB1 isoforms, methods of determining an
CC	individual's haplotype or genotype as well as methods of determining an
CC	association of a particular haplotype with a disease or trait and a
CC	composition comprising at least one genotyping oligonucleotide
CC	(especially allele-specific oligonucleotides (ASO)) for detecting a
CC	polymorphism in the CRYBB1. The isoforms or haplotypes are useful for
CC	improving the efficiency and reliability of several steps in the
CC	discovery and development of drugs for treating diseases associated with
CC	CRYBB1 activity, e.g. cataract, and can also be used by the
CC	pharmaceutical research scientist to validate CRYBB1 as a candidate
CC	target for, and in design of clinical trials of candidate drugs for,
CC	treating a specific condition drugs or disease predicted to be associated
CC	with CRYBB1 activity. The ASOs are useful as probes and primers, and for
CC	assaying a polymorphism in the target region. The present sequence is the
CC	allele specific 3' end of a PCR primer used in primer extension
CC	experiment to detect polymorphisms in CRYBB1
XX	
SQ	Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
	Query Match 36.8%; Score 7; DB 1; Length 10;
	Best Local Similarity 100.0%; Pred.No. 2.le+02;
	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	6 CGCTGTG 12
Dd	
	10 CGCTGTG 4
RESULT 378	
AAD24500/C	
ID	AAD24500 standard; DNA; 10 BP.
XX	
AC	AAD24500;
XX	
DT	07-MAR-2002 (first entry)
XX	
DE	Retinoid-regulated gene amplifying degenerate PCR primer #2.
XX	
KW	Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW	cytochrome P450; prostate cancer; drug screening; PCR primer;
KW	retinoid-regulated gene; ss.
XX	
OS	Unidentified.
XX	
PN	US6306624-B1.
XX	
PD	23-OCT-2001.
XX	
PF	25-JUN-1997; 97US-00882164.
XX	
PR	21-JUN-1996; 96US-00667546.
PR	01-OCT-1996; 96US-00724466.
PR	23-JUN-1997; 97WO-CA000440.
XX	
PA	(TOOH) UNIV QUEENS KINGSTON.
XX	
PI	Petkovich PM, White JA, Beckett BR, Jones G;
XX	
DR	WPI; 2002-033254/04.
XX	
PT	New DNA fragments having promoter activity, useful in retinoid
PT	metabolism, as well as in producing retinoic acid metabolizing cytochrome
PT	P450s that are useful as targets for the treatment of certain cancers.
XX	
PS	Disclosure; Col 13; 75pp; English.
XX	
XC	The present invention relates to retinoid (e.g., retinoic acid (RA),

CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
 CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
 CC (Bla) promoter. Transcription regulatory sequences may be used to
 CC regulate expression of the endogenous, autologous or heterologous genes
 CC operably linked to the promoter, and may be incorporated into
 CC heterologous nucleic acid constructs for use in regulated expression of
 CC transgenes. Regulated expression of cyclin D1 can be used in cancer
 CC therapies, such as breast, colon or pancreatic cancers and familial
 CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
 CC may be used in the treatment of immunological disorders, such as
 CC autoimmune diseases e.g. multiple sclerosis (MS), systemic lupus
 CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
 CC arthritis. Regulated expression of genes under the control of the HBV
 CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
 CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
 CC hepatocellular carcinoma, and in the regulated expression of liver cell-
 CC specific genes. Regulated expression of the vanH gene promoter can be
 CC used in treatment of Enterococcus infection, while regulated expression
 CC of the androgen receptor gene can be used in the treatment of prostate
 CC cancer. This sequence represents a mutated promoter region used in the
 CC invention to determine the regulatory regions involved in gene
 CC expression, described in the method of the invention
 XX
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10
 DB 8 CGCGCTG 2
 |||||

RESULT 380
 AAS95992/c
 ID AAS95992 standard; DNA; 10 BP.
 XX
 AC AAS95992;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE Human CALM1 gene allele-specific oligonucleotide #101.
 XX
 KW Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;
 KW haplotyping; SCYA3; Alzheimer's disease; drug screening;
 KW calcium-dependent signal transduction; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200179218-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 09-APR-2001; 2001WO-US011509.
 XX
 PR 12-APR-2000; 2000US-0196340P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
 XX
 DR WPI; 2002-049190/06.
 XX
 XX New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in
 PT expressing CALM1 protein for use in screening for candidate drugs to
 PT treat diseases related to CALM1 activity such as Alzheimer's disease.
 XX
 PS Claim 17; Page 14; 82pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising a sequence
 CC selected from a polymorphic variant of calmodulin 1 (CALM1). The
 CC polymorphic variant comprises an CALM1 isogene defined by a haplotype

CC selected from haplotypes 1-21 given in the specification. The
 CC polymorphisms are useful for studying the biological function of CALM1 as
 CC well as in identifying drugs targeting this protein for the treatment of
 CC a disorder related to its abnormal expression or function. The
 CC polymorphic variants may also be used in screening for compounds
 CC targeting CALM1 to treat a specific condition or disease predicted to be
 CC associated with CALM1 activity. Establishing CALM1 haplotype or haplotype
 CC pair of an individual is useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with SCYA3 activity, e.g. Alzheimer's
 CC disease and diseases involving defects in calcium-dependent signal
 CC transduction. Haplotyping the CALM1 gene in an individual is also useful
 CC in the design of clinical trials of candidate drugs for treating a
 CC specific condition or disease predicted to be associated with CALM1
 CC activity. AAS95892-AAS96018 represent human CALM1 allele- specific
 CC oligonucleotides and PCR primers of the invention
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
 DB 10 TGGCGAA 4
 |||||

RESULT 381
 ADH22188/c
 ID ADH22188 standard; DNA; 10 BP.
 XX
 AC ADH22188;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Primer extension DNA oligo for detecting CHRNG haplotypes SeqID 57.
 XX
 KW human; primer; PCR; ss; cholinergic receptor, nicotinic, gamma; CHRNG;
 KW haplotype; drug discovery; acetylcholine receptor; AChR;
 KW myasthenia gravis; screening assay.
 XX
 OS Homo sapiens.
 XX
 FN WO200222643-A1.
 XX
 PD 21-MAR-2002.
 XX
 PF 17-SEP-2001; 2001WO-US029206.
 XX
 PR 15-SEP-2000; 2000US-0232807P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Gilson CR, Koshy B, Kliem SE, Sausker EA;
 XX
 DR WPI; 2002-371968/40.
 XX
 XX New genetic variants of cholinergic receptor, nicotinic, gamma
 PT polypeptide, CHRNG gene useful for therapeutic purposes and for
 PT expressing CHRNG protein useful in identifying drugs to treat myasthenia
 PT gravis.
 XX
 PS Claim 18; SEQ ID NO 57; 107pp; English.
 XX
 XX This invention relates to novel genetic markers and variants of the gene
 CC encoding the cholinergic receptor, nicotinic, gamma polypeptide (CHRNG),
 CC located on chromosome 2q33-p34. Specifically, it refers to a set of
 CC haplotypes in the CHRNG gene, which are useful for improving the
 CC efficiency and output of the drug discovery process by the identification
 CC of drugs that can target the CHRNG protein and treat disorders associated
 CC with its abnormal expression or function. The CHRNG protein is the gamma
 CC subunit of the acetylcholine receptor (AChR), and autoantibodies directed

CC against the embryonic form of AChR play an important role in the
 CC pathogenesis of neonatal myasthenia gravis. As such, the present
 CC invention describes a method for identifying an association between a
 CC trait (such as a clinical response to a drug that targets CHRN) and a
 CC haplotype or haplotype pair of the CHRN gene. Furthermore, it is useful
 CC in screening assays, for the development of diagnostic tests and for
 CC therapeutic treatments of myasthenia gravis using gene therapy. This
 CC oligonucleotide sequence is a human primer extension DNA oligo used for
 CC detecting the CHRN haplotypes of the invention.

XX
 SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTGG 13
 |||||
 Db 10 GCTGTGG 4

RESULT 382

ACC41737
 ID ACC41737 standard; DNA; 10 BP.

XX
 AC ACC41737;

XX
 DT 21-MAY-2003 (first entry)

XX Zinc finger protein DNA-binding domain target sequence SEQ ID NO:284.

DE Zinc finger domain; zinc finger; zinc finger binding domain; probe;
 KW chimeric nucleic acid; library; PCR primer; ss.

XX Synthetic.

XX WO2003016571-A1.

XX
 PD 27-FEB-2003.

XX
 PF 17-AUG-2002; 2002WO-KR001560.

XX
 PR 17-AUG-2001; 2001US-0313402P.

XX
 PR 22-APR-2002; 2002US-0374355P.

XX (TOOL-) TOOLGEN INC.

XX Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;

XX WPI; 2003-268344/26.

XX New library comprising polypeptides having zinc finger domains, useful
 for producing chimeric nucleic acids.

XX Claim 40; Page 106; 234pp; English.

XX The present invention describes a library comprising polypeptides. Each
 CC polypeptide comprises a first or second zinc finger domain. The domains
 CC of each polypeptide are identical to a zinc finger domain from a
 CC naturally occurring protein and either do not occur in the same naturally
 CC occurring protein or occur in the same naturally occurring protein in a
 CC different configuration than in the polypeptide. The domains vary among
 CC polypeptides. Also described: (1) producing chimeric nucleic acids; (2)
 CC generating an artificial zinc finger polypeptide that specifically binds
 CC to a target DNA site; and (3) identifying a nucleic acid encoding a zinc
 CC finger polypeptide that specifically recognises a target DNA site. The
 CC library can be used for producing chimeric nucleic acids. ACC41551 to
 CC ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid
 CC sequences given in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTGG 7
 |||||
 Db 3 GGTCTGG 9

RESULT 383

ABT14391/C
 ID ABT14391 standard; DNA; 10 BP.

XX
 AC ABT14391;

XX
 DT 20-FEB-2003 (first entry)

XX Nucleic acid PCR amplification method-related RAPD PCR primer #161.
 XX Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
 KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.

XX Unidentified.

XX WO200281743-A2.

XX
 PD 17-OCT-2002.

XX
 PF 28-MAR-2002; 2002WO-GB001489.

XX
 PR 02-APR-2001; 2001GB-00008182.

XX (HAMI/) HAMILL B.

XX Hamill B;

XX WPI; 2003-075484/07.

XX Amplification of nucleotide sequences from polynucleotides by chain
 PT extension of oligonucleotide primers, comprises 2 oligonucleotides in
 PT solution, 2 attached to supports and both share complementary sequences.

XX Disclosure; Fig 17; 60pp; English.

XX The invention comprises a method for the PCR amplification of nucleic
 CC acids. The method involves a set of primers, where two of the primers are
 CC in solution and at least two other primers are attached to a solid
 CC support. The method of the invention can be used for the analysis of a
 CC nucleic acid or a mixture of nucleic acids, including: single-stranded
 CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The
 CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)
 CC PCR primer of the invention

XX Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTGG 13
 |||||
 Db 7 GCTGTGG 1

RESULT 384

ADA62122
 ID ADA62122 standard; DNA; 10 BP.

XX
 AC ADA62122;

XX
 DT 20-NOV-2003 (first entry)

XX Zinc finger target sequence DNA #77.

KW ds; target sequence; zinc finger protein;
 KW multi-finger zinc finger protein; improved affinity;
 KW improved specificity; enhanced biological activity.

XX Synthetic.

OS US2003068675-A1.

PN XX

XX US2003068675-A1.

PD 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

XX 24-MAR-1999; 99US-0126238P.

XX 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

PA XX

XX Liu Q;

PI XX

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus

PT and C-terminus that bind to subsites in 3' to 5' direction, in a target

PT site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 14; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The

CC method is useful for designing a zinc finger protein. The method provides

CC multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The

CC present sequence represents a zinc finger protein DNA target sequence.

XX Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGGAG 18

DB 4 GCGGAAG 10

RESULT 385

ADA63307

ID ADA63307 standard; DNA; 10 BP.

XX ADA63307;

AC ADA63307;

XX 20-NOV-2003 (first entry)

DT Zinc finger target sequence DNA #329.

DE ds; target sequence; zinc finger protein;

XX multi-finger zinc finger protein; improved affinity;

KW improved specificity; enhanced biological activity.

XX Synthetic.

OS US2003068675-A1.

PN XX

XX US2003068675-A1.

PD 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

XX 24-MAR-1999; 99US-0126238P.

XX 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

PA XX

XX Liu Q;

PI XX

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus

PT and C-terminus that bind to subsites in 3' to 5' direction, in a target

PT site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 14; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The

CC method is useful for designing a zinc finger protein. The method provides

CC multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The

CC present sequence represents a zinc finger protein DNA target sequence.

XX Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGGAG 18

DB 4 GCGGAAG 10

RESULT 385

ADA63307

ID ADA63307 standard; DNA; 10 BP.

XX ADA63307;

AC ADA63307;

XX 20-NOV-2003 (first entry)

DT Zinc finger target sequence DNA #329.

DE ds; target sequence; zinc finger protein;

XX multi-finger zinc finger protein; improved affinity;

KW improved specificity; enhanced biological activity.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

XX Liu Q;

PI XX

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus

PT and C-terminus that bind to subsites in 3' to 5' direction, in a target

PT site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 18; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The

CC method is useful for designing a zinc finger protein. The method provides

CC multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The

CC present sequence represents a zinc finger protein DNA target sequence.

XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13

DB 4 GCTGTGG 10

RESULT 386

ADA63696

ID ADA63696 standard; DNA; 10 BP.

XX ADA63696;

AC ADA63696;

XX 20-NOV-2003 (first entry)

DT Zinc finger target sequence DNA #460.

DE ds; target sequence; zinc finger protein;

KW multi-finger zinc finger protein; improved affinity;

KW improved specificity; enhanced biological activity.

XX Synthetic.

OS US2003068675-A1.

PN 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

XX 24-MAR-1999; 99US-0126238P.

PR 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

PA XX

XX Liu Q;

PI XX

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus

PT and C-terminus that bind to subsites in 3' to 5' direction, in a target

PT site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 20; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The

CC method is useful for designing a zinc finger protein. The method provides

CC multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The

CC present sequence represents a zinc finger protein DNA target sequence.

XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13

DB 4 GCTGTGG 10

RESULT 386

ADA63696

ID ADA63696 standard; DNA; 10 BP.

XX ADA63696;

AC ADA63696;

XX 20-NOV-2003 (first entry)

DT Zinc finger target sequence DNA #460.

DE ds; target sequence; zinc finger protein;

KW multi-finger zinc finger protein; improved affinity;

KW improved specificity; enhanced biological activity.

XX Synthetic.

OS US2003068675-A1.

PN 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

XX 24-MAR-1999; 99US-0126238P.

PR 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

PA XX

XX Liu Q;

PI XX

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus

PT and C-terminus that bind to subsites in 3' to 5' direction, in a target

PT site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 20; 34pp; English.

KW improved specificity; enhanced biological activity.

XX Synthetic.

XX US2003068675-A1.

XX 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

XX 24-MAR-1999; 99US-0126238P.

XX 24-MAR-1999; 99US-0126239P.

XX 30-JUL-1999; 99US-0146595P.

XX 30-JUL-1999; 99US-0146615P.

XX 23-MAR-2000; 2000US-00535008.

XX 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

XX Liu Q;

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus

XX and C-terminus that bind to subsites in 3' to 5' direction, in a target

XX site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 20; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The

XX method is useful for designing a zinc finger protein. The method provides

XX multi-finger zinc finger proteins with improved affinity and specificity

XX for their target sequences, as well as enhanced biological activity. The

XX present sequence represents a zinc finger protein DNA target sequence.

XX Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGGC 7

Db 3 GGTCGGC 9

RESULT 390

ADB81067

ID ADB81067 standard; DNA; 10 BP.

XX ADB81067;

XX 04-DEC-2003 (first entry)

XX LINE retro-position related SART1 oligo, SEQ ID No 27.

XX RNA retro-position; 3' UTR; LINE; APE domain; retro-transposition;

XX endonuclease domain; chromosome; gene therapy; gene transfer; ss.

XX Unidentified.

XX WO2003064644-A1.

XX 07-AUG-2003.

XX 26-NOV-2002; 2002WO-JP012317.

XX 31-JAN-2002; 2002JP-00024226.

KW improved specificity; enhanced biological activity.

XX Synthetic.

XX US2003068675-A1.

XX 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

XX 24-MAR-1999; 99US-0126238P.

XX 24-MAR-1999; 99US-0126239P.

XX 30-JUL-1999; 99US-0146595P.

XX 30-JUL-1999; 99US-0146615P.

XX 23-MAR-2000; 2000US-00535008.

XX 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

XX Liu Q;

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus

XX and C-terminus that bind to subsites in 3' to 5' direction, in a target

XX site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 20; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The

XX method is useful for designing a zinc finger protein. The method provides

XX multi-finger zinc finger proteins with improved affinity and specificity

XX for their target sequences, as well as enhanced biological activity. The

XX present sequence represents a zinc finger protein DNA target sequence.

XX Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGGC 7

Db 3 GGTCGGC 9

RESULT 390

ADB81067

ID ADB81067 standard; DNA; 10 BP.

XX ADB81067;

XX 04-DEC-2003 (first entry)

XX LINE retro-position related SART1 oligo, SEQ ID No 27.

XX RNA retro-position; 3' UTR; LINE; APE domain; retro-transposition;

XX endonuclease domain; chromosome; gene therapy; gene transfer; ss.

XX Unidentified.

XX WO2003064644-A1.

XX 07-AUG-2003.

XX 26-NOV-2002; 2002WO-JP012317.

XX 31-JAN-2002; 2002JP-00024226.

DR WPI; 2003-627609/59.

XX LINE retro-position by trans-complementation for transferring targeted,
PT specific gene or nucleic acid of e.g. endonuclease domain via
PT substitution to chromosome using virus vector, applicable in gene
PT therapy.

XX Example 5; Fig 3; 96pp; Japanese.

XX The invention relates to a novel RNA retro-position comprising the
CC transcription of an RNA containing a 3' UTR fragment of a LINE in cells;
CC and trans-positioning the ORF protein of such LINE after expressing from
CC other than the RNA. The invention further comprises a similar method in
CC which the transcription of an RNA containing a 3' UTR fragment of an APE
CC domain-carrying type site-specific LINE in cells, and expressing the ORF
CC protein of the LINE in such cells; or transcription of an RNA containing
CC 3' UTR fragment of a LINE in cells, and expressing ORF protein in such
CC cells thereby modifying a retro-transposition target site of a LINE by
CC substituting the endonuclease domain of the LINE by that of another LINE
CC via ORF protein of such LINE. The invention also includes a retro-
CC transposition vector with RNA encoding the 3' UTR fragment of a LINE but
CC not expressing the encoded ORF of the LINE; a vector encoding a protein in
CC for substitution of the endonuclease domain of an encoded ORF protein in
CC the site-specific LINE by the endonuclease domain of the encoded ORF
CC protein in another LINE; and a kit for gene transfer through retro-
CC transposition of an RNA. The method is useful for transferring targeted,
CC specific genes or nucleic acids of an endonuclease domain via
CC substitution to a chromosome using a virus vector, which is applicable in
CC gene therapy. The retro-transposition in the host is highly efficient by
CC targeting specifically at LINE, and with little damage to the host due to
CC the gene transfer. This polynucleotide sequence represents an
CC oligonucleotide used in the exemplification of the invention.

XX Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17

Db 1 TGGCGAA 7

RESULT 391

ADE14136/c

ID ADE14136 standard; DNA; 10 BP.

XX ADE14136;

XX 29-JAN-2004 (first entry)

XX Optineurin promoter motif, repeat element or regulatory region #245.

XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;

XX SNP; glaucoma; progressive ocular hypertensive disorder;

XX Glaucoma related disorder; motif; repeat element; regulatory region.

XX Homo sapiens.

XX US2003190617-A1.

XX 09-OCT-2003.

XX 06-MAR-2002; 2002US-00091281.

XX 06-MAR-2002; 2002US-00091281.

XX (SIEE/) SI E.

XX (RAYN/) RAYMOND V.

XX (MORI/) MORISSETTE J.

XX Raymond V, Morissette J, Si E;


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XX WPI; 2003-864168/80.
XX
XX New nucleic acid sequences of the optineurin gene are useful to detect
XX polymorphisms particularly single nucleotide polymorphisms in the
XX optineurin promoter to diagnose, prognose and treat glaucoma and related
XX disorders.
XX
XX Claim 11; SEQ ID NO 247; 159pp; English.
XX
XX The invention relates to an isolated nucleic acid (N1) comprising at
XX least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX promoter appearing as ADEI3890. Also included are the optineurin promoter
XX operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX detecting a single nucleotide polymorphism (SNP) in the optineurin
XX promoter, a host cell comprising the promoter operably linked to a
XX heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX in a promoter region of the optineurin gene, associated with a glaucoma
XX phenotype), detecting a SNP sequence variation in a sample containing
XX DNA, detecting the presence of an optineurin promoter sequence variation
XX in a sample containing DNA, determining the presence or increased
XX susceptibility to glaucoma or to a progressive ocular hypertensive
XX disorder resulting in loss of visual field in a patient (or the severity
XX or progression of glaucoma in a patient, comprising providing
XX amplification reaction primers that direct amplification of a selected
XX nucleic acid region containing the variation within the optineurin
XX promoter and amplifying the DNA) and detecting a polymorphism (comprising
XX obtaining a sample containing human genomic DNA, providing a nucleic acid
XX capable of detecting a SNP located within an optineurin promoter, and
XX detecting the polymorphism). The invention is used to diagnose and
XX prognose glaucoma and also to treat glaucoma related disorders. The
XX present sequence is an optineurin promoter motif, repeat element or
XX putative regulatory region.
XX
XX Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 36.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 11 TGGCGAA 17
XX Db 9 TGGCGAA 3
XX
XX RESULT 392
XX ADM22181
XX ID ADM22181 standard; DNA; 10 BP.
XX AC
XX AD 20-MAY-2004 (first entry)
XX DT
XX DE Synthetic zinc finger protein target DNA #447.
XX KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX OS Unidentified.
XX XX US2003104526-A1.
XX PN
XX PD 05-JUN-2003.
XX PF 20-NOV-2001; 2001US-00989994.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126239P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX
XX PA (LIUQ/) LIU Q.
XX PI Liu Q;
XX WPI; 2003-843091/78.
XX
XX New zinc finger protein used for recognizing triplet target subsites
XX having nucleotide G in 5'-most position of subsite, that has been
XX optimized with respect to location of subsite within target site.
XX
XX Example 6; SEQ ID NO 1654; 48pp; English.
XX
XX The invention describes a new zinc finger protein that binds to a target
XX site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
XX ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
XX comprises, in the 3' to 5' direction, first (S1), second (S2) and third
XX (S3) target subsites. The zinc finger proteins can be used for
XX recognizing triplet target subsites having the nucleotide G in the 5'-
XX most position of the subsite, that has been optimised with respect to the
XX location of the subsite within the target site. This sequence represents
XX the target polynucleotide of a synthetic zinc finger protein of the
XX invention.
XX
XX Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 36.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGTCTGG 7
XX Db 3 GGTCTGG 9
XX
XX RESULT 393
XX ADM22194
XX ID ADM22194 standard; DNA; 10 BP.
XX AC
XX AD 20-MAY-2004 (first entry)
XX DT
XX DE Synthetic zinc finger protein target DNA #460.
XX KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX OS Unidentified.
XX XX US2003104526-A1.
XX PN
XX PD 05-JUN-2003.
XX PF 20-NOV-2001; 2001US-00989994.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126239P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX
XX PA (LIUQ/) LIU Q.
XX PI Liu Q;
XX WPI; 2003-843091/78.
XX
XX New zinc finger protein used for recognizing triplet target subsites
XX having nucleotide G in 5'-most position of subsite, that has been
XX optimized with respect to location of subsite within target site.
XX
XX Example 6; SEQ ID NO 1667; 48pp; English.
XX
XX

```

CC The invention describes a new zinc finger protein that binds to a target
 CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
 CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
 CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
 CC (S3) target subsites. The zinc finger proteins can be used for
 CC recognising triplet target subsites having the nucleotide G in the 5'-
 CC most position of the subsite, that has been optimised with respect to the
 CC location of the subsite within the target site. This sequence represents
 CC the target polynucleotide of a synthetic zinc finger protein of the
 CC invention.

XX
 SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7
 |||||
 Db 3 GGTCGCG 9

RESULT 394

ADM20326

ID ADM20326 standard; DNA; 10 BP.

XX
 AC ADM20326;XX
 DT 20-MAY-2004 (first entry)

XX Synthetic zinc finger protein target DNA #77.

XX zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.

XX Unidentified.

XX US2003104526-A1.

XX
 PD 05-JUN-2003.XX
 PF 20-NOV-2001; 2001US-00989994.XX
 PR 24-MAR-1999; 99US-0126238P.XX
 PR 24-MAR-1999; 99US-0126238P.XX
 PR 30-JUL-1999; 99US-0146595P.XX
 PR 30-JUL-1999; 99US-0146615P.XX
 PR 23-MAR-2000; 2000US-00535008.XX
 PR 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

XX
 PI Liu Q;XX
 DR WPI; 2003-843091/78.

XX New zinc finger protein used for recognizing triplet target subsites
 PT having nucleotide G in 5'-most position of subsite, that has been
 PT optimized with respect to location of subsite within target site.

XX Example 6; SEQ ID NO 93; 48pp; English.

XX The invention describes a new zinc finger protein that binds to a target
 CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
 CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
 CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
 CC (S3) target subsites. The zinc finger proteins can be used for
 CC recognising triplet target subsites having the nucleotide G in the 5'-
 CC most position of the subsite, that has been optimised with respect to the
 CC location of the subsite within the target site. This sequence represents
 CC the target polynucleotide of a synthetic zinc finger protein of the
 CC invention.

XX Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCGAAG 18
 |||||
 Db 4 GGCGAAG 10

RESULT 395

ADM20325

ID ADM20325 standard; DNA; 10 BP.

XX
 AC ADM20325;XX
 DT 20-MAY-2004 (first entry)

XX Synthetic zinc finger protein target DNA #76.

XX zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.

XX Unidentified.

XX US2003104526-A1.

XX
 PD 05-JUN-2003.XX
 PF 20-NOV-2001; 2001US-00989994.XX
 PR 24-MAR-1999; 99US-0126238P.XX
 PR 24-MAR-1999; 99US-0126238P.XX
 PR 30-JUL-1999; 99US-0146595P.XX
 PR 30-JUL-1999; 99US-0146615P.XX
 PR 23-MAR-2000; 2000US-00535008.XX
 PR 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

XX
 PI Liu Q;XX
 DR WPI; 2003-843091/78.

XX New zinc finger protein used for recognizing triplet target subsites
 PT having nucleotide G in 5'-most position of subsite, that has been
 PT optimized with respect to location of subsite within target site.

XX Example 6; SEQ ID NO 92; 48pp; English.

XX The invention describes a new zinc finger protein that binds to a target
 CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
 CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
 CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
 CC (S3) target subsites. The zinc finger proteins can be used for
 CC recognising triplet target subsites having the nucleotide G in the 5'-
 CC most position of the subsite, that has been optimised with respect to the
 CC location of the subsite within the target site. This sequence represents
 CC the target polynucleotide of a synthetic zinc finger protein of the
 CC invention.

XX Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCGAAG 18
 |||||
 Db 4 GGCGAAG 10

RESULT 396

ADM21511

```

ID ADM21511 standard; DNA; 10 BP.
XX AC ADM21511;
XX DT 20-MAY-2004 (first entry)
XX DE Synthetic zinc finger protein target DNA #329.
XX KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX OS Unidentified.
XX PN US2003104526-A1.
XX PD 05-JUN-2003.
XX PF 20-NOV-2001; 2001US-00989994.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126239P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (LIUQ/) LIU Q.
XX PI Liu Q;
XX PF WPI; 2003-843091/78.
XX PR New zinc finger protein used for recognizing triplet target subsites
PT having nucleotide G in 5'-most position of subsite, that has been
PT optimized with respect to location of subsite within target site.
XX PS Example 6; SEQ ID NO 1278; 48pp; English.
XX PX The invention describes a new zinc finger protein that binds to a target
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC (S3) target subsites. The zinc finger proteins can be used for
CC recognising triplet target subsites having the nucleotide G in the 5'-
CC most position of the subsite, that has been optimised with respect to the
CC location of the subsite within the target site. This sequence represents
CC the target polynucleotide of a synthetic zinc finger protein of the
CC invention.
XX SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
DB 4 GCTGTGG 10

RESULT 397
ADM22180
ID ADM22180 standard; DNA; 10 BP.
XX AC ADM22180;
XX DT 20-MAY-2004 (first entry)
XX DE Synthetic zinc finger protein target DNA #446.
XX KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX OS Unidentified.
XX PN ADM22180 standard; DNA; 10 BP.
XX PD 05-JUN-2003.
XX PF 20-NOV-2001; 2001US-00989994.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126239P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (LIUQ/) LIU Q.
XX PI Liu Q;
XX PF WPI; 2003-843091/78.
XX PR New zinc finger protein used for recognizing triplet target subsites
PT having nucleotide G in 5'-most position of subsite, that has been
PT optimized with respect to location of subsite within target site.
XX PS Example 6; SEQ ID NO 1278; 48pp; English.
XX PX The invention describes a new zinc finger protein that binds to a target
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC (S3) target subsites. The zinc finger proteins can be used for
CC recognising triplet target subsites having the nucleotide G in the 5'-
CC most position of the subsite, that has been optimised with respect to the
CC location of the subsite within the target site. This sequence represents
CC the target polynucleotide of a synthetic zinc finger protein of the
CC invention.
XX SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
DB 4 GCTGTGG 10

RESULT 397
ADM22180
ID ADM22180 standard; DNA; 10 BP.
XX AC ADM22180;
XX DT 20-MAY-2004 (first entry)
XX DE Synthetic zinc finger protein target DNA #446.
XX KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX OS Unidentified.
XX PN ADM22180 standard; DNA; 10 BP.
XX PD 05-JUN-2003.
XX PF 20-NOV-2001; 2001US-00989994.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126239P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (LIUQ/) LIU Q.
XX PI Liu Q;
XX PF WPI; 2003-843091/78.
XX PR New zinc finger protein used for recognizing triplet target subsites
PT having nucleotide G in 5'-most position of subsite, that has been
PT optimized with respect to location of subsite within target site.
XX PS Example 6; SEQ ID NO 1278; 48pp; English.
XX PX The invention describes a new zinc finger protein that binds to a target
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC (S3) target subsites. The zinc finger proteins can be used for
CC recognising triplet target subsites having the nucleotide G in the 5'-
CC most position of the subsite, that has been optimised with respect to the
CC location of the subsite within the target site. This sequence represents
CC the target polynucleotide of a synthetic zinc finger protein of the
CC invention.
XX SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
DB 4 GCTGTGG 10

RESULT 398
ADH57701/c
ID ADH57701 standard; DNA; 10 BP.
XX AC ADH57701;
XX DT 25-MAR-2004 (first entry)
XX DE Extendable oligo E190 for DNA sequencing and PCR amplification.
XX KW ss; primer library; extendable oligo; EO; ligation chain reaction; LCR;
XX KW rolling circle amplification; strand displacement amplification;
XX KW isothermal DNA amplification; biotechnology; agriculture;
XX KW medical research; 2,4 diaminopurine nucleotide analogue; PCR; primer.
XX OS Synthetic.
XX PN WO2003093500-A1.
XX PR 13-NOV-2003.
XX PF 24-DEC-2002; 2002WO-AU001763.
XX PR 01-MAY-2002; 2002AU-00002045.
XX PA (NUCL-) NUCLEICS PTY LTD.

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PN US2003104526-A1.
XX PD 05-JUN-2003.
XX PF 20-NOV-2001; 2001US-00989994.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126239P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (LIUQ/) LIU Q.
XX PI Liu Q;
XX PF WPI; 2003-843091/78.
XX PR New zinc finger protein used for recognizing triplet target subsites
PT having nucleotide G in 5'-most position of subsite, that has been
PT optimized with respect to location of subsite within target site.
XX PS Example 6; SEQ ID NO 1653; 48pp; English.
XX PX The invention describes a new zinc finger protein that binds to a target
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC (S3) target subsites. The zinc finger proteins can be used for
CC recognising triplet target subsites having the nucleotide G in the 5'-
CC most position of the subsite, that has been optimised with respect to the
CC location of the subsite within the target site. This sequence represents
CC the target polynucleotide of a synthetic zinc finger protein of the
CC invention.
XX SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTGG 7
DB 3 GGTCTGG 9

RESULT 398
ADH57701/c
ID ADH57701 standard; DNA; 10 BP.
XX AC ADH57701;
XX DT 25-MAR-2004 (first entry)
XX DE Extendable oligo E190 for DNA sequencing and PCR amplification.
XX KW ss; primer library; extendable oligo; EO; ligation chain reaction; LCR;
XX KW rolling circle amplification; strand displacement amplification;
XX KW isothermal DNA amplification; biotechnology; agriculture;
XX KW medical research; 2,4 diaminopurine nucleotide analogue; PCR; primer.
XX OS Synthetic.
XX PN WO2003093500-A1.
XX PR 13-NOV-2003.
XX PF 24-DEC-2002; 2002WO-AU001763.
XX PR 01-MAY-2002; 2002AU-00002045.
XX PA (NUCL-) NUCLEICS PTY LTD.

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XX
PI Tillet D, Thomas T;
XX
XX WPI; 2004-053046/05.
XX
PT Increasing the affinity of an extendable oligonucleotide (EO) for a
PT target nucleic acid, for providing primers having improved specificity,
PT comprises hybridization of the EO to a template oligonucleotide (TO) and
PT extension of the EO.
XX
XX Example 9; Page 41; 85pp; English.
XX
XX This invention relates to a novel method for the optimisation of primer
CC libraries. Specifically, it refers to increasing the affinity of short
CC oligonucleotide primers, also known as extendable oligos (EOs), for their
CC template sequences. The present invention describes improved methods for
CC sequencing and the linear and exponential amplification of DNA that can
CC be useful for PCR, RT-PCR, ligation chain reaction (LCR), rolling circle
CC amplification, strand displacement amplification and isothermal DNA
CC amplification. Accordingly, these extendable oligos with improved
CC specificity and affinity are particularly important in fields ranging
CC from biotechnology and agriculture to medical research. This
CC oligonucleotide sequence is an extendable oligonucleotide that includes
CC an adenine replacement 2,4 diaminopurine nucleotide analogue in the catch
CC region, and is useful for both DNA sequencing reactions and PCR
CC amplification in an exemplification of the invention.
XX
SQ Sequence 10 BP; 0 A; 5 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGAGG 19
DB 10 GCGAGG 4

RESULT 399
ADII3679
ID ADII3679 standard; DNA; 10 BP.
XX
AC ADII3679;
XX
DT 22-APR-2004 (first entry)
XX
DE Extracellular tumour endothelial marker standard tag SEQ ID NO:54.
XX
KW tumour endothelial marker; TEM; endothelial cell regulation;
KW neangiogenesis inhibition; neangiogenesis screening;
KW neangiogenesis promotion; neangiogenesis; tumour; wound healing;
KW cytostatic; vulnery; human; standard tag; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
PN WO2004005883-A2.
XX
PD 15-JAN-2004.
XX
XX 02-JUL-2003; 2003WO-US016250.
XX
PR 02-JUL-2002; 2002US-0393023P.
PR 01-APR-2003; 2003US-0458964P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
XX St Croix B, Kinzler KW, Vogelstein B;
PI WPI; 2004-142995/14.
XX
XX Use of tumor endothelial marker proteins for inhibiting neangiogenesis,
PT screening for neangiogenesis, promoting neangiogenesis, identifying

PT candidate drugs for treating tumors or promoting wound healing.
XX
XX Disclosure; SEQ ID NO 54; 113pp; English.
XX
CC The present invention describes the use of tumour endothelial marker
CC (TEM) proteins for identifying a ligand involved in endothelial cell
CC regulation, inhibiting neangiogenesis, screening for neangiogenesis,
CC promoting neangiogenesis, identifying candidate drugs for treating
CC tumours or promoting wound healing or identifying endothelial cells. Also
CC described: (1) identification of a ligand involved in endothelial cell
CC regulation; (2) inhibiting neangiogenesis; (3) promoting neangiogenesis
CC in a patient; (4) screening for neangiogenesis in a patient; (5)
CC identify candidate drugs for treating tumours or promoting wound healing;
CC and (6) identifying endothelial cells. TEM proteins have cytostatic and
CC vulnerary activities. The TEM proteins are useful for identifying a
CC ligand involved in endothelial cell regulation, inhibiting
CC neangiogenesis, screening for neangiogenesis, promoting tumours or
CC neangiogenesis, identifying candidate drugs for treating tumours or
CC promoting wound healing or identifying endothelial cells. The present
CC sequence represents an extracellular tumour endothelial marker standard
CC tag oligonucleotide, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
DB 1 GCTGTGG 7

RESULT 400
ADL70389/c
ID ADL70389 standard; DNA; 10 BP.
XX
XX AC ADL70389;
XX
XX 20-MAY-2004 (first entry)
XX
DE Enhancer sequence for nucleic acid detection by tail cleavage assay.
XX
KW Nucleic acid detection; Tail cleavage assay; ss.
XX
OS Synthetic.
XX
PN WO2004018626-A2.
XX
PD 04-MAR-2004.
XX
XX 20-AUG-2003; 2003WO-US026133.
XX
XX 21-AUG-2002; 2002US-0405642P.
XX
XX (EPOC-) EPOCH BIOSCIENCES INC.
XX
XX Kutayavin IV, Milesi D, Hoekstra M;
PI WPI; 2004-248069/23.
XX
XX Detecting target nucleic acid in sample, comprises contacting sample with
PT apurinic/aprimidinic site probe and endonuclease, incubating mixture to
PT cleave phosphodiester bond and detecting reporter group.
XX
XX Example 3; Page 34; 61pp; English.
XX
XX The present invention provides a novel method for detection and/or
CC genotyping of nucleic acids that utilises the specificity of an abasic
CC (apurinic/aprimidinic) (AP) endonuclease. An AP site probe is used that
CC comprises an oligonucleotide which hybridises to a target nucleic acid
CC and a functional tail composed of a detectable reporter group and an AP

CC endonuclease cleavage site. The functional tail is attached through a
 CC phosphodiester bond of a phosphate group to the 3' terminal nucleotide of
 CC the oligonucleotide, and the reporter group is not detected when the
 CC functional tail is attached to the oligonucleotide. Methods of detecting
 CC a target nucleic acid involve contacting the sample with an AP site probe
 CC and an AP endonuclease, incubating under conditions that allow the AP
 CC endonuclease to cleave the phosphodiester bond, and detecting the
 CC reporter group on the cleaved functional tail. The method is exquisitely
 CC sensitive to the detection of single base pair mismatches between the
 CC probe and target because the AP endonuclease preferentially cleaves the
 CC phosphodiester bond when the oligonucleotide is hybridised with a fully
 CC complementary nucleic acid sequence. The present sequence is that of an
 CC enhancer sequence, which was used in an example from the invention
 CC illustrating the substrate specificity of *Escherichia coli* endonuclease
 CC IV. The enhancer hybridises to the 5' end of a target nucleic acid
 CC ADL70387 and is used to support the tail cleavage reaction.
 CC
 SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCG 15
 Db 8 TGTGGCG 2
 |||||

RESULT 401
 ADN36844/c
 ID ADN36844 standard; RNA; 10 BP.

AC ADN36844;

DT 15-JUL-2004 (first entry)

DE West Nile virus detection-related oligonucleotide probe SeqID166.

XX hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.

OS West Nile virus.

XX Key Location/Qualifiers
 FH modified_base 1..10
 FT /*tag= a
 FT /mod_base= OTHER

FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
 XX

PN WO2004036190-A2.

XX

PD 29-APR-2004.

XX 10-OCT-2003; 2003WO-US033639.

XX 16-OCT-2002; 2002US-0418891P.

PR 25-NOV-2002; 2002US-0429006P.

PR 24-FEB-2003; 2003US-0449810P.

XX (GENP-) GEN-PROBE INC.

PA Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

PI WPI; 2004-389590/36.

XX New hybridization assay probe comprising target-complementary sequence of

PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX Claim 43; SEQ ID NO 166; 135pp; English.

XX This invention relates to a novel hybridisation assay probe, for

CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.
 XX

SQ Sequence 10 BP; 0 A; 4 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGAAGG 19
 Db 10 GCGAAGG 4
 |||||

RESULT 402

ADR16068

ID ADR16068 standard; DNA; 10 BP.

AC ADR16068;

DT 04-NOV-2004 (first entry)

XX Loquat crown-gall disease resistance gene-specific PCR primer #1.

DE loquat; crown-gall disease resistance gene; marker;

KW crown-gall disease resistant seedling; PCR; primer; ss.

XX Eriobotrya japonica.

XX JP2004229571-A.

XX 19-AUG-2004.

XX 30-JAN-2003; 2003JP-00022874.

XX 30-JAN-2003; 2003JP-00022874.

XX (NAGA-) NAGASAKI KEN PREFECTURE.

XX WPI; 2004-586543/57.

XX Novel loquat crown-gall disease resistant gene, useful as a marker for
 PT identifying loquat plant resistant to crown-gall disease.

XX Claim 3; SEQ ID NO 3; 9pp; Japanese.

XX The invention comprises two DNA sequences of a loquat crown-gall disease
 CC resistance gene, the invention also comprises PCR primers that are
 CC specific to this gene. The loquat crown-gall disease resistance gene DNA
 CC sequences of the invention are useful as a marker for identifying loquat
 CC crown-gall disease resistant seedlings. The present DNA sequence
 CC represents a PCR primer that is specific for the loquat crown-gall
 CC disease resistance gene of the invention.
 XX

SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGAAGG 19
 Db 2 GCGAAGG 8
 |||||

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XX DE Hypoxia-related tumorigenesis-related SAGE tag #39.
XX screening; hypoxia-related tumorigenesis;
XX hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX OS Unidentified.
XX PN WO2004092198-A2.
XX PD 28-OCT-2004.
XX PF 09-APR-2004; 2004WO-US011087.
XX PW 09-APR-2003; 2003US-0461712P.
XX PA (GENZ ) GENZYME CORP.
XX PI Nacht M;
XX DR WPI; 2004-758333/74.
XX PT Identifying agents that alter biological activity of a polypeptide
XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis
XX comprises contacting an agent with a target cell and monitoring activity
XX of expressed product.
XX PS Disclosure; Page 57; 100pp; English.
XX CC The invention comprises a method of screening for candidate agents
XX capable of altering the biological activity of a protein encoded by a
XX nucleotide involved in hypoxia-related tumorigenesis. The method of the
XX invention involves contacting a test agent with a target cell expressing
XX the nucleotide, and monitoring the activity of the expressed protein
XX product; if the test agent modifies the activity of the expressed protein
XX then this is a candidate agent. The method of the invention is useful for
XX modifying hypoxia-induced gene regulation and for diagnosing, prognosing
XX or treating tumours. The present DNA sequence represents a SAGE tag that
XX was used in the exemplification of the invention.
XX SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
Db 10 CTGTGGC 4
|||||

RESULT 405
ADU19824
ID ADU19824 standard; DNA; 10 BP.
XX AC ADU19824;
XX DT 13-JAN-2005 (first entry)
XX DE Hypoxia-related tumorigenesis-related SAGE tag #1615.
XX screening; hypoxia-related tumorigenesis;
XX hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX OS Unidentified.
XX PN WO2004092198-A2.
XX PD 28-OCT-2004.
XX PF 09-APR-2004; 2004WO-US011087.
XX PW 09-APR-2003; 2003US-0461712P.
XX PR 09-APR-2003; 2003US-0461712P.

RESULT 404
ADU18248/c
ID ADU18248 standard; DNA; 10 BP.
XX AC ADU18248;
XX DT 13-JAN-2005 (first entry)

The present invention relates to a method for preparing a composition for
inhibiting recruitment of perivascular cells of smooth muscle type using
a VE-statin protein (I; ADR27861-ADR27863 and ADR27902). VE-statins,
soluble factors secreted by endothelial cells of the blood vessels, block
recruitment of perivascular smooth muscle cells (but do not affect their
proliferation), so inhibit angiogenesis. VE-statins, also their peptide
fragments, nucleic acids encoding them and vectors containing this
nucleic acid, are used for treating cancer, retinopathy, atherosclerosis
and restenosis, including in gene therapy. The VE-statin nucleic acids
can also be used to produce transgenic animals (for studying the VE-
statin proteins and genes); the VE-statins are used to screen for
specific (ant)agonists, and antibodies specific for VE-statins can be
used to determine expression profiles, particularly for diagnosis of
diseases associated with VE-statins. The present sequence was used to
illustrate the structure of the murine VE-statin gene.

Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
Db 8 GCTGTGG 2
|||||

RESULT 404
ADU18248/c
ID ADU18248 standard; DNA; 10 BP.
XX AC ADU18248;
XX DT 13-JAN-2005 (first entry)

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XX DE Hypoxia-related tumorigenesis-related SAGE tag #39.
XX screening; hypoxia-related tumorigenesis;
XX hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX OS Unidentified.
XX PN WO2004092198-A2.
XX PD 28-OCT-2004.
XX PF 09-APR-2004; 2004WO-US011087.
XX PW 09-APR-2003; 2003US-0461712P.
XX PA (GENZ ) GENZYME CORP.
XX PI Nacht M;
XX DR WPI; 2004-758333/74.
XX PT Identifying agents that alter biological activity of a polypeptide
XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis
XX comprises contacting an agent with a target cell and monitoring activity
XX of expressed product.
XX PS Disclosure; Page 57; 100pp; English.
XX CC The invention comprises a method of screening for candidate agents
XX capable of altering the biological activity of a protein encoded by a
XX nucleotide involved in hypoxia-related tumorigenesis. The method of the
XX invention involves contacting a test agent with a target cell expressing
XX the nucleotide, and monitoring the activity of the expressed protein
XX product; if the test agent modifies the activity of the expressed protein
XX then this is a candidate agent. The method of the invention is useful for
XX modifying hypoxia-induced gene regulation and for diagnosing, prognosing
XX or treating tumours. The present DNA sequence represents a SAGE tag that
XX was used in the exemplification of the invention.
XX SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
Db 10 CTGTGGC 4
|||||

RESULT 405
ADU19824
ID ADU19824 standard; DNA; 10 BP.
XX AC ADU19824;
XX DT 13-JAN-2005 (first entry)
XX DE Hypoxia-related tumorigenesis-related SAGE tag #1615.
XX screening; hypoxia-related tumorigenesis;
XX hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX OS Unidentified.
XX PN WO2004092198-A2.
XX PD 28-OCT-2004.
XX PF 09-APR-2004; 2004WO-US011087.
XX PW 09-APR-2003; 2003US-0461712P.

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XX (GENZ) GENZYME CORP.
 XX Nacht M;
 XX WPI; 2004-758333/74.
 XX Identifying agents that alter biological activity of a polypeptide
 PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis
 PT comprises contacting an agent with a target cell and monitoring activity
 PT of expressed product.
 XX Disclosure; Page 88; 100pp; English.
 XX The invention comprises a method of screening for candidate agents
 CC capable of altering the biological activity of a protein encoded by a
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the
 CC invention involves; contacting a test agent with a target cell expressing
 CC the nucleotide, and monitoring the activity of the expressed protein
 CC product; if the test agent modifies the activity of the expressed protein
 CC then this is a candidate agent. The method of the invention is useful for
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
 CC or treating tumours. The present DNA sequence represents a SAGE tag that
 CC was used in the exemplification of the invention.
 XX Sequence 10 BP; 0 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
 SQ Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 TGTGGCG 15
 DB 1 TGTGGCG 7
 RESULT 406
 ADU18636/c
 ID ADU18636 standard; DNA; 10 BP.
 AC ADU18636;
 DT 13-JAN-2005 (first entry)
 DE Hypoxia-related tumorigenesis-related SAGE tag #427.
 KW screening; hypoxia-related tumorigenesis;
 KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
 XX Unidentified.
 XX WO2004092198-A2.
 XX 28-OCT-2004.
 XX 09-APR-2004; 2004WO-US011087.
 XX 09-APR-2003; 2003US-0461712P.
 XX (GENZ) GENZYME CORP.
 XX Nacht M;
 XX WPI; 2004-758333/74.
 XX Identifying agents that alter biological activity of a polypeptide
 PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis
 PT comprises contacting an agent with a target cell and monitoring activity
 PT of expressed product.
 XX Disclosure; Page 64; 100pp; English.
 XX The invention comprises a method of screening for candidate agents

CC capable of altering the biological activity of a protein encoded by a
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the
 CC invention involves; contacting a test agent with a target cell expressing
 CC the nucleotide, and monitoring the activity of the expressed protein
 CC product; if the test agent modifies the activity of the expressed protein
 CC then this is a candidate agent. The method of the invention is useful for
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
 CC or treating tumours. The present DNA sequence represents a SAGE tag that
 CC was used in the exemplification of the invention.
 XX Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
 SQ Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CTGTGGC 14
 DB 9 CTGTGGC 3
 RESULT 407
 ADU18717/c
 ID ADU18717 standard; DNA; 10 BP.
 XX ADU18717;
 XX 13-JAN-2005 (first entry)
 XX Hypoxia-related tumorigenesis-related SAGE tag #508.
 DE screening; hypoxia-related tumorigenesis;
 KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
 XX Unidentified.
 XX WO2004092198-A2.
 XX 28-OCT-2004.
 XX 09-APR-2004; 2004WO-US011087.
 XX 09-APR-2003; 2003US-0461712P.
 XX (GENZ) GENZYME CORP.
 XX Nacht M;
 XX WPI; 2004-758333/74.
 XX Identifying agents that alter biological activity of a polypeptide
 PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis
 PT comprises contacting an agent with a target cell and monitoring activity
 PT of expressed product.
 XX Disclosure; Page 65; 100pp; English.
 XX The invention comprises a method of screening for candidate agents
 CC capable of altering the biological activity of a protein encoded by a
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the
 CC invention involves; contacting a test agent with a target cell expressing
 CC the nucleotide, and monitoring the activity of the expressed protein
 CC product; if the test agent modifies the activity of the expressed protein
 CC then this is a candidate agent. The method of the invention is useful for
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
 CC or treating tumours. The present DNA sequence represents a SAGE tag that
 CC was used in the exemplification of the invention.
 XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
 SQ Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      8 CTGTGGC 14
Db      7 CTGTGGC 1

RESULT 408
ADU66846/c
ID      ADU66846 standard; DNA; 10 BP.
XX      AC
XX      AC
XX      AC
DT      10-FEB-2005 (first entry)
XX      XX
XX      XX
DE      ZP450RAI gene isolating PCR primer, SEQ:25.
XX      XX
KW      Retinoic acid-inducible retinoid metabolizing protein; cytochrome P450;
KW      CYP26; cancer; actinic keratosis; tumour; basal cell carcinoma; RA; acne;
KW      psoriasis; cytostatic; keratolytic; antiseborrheic; dermatological;
KW      antipsoriatic; PCR; primer; ss; ZP450RAI.
XX      XX
OS      Danio rerio.
XX      XX
XX      US2004235057-A1.
XX      XX
XX      25-NOV-2004.
XX      XX
XX      28-MAY-2004; 2004US-00855595.
XX      XX
PR      21-JUN-1996; 96US-00667546.
PR      01-OCT-1996; 96US-00724466.
PR      23-JUN-1997; 97WO-CA000440.
PR      25-JUN-1997; 97US-00882164.
PR      25-SEP-2000; 2000US-00668482.
XX      XX
PA      (TOOH ) UNIV QUEENS KINGSTON.
XX      XX
PI      Petkovich PM, White JA, Beckett BR, Jones G;
XX      WPI; 2004-832945/82.
XX      XX
XX      Novel antibody specifically binding to protein that oxidizes retinoid,
XX      useful for inhibiting retinoic acid hydroxylation in human.
XX      XX
PS      Disclosure; SEQ ID NO 25; 78pp; English.
XX      XX
CC      The invention relates to retinoic acid (RA)-inducible retinoid
CC      metabolizing proteins found in human (hp450RAI), mouse (mp450RAI) and
CC      zebrafish (zp450RAI) and to nucleic acid molecules encoding such
CC      proteins. P450RAI is a novel member of cytochrome P450 family and is also
CC      referred to as CYP26. The invention is useful for determining protein
CC      which oxidizes retinoid. It is also useful for inhibiting RA
CC      hydroxylation in an organism such as human who is need of treatment
CC      against a disease chosen from cancer, actinic keratosis, secondary tumour
CC      of the head and/or neck, basal cell carcinoma, skin cancer, acne or
CC      psoriasis. The present sequence is a PCR primer used to isolate ZP450RAI
CC      gene using differential display procedure.
XX      XX
SQ      Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCGGAA 17
Db      9 TGGCGGAA 3

RESULT 409
ADV90786/c
ID      ADV90786 standard; DNA; 10 BP.
XX      AC
XX      AC
XX      AC
DT      19-MAY-2005 (first entry)
XX      XX
XX      XX

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AC      ADV90786;
XX      XX
DT      10-MAR-2005 (first entry)
XX      XX
DE      Degenerate primer, SEQ ID 25.
XX      XX
KW      Drug screening; PCR; primer; ss.
XX      XX
OS      Synthetic.
XX      XX
XX      US2004259074-A1.
XX      XX
XX      23-DEC-2004.
XX      XX
XX      28-MAY-2004; 2004US-00855532.
XX      XX
PR      21-JUN-1996; 96US-00667546.
PR      01-OCT-1996; 96US-00724466.
PR      23-JUN-1997; 97WO-CA000440.
PR      25-JUN-1997; 97US-00882164.
PR      25-SEP-2000; 2000US-00668482.
XX      XX
PA      (TOOH ) UNIV QUEENS KINGSTON.
XX      XX
PI      Petkovich PM, White JA, Beckett BR, Jones G;
XX      WPI; 2005-078941/09.
XX      XX
XX      Screening drugs for their effect on activity of retinoid metabolizing
XX      protein, by exposing cell transfected with nucleic acid molecule encoding
XX      protein and expressing protein, to drug, determining effect of drug on
XX      activity of protein.
XX      XX
PS      Disclosure; SEQ ID NO 25; 78pp; English.
XX      XX
CC      The present invention relates to novel retinoic acid-inducible, retinoid-
CC      metabolizing proteins (ADV90763, ADV90765 and ADV90793) and their coding
CC      sequences (ADV90764, ADV90766 and ADV90792). The retinoid-metabolizing
CC      proteins contain a heme-binding motif characteristic of the cytochrome
CC      P450 proteins. The P450RAI family has been designated CYP26. The retinoid
CC      -metabolizing proteins are useful for screening (M1) drugs for their
CC      effect on the activity of the retinoid-metabolizing proteins. (M1)
CC      involves exposing cells transfected with a retinoid-metabolizing protein
CC      coding sequence to a drug, where the transfected cell expresses the
CC      protein; and determining the effect of the drug on the activity of the
CC      protein, where the protein oxidizes a retinoid or hydroxylates a retinoid
CC      at the C4-position of the beta-ionone ring. The drugs screened by (M1),
CC      are useful for inhibiting retinoic acid metabolism, preferably retinoic
CC      acid hydroxylation in an organism for treating diseases such as cancer,
CC      actinic keratosis, oral leukoplakia, secondary tumor of head and/or neck,
CC      basal cell carcinoma, skin cancer, premalignancy associated actinic
CC      keratosis, acne, psoriasis, ichthyosis, eczema, etc. The present primer
CC      was used during differential mRNA display.
XX      XX
SQ      Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCGGAA 17
Db      9 TGGCGGAA 3

RESULT 410
ADY62603/c
ID      ADY62603 standard; DNA; 10 BP.
XX      XX
XX      AC
XX      AC
XX      ADY62603;
XX      XX
DT      19-MAY-2005 (first entry)
XX      XX

```


DE Zebrafish P450RAI cDNA differential display oligo #14.
 KW DNA purification; retinoic acid; microsome; metabolism; primer; ss.
 XX
 OS Danio rerio.
 XX
 PN US6861238-B1.
 XX
 PD 01-MAR-2005.
 XX
 XX 25-SEP-2000; 2000US-00668482.
 PF
 XX 21-JUN-1996; 96US-00667546.
 PR
 PR 01-OCT-1996; 96US-00724466.
 PR
 PR 23-JUN-1997; 97WO-CA000440.
 PR
 PR 25-JUN-1997; 97US-00882164.
 XX
 XX (TOOH) UNIV QUEENS KINGSTON.
 PA
 PI Petkovich PM, White JA, Beckett BR, Jones G;
 XX
 DR WPI; 2005-201182/21.
 XX
 XX Microsomal preparation of a cell transfected with a nucleic acid molecule
 PT encoding a protein that oxidizes/hydroxylates all-trans retinoic acid at
 PT the C4-position of beta-ionone ring, useful for metabolizing retinoic
 PT acid in a cell.
 XX
 XX Disclosure; SEQ ID NO 25; 65pp; English.
 PS
 XX The invention relates to a microsomal preparation of a cell that has been
 CC transfected with a nucleic acid molecule encoding a protein, or of its
 CC descendant cell, where the protein oxidizes or hydroxylates all-trans
 CC retinoic acid at the C4-position of the beta-ionone ring, the nucleic
 CC acid molecule comprising a nucleotide sequence that hybridizes under high
 CC stringency conditions, where high stringency conditions include a wash
 CC step of about 0.2XSSC at 65 deg. C, to a polynucleotide having a fully
 CC defined 1850 base pairs sequence given in the specification, the
 CC microsomal preparation comprising the protein. The microsomal preparation
 CC is useful for metabolizing retinoic acid in an organism or cell. This
 CC sequence corresponds to an oligonucleotide used for differential display
 CC analysis of the zebrafish P450RAI gene which encodes the P450RAI protein
 CC involved in retinoic acid metabolism.
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TGGCGGAA 17
 Db 9 TGGCGGAA 3
 RESULT 411
 ADY95141
 ID ADY95141 standard; DNA; 10 BP.
 XX
 AC ADY95141;
 XX
 XX 16-JUN-2005 (first entry)
 DT
 XX Oligonucleotide related to photo dynamic therapy, ODN2-fw.
 DE
 XX ss; photo dynamic therapy; DNA damage.
 KW
 XX Synthetic.
 OS
 XX WO2005030329-A1.
 PN
 XX 07-APR-2005.
 PD
 XX

PF 29-MAR-2004; 2004WO-JP004472.
 XX
 PR 29-SEP-2003; 2003JP-00338082.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
 XX
 PI Majima T, Kawai K;
 XX
 DR WPI; 2005-305912/31.
 XX
 XX Biomolecule damaging method involves irradiating photosensitized
 PT substance with optical beams of different wavelength, so as to induce
 PT multiple excitations of photosensitized substance.
 XX
 XX Example 2; SEQ ID NO 3; 49pp; Japanese.
 PS
 XX The invention relates to a method whereby photosensitized substance is
 CC irradiated with optical beams of different wavelength, so as to induce
 CC multiple excitations of photosensitized substance. Also included is a
 CC biomolecule damaging apparatus. The method is used for damaging
 CC biomolecules, by photosensitized one-electron oxidation reaction in photo
 CC dynamic therapy. The methods enables damaging of the biomolecules
 CC effectively and quickly, while reducing the strain on patients and the
 CC workload of doctors. The present sequence is an oligonucleotide used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TCGCGCT 9
 Db 3 TCGCGCT 9
 RESULT 412
 ADY95142/C
 ID ADY95142 standard; DNA; 10 BP.
 XX
 AC ADY95142;
 XX
 XX 16-JUN-2005 (first entry)
 DT
 XX Oligonucleotide related to photo dynamic therapy, ODN2-rev.
 DE
 XX ss; photo dynamic therapy; DNA damage.
 KW
 XX Synthetic.
 OS
 XX WO2005030329-A1.
 PN
 XX 07-APR-2005.
 PD
 XX 29-MAR-2004; 2004WO-JP004472.
 PF
 XX 29-SEP-2003; 2003JP-00338082.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
 PA
 XX Majima T, Kawai K;
 PI
 XX WPI; 2005-305912/31.
 DR
 XX Biomolecule damaging method involves irradiating photosensitized
 PT substance with optical beams of different wavelength, so as to induce
 PT multiple excitations of photosensitized substance.
 XX
 XX Example 2; SEQ ID NO 4; 49pp; Japanese.
 PS
 XX The invention relates to a method whereby photosensitized substance is
 CC irradiated with optical beams of different wavelength, so as to induce
 CC multiple excitations of photosensitized substance.

CC multiple excitations of photosensitized substance. Also included is a
CC biomolecule damaging apparatus. The method is used for damaging
CC biomolecules, by photosensitized one-electron oxidation reaction in photo
CC dynamic therapy. The methods enables damaging of the biomolecules
CC effectively and quickly, while reducing the strain on patients and the
CC workload of doctors. The present sequence is an oligonucleotide used in
CC the exemplification of the invention.

XX Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCT 9
|||||
Db 8 TCGCGCT 2

RESULT 413

ADY95147
ID ADY95147 standard; DNA; 10 BP.

XX AC ADY95147;

DT 16-JUN-2005 (first entry)

XX Oligonucleotide related to photo dynamic therapy, ODN3-fw.

XX ss; photo dynamic therapy; DNA damage.

XX Synthetic.

XX WO2005030329-A1.

XX 07-APR-2005.

XX 29-MAR-2004; 2004WO-JP004472.

XX 29-SEP-2003; 2003JP-00338082.

XX (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.

XX Majima T, Kawai K;

XX WPI; 2005-305912/31.

XX Biomolecule damaging method involves irradiating photosensitized
PT substance with optical beams of different wavelength, so as to induce
PT multiple excitations of photosensitized substance.

XX Disclosure; SEQ ID NO 9; 49pp; Japanese.

XX The invention relates to a method whereby photosensitized substance is
CC irradiated with optical beams of different wavelength, so as to induce
CC multiple excitations of photosensitized substance. Also included is a
CC biomolecule damaging apparatus. The method is used for damaging
CC biomolecules, by photosensitized one-electron oxidation reaction in photo
CC dynamic therapy. The methods enables damaging of the biomolecules
CC effectively and quickly, while reducing the strain on patients and the
CC workload of doctors. The present sequence is an oligonucleotide used in
CC the exemplification of the invention.

XX Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCT 9
|||||
Db 3 TCGCGCT 9

RESULT 414

ADY95148/c
ID ADY95148 standard; DNA; 10 BP.

XX AC ADY95148;

DT 16-JUN-2005 (first entry)

XX Oligonucleotide related to photo dynamic therapy, ODN3-fw.

XX ss; photo dynamic therapy; DNA damage.

XX Synthetic.

XX WO2005030329-A1.

XX 07-APR-2005.

XX 29-MAR-2004; 2004WO-JP004472.

XX 29-SEP-2003; 2003JP-00338082.

XX (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.

XX Majima T, Kawai K;

XX WPI; 2005-305912/31.

XX Biomolecule damaging method involves irradiating photosensitized
PT substance with optical beams of different wavelength, so as to induce
PT multiple excitations of photosensitized substance.

XX Disclosure; SEQ ID NO 10; 49pp; Japanese.

XX The invention relates to a method whereby photosensitized substance is
CC irradiated with optical beams of different wavelength, so as to induce
CC multiple excitations of photosensitized substance. Also included is a
CC biomolecule damaging apparatus. The method is used for damaging
CC biomolecules, by photosensitized one-electron oxidation reaction in photo
CC dynamic therapy. The methods enables damaging of the biomolecules
CC effectively and quickly, while reducing the strain on patients and the
CC workload of doctors. The present sequence is an oligonucleotide used in
CC the exemplification of the invention.

XX Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCT 9
|||||
Db 8 TCGCGCT 2

Search completed: May 9, 2006, 15:49:46
Job time : 1 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 15:51:35 ; Search time 0.001 Seconds
(without alignments)
66.234 Million cell updates/sec

Title: US-09-904-968A-19-COPY

Perfect score: 19

Sequence: 1 ggtcgctgtggaagg 19

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 154 seqs, 1743 residues

Total number of hits satisfying chosen parameters: 308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 154 summaries

Database : pubmaindb19.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1	US-09-904-968A-19
2	11	57.9	13	1	US-10-257-017B-116243
3	11	57.9	13	1	US-10-257-017B-116244
4	10.4	54.7	14	1	US-09-847-601B-115
5	10	52.6	12	1	US-10-994-626-27
6	10	52.6	12	1	US-11-078-601-46
7	10	52.6	13	1	US-10-257-017B-20773
8	10	52.6	13	1	US-10-257-017B-20774
9	9.8	51.6	13	1	US-10-257-017B-23021
10	9.8	51.6	13	1	US-10-257-017B-23022
11	9.8	51.6	13	1	US-10-257-017B-88973
12	9.8	51.6	13	1	US-10-257-017B-88974
13	9.8	51.6	13	1	US-10-257-017B-88989
14	9.8	51.6	13	1	US-10-257-017B-88990
15	9.8	51.6	13	1	US-10-257-017B-117103
16	9.8	51.6	13	1	US-10-257-017B-117104
17	9.8	51.6	14	1	US-10-291-230-33
18	9.8	51.6	14	1	US-10-291-249-33
19	9.4	49.5	12	1	US-10-257-017B-284862
20	9.4	49.5	12	1	US-10-257-017B-290687
21	9.4	49.5	12	1	US-10-257-017B-350230
22	9.4	49.5	13	1	US-10-257-017B-53147
23	9.4	49.5	13	1	US-10-257-017B-53148
24	9.4	49.5	13	1	US-10-257-017B-63161
25	9.4	49.5	13	1	US-10-257-017B-63162
26	9.4	49.5	13	1	US-10-257-017B-77009
27	9.4	49.5	13	1	US-10-257-017B-77010
28	9.4	49.5	13	1	US-10-257-017B-86991
29	9.4	49.5	13	1	US-10-257-017B-86992
30	9.4	49.5	13	1	US-10-257-017B-103959
31	9.4	49.5	13	1	US-10-257-017B-103960
32	9.4	49.5	13	1	US-10-257-017B-104971
33	9.4	49.5	13	1	US-10-257-017B-104972

Sequence 116159,	1	US-10-257-017B-116159	13	49.5	9.4	34
Sequence 116160,	1	US-10-257-017B-116160	13	49.5	9.4	35
Sequence 116241,	1	US-10-257-017B-116241	13	49.5	9.4	36
Sequence 116242,	1	US-10-257-017B-116242	13	49.5	9.4	37
Sequence 219517,	1	US-10-257-017B-219517	13	49.5	9.4	38
Sequence 219518,	1	US-10-257-017B-219518	13	49.5	9.4	39
Sequence 219519,	1	US-10-257-017B-219519	13	49.5	9.4	40
Sequence 219520,	1	US-10-257-017B-219520	13	49.5	9.4	41
Sequence 232663,	1	US-10-257-017B-232663	13	49.5	9.4	42
Sequence 232664,	1	US-10-257-017B-232664	13	49.5	9.4	43
Sequence 285117,	1	US-10-257-017B-285117	13	49.5	9.4	44
Sequence 285118,	1	US-10-257-017B-285118	13	49.5	9.4	45
Sequence 16, Appl	1	US-10-994-626-16	13	49.5	9.4	46
Sequence 42, Appl	1	US-11-078-601-42	13	49.5	9.4	47
Sequence 18, Appl	1	US-08-825-486-18	10	47.4	9	48
Sequence 18, Appl	1	US-08-870-434-18	10	47.4	9	49
Sequence 18, Appl	1	US-09-372-044-18	10	47.4	9	50
Sequence 18, Appl	1	US-09-560-150-18	10	47.4	9	51
Sequence 18, Appl	1	US-10-067-741-18	10	47.4	9	52
Sequence 18, Appl	1	US-10-067-741-18	10	47.4	9	53
Sequence 303992,	1	US-10-257-017B-303992	12	46.3	8.8	54
Sequence 289187,	1	US-10-257-017B-289187	12	46.3	8.8	55
Sequence 324838,	1	US-10-257-017B-324838	12	46.3	8.8	56
Sequence 359284,	1	US-10-257-017B-359284	12	44.2	8.4	57
Sequence 250, App	1	US-10-033-145-250	10	44.2	8.4	58
Sequence 273, App	1	US-10-330-627-903	10	44.2	8.4	59
Sequence 903, App	1	US-10-487-934-173	10	44.2	8.4	60
Sequence 173, App	1	US-10-314-322-305	11	44.2	8.4	61
Sequence 305, App	1	US-10-450-797-16	11	44.2	8.4	62
Sequence 16, Appl	1	US-10-450-797-923	11	44.2	8.4	63
Sequence 923, App	1	US-09-949-041A-50	12	44.2	8.4	64
Sequence 50, Appl	1	US-10-257-017B-271986	12	44.2	8.4	65
Sequence 271986,	1	US-10-257-017B-271986	12	44.2	8.4	66
Sequence 273770,	1	US-10-257-017B-273770	12	44.2	8.4	67
Sequence 290024,	1	US-10-257-017B-290024	12	44.2	8.4	68
Sequence 290182,	1	US-10-257-017B-290182	12	44.2	8.4	69
Sequence 290343,	1	US-10-257-017B-290343	12	44.2	8.4	70
Sequence 290346,	1	US-10-257-017B-290346	12	44.2	8.4	71
Sequence 295960,	1	US-10-257-017B-295960	12	44.2	8.4	72
Sequence 295962,	1	US-10-257-017B-295962	12	44.2	8.4	73
Sequence 306594,	1	US-10-257-017B-306594	12	44.2	8.4	74
Sequence 312013,	1	US-10-257-017B-312013	12	44.2	8.4	75
Sequence 312889,	1	US-10-257-017B-312889	12	44.2	8.4	76
Sequence 317080,	1	US-10-257-017B-317080	12	44.2	8.4	77
Sequence 323594,	1	US-10-257-017B-323594	12	44.2	8.4	78
Sequence 325659,	1	US-10-257-017B-325659	12	44.2	8.4	79
Sequence 326801,	1	US-10-257-017B-326801	12	44.2	8.4	80
Sequence 329721,	1	US-10-257-017B-329721	12	44.2	8.4	81
Sequence 350774,	1	US-10-257-017B-350774	12	44.2	8.4	82
Sequence 364089,	1	US-10-257-017B-364089	12	44.2	8.4	83
Sequence 28, Appl	1	US-10-912-032-28	10	42.1	8	84
Sequence 1534, App	1	US-10-033-145-1534	10	42.1	8	85
Sequence 718, App	1	US-10-330-627-718	10	42.1	8	86
Sequence 108, App	1	US-10-257-021-108	10	42.1	8	87
Sequence 326, App	1	US-10-293-222-326	10	42.1	8	88
Sequence 119, App	1	US-10-487-934-119	10	42.1	8	89
Sequence 266, App	1	US-10-487-934-266	10	42.1	8	90
Sequence 8, Appl	1	US-10-037-677-8	11	41.1	7.8	91
Sequence 10, Appl	1	US-10-215-571-10	11	41.1	7.8	92
Sequence 10, Appl	1	US-10-719-571-10	11	41.1	7.8	93
Sequence 851, App	1	US-10-450-797-851	11	41.1	7.8	94
Sequence 985, App	1	US-10-450-797-985	11	41.1	7.8	95
Sequence 1022, App	1	US-10-450-797-1022	11	41.1	7.8	96
Sequence 8, Appl	1	US-10-754-408-8	10	38.9	7.4	97
Sequence 12, Appl	1	US-09-775-743A-12	10	38.9	7.4	98
Sequence 9, Appl	1	US-09-848-537A-9	10	38.9	7.4	99
Sequence 1209, App	1	US-10-033-145-1209	10	38.9	7.4	100
Sequence 1502, App	1	US-10-033-145-1502	10	38.9	7.4	101
Sequence 1908, App	1	US-10-033-145-1908	10	38.9	7.4	102
Sequence 2103, App	1	US-10-033-145-2103	10	38.9	7.4	103
Sequence 279, App	1	US-10-330-627-279	10	38.9	7.4	104
Sequence 280, App	1	US-10-330-627-280	10	38.9	7.4	105
Sequence 447, App	1	US-10-330-627-447	10	38.9	7.4	106
Sequence 586, App	1	US-10-330-627-586	10	38.9	7.4	106

Published-Applications-NA-Main

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C 107 7.4 38.9 10 1 US-10-330-627-734 Sequence 734, App
108 7.4 38.9 10 1 US-10-330-627-1025 Sequence 1025, Ap
109 7.4 38.9 10 1 US-10-330-627-1064 Sequence 1064, Ap
110 7.4 38.9 10 1 US-10-197-019-109 Sequence 109, App
111 7.4 38.9 10 1 US-10-293-222-205 Sequence 205, App
112 7.4 38.9 10 1 US-10-723-940-92 Sequence 92, Appl
113 7.4 38.9 10 1 US-10-487-934-14 Sequence 14, Appl
114 7.4 38.9 10 1 US-10-487-934-123 Sequence 123, App
115 7.4 38.9 10 1 US-10-487-934-184 Sequence 184, App
116 7.4 38.9 10 1 US-10-784-589-12 Sequence 12, Appl
117 7.4 38.9 10 1 US-10-987-549-29 Sequence 29, Appl
118 7.4 38.9 10 1 US-10-987-549-30 Sequence 30, Appl
119 7.4 38.9 10 1 US-11-035-899-259 Sequence 259, App
120 7.4 38.9 10 1 US-11-035-899-260 Sequence 260, App
121 7 36.8 10 1 US-09-867-262-5 Sequence 5, Appli
122 7 36.8 10 1 US-09-885-551A-6 Sequence 6, Appli
123 7 36.8 10 1 US-09-990-186-92 Sequence 92, Appl
124 7 36.8 10 1 US-09-990-186-93 Sequence 93, Appl
125 7 36.8 10 1 US-09-990-186-1278 Sequence 1278, Ap
126 7 36.8 10 1 US-09-990-186-1653 Sequence 1653, Ap
127 7 36.8 10 1 US-09-990-186-1654 Sequence 1654, Ap
128 7 36.8 10 1 US-09-990-186-1667 Sequence 1667, Ap
129 7 36.8 10 1 US-09-989-994-92 Sequence 92, Appl
130 7 36.8 10 1 US-09-989-994-93 Sequence 93, Appl
131 7 36.8 10 1 US-09-989-994-1278 Sequence 1278, Ap
132 7 36.8 10 1 US-09-989-994-1653 Sequence 1653, Ap
133 7 36.8 10 1 US-09-989-994-1654 Sequence 1654, Ap
134 7 36.8 10 1 US-09-989-994-1667 Sequence 1667, Ap
135 7 36.8 10 1 US-10-087-426-6 Sequence 6, Appli
136 7 36.8 10 1 US-10-033-145-299 Sequence 299, App
137 7 36.8 10 1 US-10-033-145-527 Sequence 527, App
138 7 36.8 10 1 US-10-033-145-1855 Sequence 1855, Ap
139 7 36.8 10 1 US-10-033-145-2019 Sequence 2019, Ap
140 7 36.8 10 1 US-10-108-077-6 Sequence 6, Appli
141 7 36.8 10 1 US-10-142-111-23 Sequence 23, Appl
142 7 36.8 10 1 US-10-223-765-284 Sequence 284, App
143 7 36.8 10 1 US-10-330-627-524 Sequence 524, App
144 7 36.8 10 1 US-10-091-281-247 Sequence 247, App
145 7 36.8 10 1 US-10-422-523-28 Sequence 28, Appl
146 7 36.8 10 1 US-10-029-221C-5 Sequence 5, Appli
147 7 36.8 10 1 US-10-816-079-27 Sequence 27, Appl
148 7 36.8 10 1 US-10-855-595-25 Sequence 25, Appl
149 7 36.8 10 1 US-10-631-544-6 Sequence 6, Appli
150 7 36.8 10 1 US-10-855-532-25 Sequence 25, Appl
151 7 36.8 10 1 US-10-688-489-166 Sequence 166, App
152 7 36.8 10 1 US-10-398-271-14 Sequence 14, Appl
153 7 36.8 10 1 US-10-987-549-31 Sequence 31, Appl
154 7 36.8 10 1 US-10-987-549-32 Sequence 32, Appl
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ALIGNMENTS

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RESULT 1
US-09-904-968A-19
; Sequence 19, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHADDEEKITCHAREN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JH01680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
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; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer IF1
US-09-904-968A-19

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGGCTGTGGCGAAGG 19
|||||
DB 1 GGTGCGGCTGTGGCGAAGG 19
|||||

RESULT 2
US-10-257-017B-116243
; Sequence 116243, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116243
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029111
US-10-257-017B-116243

Query Match 57.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
|||||
DB 2 TGTGGCGAAGG 12
|||||

RESULT 3
US-10-257-017B-116244/c
; Sequence 116244, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116244
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029111
US-10-257-017B-116244
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Query Match 57.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGCGGAAG 19
| | | | | | | | | |
DB 12 TGTGCGGAAG 2

RESULT 4
US-09-847-601B-115
; Sequence 115, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; TITLE OF INVENTION: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-115

Query Match 54.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGCGGAAG 19
| : | | | | | | | | | |
DB 1 CUGUGGAGAAG 12

RESULT 5
US-10-994-626-27/c
; Sequence 27, Application US/10994626
; Publication No. US20050112677A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A substrate having an oxide layer, method for detecting a target
; FILE REFERENCE: PN051212
; CURRENT APPLICATION NUMBER: US/10/994,626
; CURRENT FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe oligonucleotide
US-10-994-626-27

Query Match 52.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGCGGAAG 18

Query Match 57.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGCGGAAG 19
| | | | | | | | | |
DB 12 TGTGCGGAAG 2

RESULT 4
US-09-847-601B-115
; Sequence 115, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; TITLE OF INVENTION: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-115

Query Match 54.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGCGGAAG 19
| : | | | | | | | | | |
DB 1 CUGUGGAGAAG 12

RESULT 5
US-10-994-626-27/c
; Sequence 27, Application US/10994626
; Publication No. US20050112677A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A substrate having an oxide layer, method for detecting a target
; FILE REFERENCE: PN051212
; CURRENT APPLICATION NUMBER: US/10/994,626
; CURRENT FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe oligonucleotide
US-10-994-626-27

Query Match 52.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGCGGAAG 18

DB 10 TGTGCGGAAG 1
| | | | | | | | | |

RESULT 6
US-11-078-601-46/c
; Sequence 46, Application US/11078601
; Publication No. US20050202492A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A microarray having probe polynucleotide spots binding to a same
; TITLE OF INVENTION: target polynucleotide fragment maximally apart therebetween and
; TITLE OF INVENTION: method of producing the same
; FILE REFERENCE: PN052961
; CURRENT APPLICATION NUMBER: US/11/078,601
; CURRENT FILING DATE: 2005-03-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 46
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe polynucleotide
US-11-078-601-46

Query Match 52.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGCGGAAG 18
| | | | | | | | | |
DB 10 TGTGCGGAAG 1

RESULT 7
US-10-257-017B-20773
; Sequence 20773, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 20773
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004222
US-10-257-017B-20773

Query Match 52.6%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGCGGAAG 18
| | | | | | | | | |
DB 1 TGTGCGGAAG 10

RESULT 8
US-10-257-017B-20774/c
; Sequence 20774, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:

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; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 20774
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004222
US-10-257-017B-20774

Query Match          52.6%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
Db 13 TGTGGCGAAG 4

RESULT 9
US-10-257-017B-23021
; Sequence 23021, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 23021
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004520
US-10-257-017B-23021

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.8%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGCGCTGTGG 13
Db 1 GGTGCGCTGTGG 13

RESULT 10
US-10-257-017B-23022/c
; Sequence 23022, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 20774
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004520
US-10-257-017B-20774

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGCGCTGTGG 13
Db 1 GGTGCGCTGTGG 13

RESULT 11
US-10-257-017B-88973
; Sequence 88973, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88973
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022356
US-10-257-017B-88973

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCG 15
Db 1 TCGCGCTGTGGCG 13

RESULT 12
US-10-257-017B-88974/c
; Sequence 88974, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88974
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022356
US-10-257-017B-88973
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022356
US-10-257-017B-88974

Query Match 51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCGCGCTGTGCG 15
| | | | | | | | | |
Db 13 TCGCGCTGTGCG 1

RESULT 13
US-10-257-017B-88989
; Sequence 88989, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88989
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022356
US-10-257-017B-88989

Query Match 51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCGCGCTGTGCG 15
| | | | | | | | | |
Db 1 TCGCGCGGTGCG 13

RESULT 14
US-10-257-017B-88990/c
; Sequence 88990, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88990
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022356
US-10-257-017B-88990

Query Match 51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TCGCGCTGTGCG 15
| | | | | | | | | |
Db 13 TCGCGCGGTGCG 1

RESULT 15
US-10-257-017B-117103
; Sequence 117103, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117103
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029306
US-10-257-017B-117103

Query Match 51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGCGGAAG 19
| | | | | | | | | |
Db 1 GTTGTGTGAAG 13

RESULT 16
US-10-257-017B-117104/c
; Sequence 117104, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117104
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029306
US-10-257-017B-117104

Query Match 51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGCGGAAG 19
| | | | | | | | | |
Db 13 GTTGTGTGAAG 1

```
RESULT 17
US-10-291-230-33
; Sequence 33, Application US/10291230
; Publication No. US20030108939A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.A
; CURRENT APPLICATION NUMBER: US/10/291,230
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-10-291-230-33

Query Match          51.6%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY      2  GTGCGCGCTGTGGC 14
        ||| ||||| |||
Db       2  GTGCGCGCTGTGGC 14

RESULT 18
US-10-291-249-33
; Sequence 33, Application US/10291249
; Publication No. US20030119041A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.B
; CURRENT APPLICATION NUMBER: US/10/291,249
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-10-291-249-33

Query Match          51.6%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY      2  GTGCGCGCTGTGGC 14
        ||| ||||| |||
Db       2  GTGCGCGCTGTGGC 14

RESULT 19
US-10-257-017B-284862/c
; Sequence 284862, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 284862
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012030
US-10-257-017B-284862

Query Match          49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      5  GCGCTGTGGCG 15
        ||| |||||
Db      11 GCGCGTGGCG 1

RESULT 20
US-10-257-017B-290687/c
; Sequence 290687, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290687
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014474
US-10-257-017B-290687

Query Match          49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      9  TGTGGCGAAGG 19
        ||| |||||
Db     12 TGTGGGGAAGG 2

RESULT 21
US-10-257-017B-350230/c
; Sequence 350230, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```



```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350230
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008276
US-10-257-017B-350230

Query Match          49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TGTGGCGAAGG 2

RESULT 22
US-10-257-017B-53147
; Sequence 53147, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 53147
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014679
US-10-257-017B-53147

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 2 TGTGGCGAAGG 12

RESULT 23
US-10-257-017B-53148/c
; Sequence 53148, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
```

```
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 53148
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014679
US-10-257-017B-53148

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TGTGGCGAAGG 2

RESULT 24
US-10-257-017B-63161
; Sequence 63161, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 63161
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016688
US-10-257-017B-63161

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 2 TGTGGCGAAGG 12

RESULT 25
US-10-257-017B-63162/c
; Sequence 63162, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 63162
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016688
US-10-257-017B-63162

Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
| | | | | | | | | |
DB 12 TTGTGGCGAAGG 2

RESULT 26

US-10-257-017B-77009
; Sequence 77009, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 77009
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019655
US-10-257-017B-77009

Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
| | | | | | | | | |
DB 2 GTCGCGTTGTG 12

RESULT 27

US-10-257-017B-77010/c
; Sequence 77010, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 77010
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019655
US-10-257-017B-77010

Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
| | | | | | | | | |
DB 12 GTCGCGTTGTG 2

RESULT 28

US-10-257-017B-86991
; Sequence 86991, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 86991
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021858
US-10-257-017B-86991

Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
| | | | | | | | | |
DB 3 TGTGGCGAAGG 13

RESULT 29

US-10-257-017B-86992/c
; Sequence 86992, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 86992
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021858
US-10-257-017B-86992

Query Match 49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
| | | | | | | | | |
DB 11 TGTGGCGAAGG 1

RESULT 30

```
US-10-257-017B-103959
; Sequence 103959, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103959
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025999
US-10-257-017B-103959

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGT 11
    ||||| |||
Db 1 GGTCGCGCTGT 11

RESULT 31
US-10-257-017B-103960/c
; Sequence 103960, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103960
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025999
US-10-257-017B-103960

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGT 11
    ||||| |||
Db 13 GGTCGCGCTGT 3

RESULT 32
US-10-257-017B-104971
; Sequence 104971, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
```

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 104971
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026284
US-10-257-017B-104971

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCGAAGG 19
    ||||| |||||
Db 1 TGTGGCGAAGG 11

RESULT 33
US-10-257-017B-104972/c
; Sequence 104972, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 104972
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026284
US-10-257-017B-104972

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCGAAGG 19
    ||||| |||||
Db 13 TGTGGCGAAGG 3

RESULT 34
US-10-257-017B-116159
; Sequence 116159, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116159
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029108
US-10-257-017B-116159

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
Db   2 TGTGGCGAAGG 12

RESULT 35
US-10-257-017B-116160/c
; Sequence 116160, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116160
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029108
US-10-257-017B-116160

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
Db   2 TGTGGCGGAGG 2

RESULT 36
US-10-257-017B-116241
; Sequence 116241, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116241
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029111
```

```
US-10-257-017B-116241

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
Db   2 TGTGGTGAAGG 12

RESULT 37
US-10-257-017B-116242/c
; Sequence 116242, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116242
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029111
US-10-257-017B-116242

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
Db   12 TGTGGTGAAGG 2

RESULT 38
US-10-257-017B-219517
; Sequence 219517, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 219517
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053391
US-10-257-017B-219517

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
```

```
Db          2 TGTGGCGAAGG 12
||||| |||||
RESULT 39
US-10-257-017B-219518/c
; Sequence 219518, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 219518
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053391
US-10-257-017B-219518
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          9 TGTGGCGAAGG 19
||||| |||||
Db          2 TGTGGCGAAGG 2
||||| |||||
RESULT 40
US-10-257-017B-219519
; Sequence 219519, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 219519
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053391
US-10-257-017B-219519
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          9 TGTGGCGAAGG 19
||||| |||||
Db          2 TGTGGCGAAGG 12
||||| |||||
RESULT 41
US-10-257-017B-219520/c
; Sequence 219520, Application US/10257017B
```

```
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 219520
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053391
US-10-257-017B-219520
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          9 TGTGGCGAAGG 19
||||| |||||
Db          2 TGTGGCGAAGG 2
||||| |||||
RESULT 42
US-10-257-017B-232663
; Sequence 232663, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 232663
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0056734
US-10-257-017B-232663
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          9 TGTGGCGAAGG 19
||||| |||||
Db          2 TGTGGCGAAGG 12
||||| |||||
RESULT 43
US-10-257-017B-232664/c
; Sequence 232664, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 232664
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0056734
US-10-257-017B-232664
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 232864
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0056734
US-10-257-017B-232864

Query Match      49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
Db  12 TGGGGCGAAGG 2

RESULT 44
US-10-257-017B-265117
; Sequence 265117, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 265117
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0064243
US-10-257-017B-265117

Query Match      49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
Db  2 TGTGACGAAGG 12

RESULT 45
US-10-257-017B-265118/c
; Sequence 265118, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 265118
```

```
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0064243
US-10-257-017B-265118

Query Match      49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 TGTGGCGAAGG 19
Db  12 TGTGACGAAGG 2

RESULT 46
US-10-994-626-16
; Sequence 16, Application US/10994626
; Publication No. US20050112677A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A substrate having an oxide layer, method for detecting a target
; TITLE OF INVENTION: substance using the same and optical sensor containing the same
; FILE REFERENCE: PN051212
; CURRENT APPLICATION NUMBER: US/10/994,626
; CURRENT FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 16
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe oligonucleotide
US-10-994-626-16

Query Match      49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3 TCGCGCTGTGG 13
Db  3 TCCCGCTGTGG 13

RESULT 47
US-11-078-601-42
; Sequence 42, Application US/11078601
; Publication No. US20050202492A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A microarray having probe polynucleotide spots binding to a same
; TITLE OF INVENTION: target polynucleotide fragment maximally apart therebetween and
; TITLE OF INVENTION: method of producing the same
; FILE REFERENCE: PN052961
; CURRENT APPLICATION NUMBER: US/11/078,601
; CURRENT FILING DATE: 2005-03-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 42
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe polynucleotide
US-11-078-601-42

Query Match      49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3 TCGCGCTGTGG 13
```

Db || |||||
 3 TCCCGCTGTGG 13

RESULT 48

US-08-825-486-18/c
; Sequence 18, Application US/08825486
; Publication No. US20020016303A1
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,486
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/799,910
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-077-999
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-825-486-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGCGCGAAG 18
 |||||
Db 10 GTGCGCGAAG 2

RESULT 49

US-08-870-434-18/c
; Sequence 18, Application US/08870434
; Publication No. US20020034736A1
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY

COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,434
FILING DATE: 06-JUN-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-870-434-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGCGCGAAG 18
 |||||
Db 10 GTGCGCGAAG 2

RESULT 50

US-09-372-044-18/c
; Sequence 18, Application US/09372044A
; Patent No. US20020102603A1
; GENERAL INFORMATION:
; APPLICANT: Dean Falb et al.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease
; FILE REFERENCE: 7853-152
; CURRENT APPLICATION NUMBER: US/09/372,044A
; CURRENT FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-044-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGCGCGAAG 18
 |||||
Db 10 GTGCGCGAAG 2

RESULT 51

US-09-560-150-18/c
; Sequence 18, Application US/09560150
; Publication No. US20030073076A1
; GENERAL INFORMATION:

APPLICANT: FALB, Dean A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; FILE REFERENCE: 7853-126
; CURRENT APPLICATION NUMBER: US/09/560,150
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/126,640
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 08/870,434
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/799,910
; PRIOR FILING DATE: 1997-02-13
; PRIOR APPLICATION NUMBER: 60/011,787
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-560-150-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
|||||
Db 10 GTGGCGAAG 2

RESULT 52
US-10-067-741-18/c
; Sequence 18, Application US/10067741
; Publication No. US20030097668A1
; GENERAL INFORMATION:
; APPLICANT: Dean A. Falb
; APPLICANT: Katherine Galvin
; APPLICANT: Michael Donovan
; APPLICANT: Dennis Huszar
; APPLICANT: Michael A. Gimbrone, Jr.
; TITLE OF INVENTION: Compositions and Methods for the Treatment and
; TITLE OF INVENTION: Diagnosis of
; TITLE OF INVENTION: Cardiovascular Disease
; FILE REFERENCE: 7853-140-999
; CURRENT APPLICATION NUMBER: US/10/067,741
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/288,292
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 08/870,434
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/799,910
; PRIOR FILING DATE: 1997-02-13
; PRIOR APPLICATION NUMBER: 60/011,787
; PRIOR FILING DATE: 1996-02-16
; PRIOR APPLICATION NUMBER: 08/485,573
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/386,844
; PRIOR FILING DATE: 1995-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-741-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
|||||
Db 10 GTGGCGAAG 2

RESULT 53
US-10-257-017B-303992/c
; Sequence 303992, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303992
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020735
US-10-257-017B-303992

Query Match 47.4%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAA 17
|||||
Db 10 TGTGGCGAA 2

RESULT 54
US-10-257-017B-289187
; Sequence 289187, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 289187
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013829
US-10-257-017B-289187

Query Match 46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCTGTGGCGA 16
|||||
Db 1 GGGTTGTGGCGA 12

RESULT 55
US-10-257-017B-324838/c


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; Sequence 324838, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 324838
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0032252
US-10-257-017B-324838

Query Match      46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGGAG 18
Db 12 GATGTGGCGGAG 1

RESULT 56
US-10-257-017B-359284/c
; Sequence 359284, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359284
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008283
US-10-257-017B-359284

Query Match      46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CGCGTGTGGCG 15
Db 12 CGCGTGTGGAG 1

RESULT 57
US-10-033-145-250/c
; Sequence 250, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

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; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-250

Query Match      44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCGGCTG 10
Db 10 GGGCGGCGTG 1

RESULT 58
US-10-033-145-273
; Sequence 273, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-273

Query Match      44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CGCTGTGGCG 15
Db 1 CGCTGTGGCG 10

RESULT 59
US-10-330-627-903/c
; Sequence 903, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107,00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 903
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-10-330-627-903

Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGGCTG 10
||| |||||
DB 10 GGGCGGCTG 1

RESULT 60

US-10-487-934-173
; Sequence 173, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kintzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-173

Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
||||| |||||
DB 1 CGCTGTGGCG 10

RESULT 61

US-10-314-322-305
; Sequence 305, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; HEALING
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-305

Query Match 44.2%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCGA 16
||||| |||||
DB 1 GCTGTGGCGA 10

RESULT 62

US-10-450-797-16
; Sequence 16, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-16

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
||||| |||||
DB 1 GTGGCGAATG 10

RESULT 63

US-10-450-797-923/c
; Sequence 923, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 923
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-923

Query Match 44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
||||| |||||
DB 11 GTGGAGAAGG 2

```
RESULT 64
US-09-949-041A-50/c
; Sequence 50, Application US/09949041A
; Publication No. US20030104387A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Meng
; APPLICANT: Woo, Hok
; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Rif
; FILE OF INVENTION: Resistance
; FILE REFERENCE: fp4637
; CURRENT APPLICATION NUMBER: US/09/949,041A
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-949-041A-50

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
Db 11 GCGCTGGGC 2

RESULT 65
US-10-257-017B-271986
; Sequence 271986, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 271986
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002677
US-10-257-017B-271986

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGCGGAAG 19
Db 2 GAGGCGAAG 11

RESULT 66
US-10-257-017B-273770
; Sequence 273770, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
```

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 273770
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003303
US-10-257-017B-273770

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
Db 2 TGTGGTGAAG 11

RESULT 67
US-10-257-017B-290024/c
; Sequence 290024, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290024
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014187
US-10-257-017B-290024

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
Db 12 TGTGGCGAGG 3

RESULT 68
US-10-257-017B-290182
; Sequence 290182, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290182
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014238
US-10-257-017B-290182

Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCGCTGTGG 13
||| |||
Db 2 CGCGCGTGG 11

RESULT 69
US-10-257-017B-290343/c
; Sequence 290343, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290343
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014318
US-10-257-017B-290343

Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
||| |||
Db 12 TGTGGCGAAG 3

RESULT 70
US-10-257-017B-290346/c
; Sequence 290346, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290346
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014318

US-10-257-017B-290346

Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
||| |||
Db 12 TGTGGCGAAG 3

RESULT 71
US-10-257-017B-295960
; Sequence 295960, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295960
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016826
US-10-257-017B-295960

Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
||| |||
Db 1 GTGGCGTAGG 10

RESULT 72
US-10-257-017B-295962
; Sequence 295962, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295962
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016826
US-10-257-017B-295962

Query Match 44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19

```
Db      1 GTGGCGTAGG 10
||||| |||
RESULT 73
US-10-257-017B-306594/c
; Sequence 306594, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306594
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022080
US-10-257-017B-306594
Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAGG 19
||||| |||
Db      10 GTGGAGAAGG 1

RESULT 74
US-10-257-017B-312013
; Sequence 312013, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 312013
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0024800
US-10-257-017B-312013
Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCGCGTGTG 12
||||| |||
Db      3 TCGCGTGTG 12

RESULT 75
US-10-257-017B-312889
; Sequence 312889, Application US/10257017B
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; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 312889
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide-Primer
US-10-257-017B-312889
Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAGG 19
||||| |||
Db      3 GTAGCGAAGG 12

RESULT 76
US-10-257-017B-317080
; Sequence 317080, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317080
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027806
US-10-257-017B-317080
Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCTGTGGCGA 16
||||| |||
Db      3 GGTGTGGCGA 12

RESULT 77
US-10-257-017B-323594
; Sequence 323594, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
```

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; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323594
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031477
US-10-257-017B-323594

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
DB 1 GTGGCGAAGG 10

RESULT 78
US-10-257-017B-325659
; Sequence 325659, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 325659
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0032649
US-10-257-017B-325659

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
DB 3 TGTGGCGAGG 12

RESULT 79
US-10-257-017B-326801
; Sequence 326801, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 326801
```

```
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033283
US-10-257-017B-326801

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
DB 1 GTGGCGAAGG 10

RESULT 80
US-10-257-017B-329721/c
; Sequence 329721, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329721
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0035109
US-10-257-017B-329721

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
DB 11 TGTGGGAGAAG 2

RESULT 81
US-10-257-017B-350774
; Sequence 350774, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350774
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046869
US-10-257-017B-350774
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Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGCGGAAG 18
   ||| |||||
Db 2 TGTGCGGAAG 11

RESULT 82
US-10-257-017B-364089/c
; Sequence 364089, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 364089
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0006574
US-10-257-017B-364089

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGCGGAAG 19
   ||| |||||
Db 10 GTGCGGAAG 1

RESULT 83
US-10-912-032-28/c
; Sequence 28, Application US/10912032
; Publication No. US20050089893A1
; GENERAL INFORMATION:
; APPLICANT: Lopez, Martin J.
; APPLICANT: Eritja, Ramon
; APPLICANT: Munzer, Martin
; TITLE OF INVENTION: Methods and Compositions for In Vitro and In Vivo Use of Parallel
; TITLE OF INVENTION: Stranded Hairpins and Triplex Structures as Nucleic Acid Ligands
; FILE REFERENCE: 040358
; CURRENT APPLICATION NUMBER: US/10/912,032
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/493,092
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: hairpin component
US-10-912-032-28

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGCGGAAG 19
   | |||||

```

```

Db 12 GAGCGGAAG 3

RESULT 84
US-10-033-145-1534
; Sequence 1534, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1534
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-033-145-1534

Query Match      42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAAG 18
   |||||
Db 3 TGGCGAAG 10

RESULT 85
US-10-330-627-718
; Sequence 718, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 718
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-330-627-718

Query Match      42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGTG 12
   |||||
Db 3 GCGCTGTG 10

RESULT 86
US-10-257-021-108
; Sequence 108, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.

```

```
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.036902
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-021-108
```

```
Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 TCGCGCTG 10
    |||||
Db 2 TCGCGCTG 9
```

```
RESULT 87
US-10-293-222-326
; Sequence 326, Application US/10293322
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 326
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-326
```

```
Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 GCGCTGTG 12
    |||||
Db 3 GCGCTGTG 10
```

```
RESULT 88
US-10-487-934-119
; Sequence 119, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
```

```
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-119
```

```
Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 8 CTGTGCG 15
    |||||
Db 2 CTGTGCG 9
```

```
RESULT 89
US-10-487-934-266
; Sequence 266, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 266
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-266
```

```
Query Match 42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 GCGCTGTG 12
    |||||
Db 3 GCGCTGTG 10
```

```
RESULT 90
US-10-037-677-8
; Sequence 8, Application US/10037677
; Publication No. US20020173003A1
; GENERAL INFORMATION:
; APPLICANT: Schellenberger, Volker
; APPLICANT: Liu, Amy D.
; APPLICANT: Selifonova, Olga V.
; TITLE OF INVENTION: Directed Evolution of Microorganisms
; FILE REFERENCE: GC560
; CURRENT APPLICATION NUMBER: US/10/037,677
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/314,847
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 11
```



```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pos102 mutd mutated gene
US-10-037-677-8

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 GTGCGGCTGTG 12
Db   1 GTGCGGCTGTG 11

RESULT 91
US-10-215-647-10
; Sequence 10, Application US/10215647
; Publication No. US20030129170A1
; GENERAL INFORMATION:
; APPLICANT: IACOVITTI, LORRAINE
; APPLICANT: KESSLER, MARK A.
; TITLE OF INVENTION: HUMAN TYROSINE HYDROXYLASE PROMOTER AND USES THEREOF
; FILE REFERENCE: 003252-52860
; CURRENT APPLICATION NUMBER: US/10/215,647
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/942,325
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/228,931
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-215-647-10

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5 GCGCTGTGGCG 15
Db   1 GCGTGTGGCG 11

RESULT 92
US-10-719-571-10
; Sequence 10, Application US/10719571
; Publication No. US20040086972A1
; GENERAL INFORMATION:
; APPLICANT: Schellenberger, Volker
; APPLICANT: Liu, Amy D.
; APPLICANT: Selifonova, Olga V.
; TITLE OF INVENTION: Directed Evolution of Microorganisms
; FILE REFERENCE: GC560-D1
; CURRENT APPLICATION NUMBER: US/10/719,571
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 09/314,847
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pos102 mutd mutated gene
US-10-719-571-10

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  8 CTGTGGCGAAG 18
Db   11 CTGGGGCTAAG 1

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  8 CTGTGGCGAAG 18
Db   11 CTGGGGCTAAG 1

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 GTGCGGCTGTG 12
Db   1 GTGCGGCTGTG 11

RESULT 93
US-10-450-797-851/c
; Sequence 851, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Contradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 851
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-851

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  4 CGCGCTGTGGC 14
Db   11 CTGCGTGGGCG 1

RESULT 94
US-10-450-797-985/c
; Sequence 985, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Contradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 985
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-985

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  8 CTGTGGCGAAG 18
Db   11 CTGGGGCTAAG 1
```

RESULT 95
US-10-450-797-1022
; Sequence 1022, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1022
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1022

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAG 18
||| ||| |||
DB 1 CTGGGGGGAAG 11

RESULT 96
US-10-754-408-8
; Sequence 8, Application US/10754408
; Publication No. US20040203035A1
; GENERAL INFORMATION:
; APPLICANT: Maet, Andrea L.
; APPLICANT: Dorn, Erin
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Accolla, Molly
; APPLICANT: Wigdal, Susan S.
; TITLE OF INVENTION: Connexin Allele Detection Assays
; FILE REFERENCE: FORS-08724
; CURRENT APPLICATION NUMBER: US/10/754,408
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-754-408-8

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGCG 14
||| ||| |||
DB 1 CGCGCCGAGGC 11

RESULT 97
US-09-775-743A-12/c
; Sequence 12, Application US/09775743A
; Patent No. US20020058619A1
; GENERAL INFORMATION:
; APPLICANT: Supratek Pharma, Inc.

; TITLE OF INVENTION: Vascular Endothelial Growth/Factor Receptor
; FILE REFERENCE: 082181-36154
; CURRENT APPLICATION NUMBER: US/09/775,743A
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/180,568
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chemical
; OTHER INFORMATION: synthesis
US-09-775-743A-12

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9
||| ||| |||
DB 10 GGTGGCGCT 2

RESULT 98
US-09-848-537A-9/c
; Sequence 9, Application US/09848537A
; Patent No. US20020137684A1
; GENERAL INFORMATION:
; APPLICANT: Tchistiakova, Liudmila
; APPLICANT: Li, Shengmin
; APPLICANT: Pietrzynski, Grzegorz
; APPLICANT: Alakhov, Valery
; TITLE OF INVENTION: Ligand For Enhancing Oral And CNS Delivery of
; FILE REFERENCE: 082181-36910
; CURRENT APPLICATION NUMBER: US/09/848,537A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
US-09-848-537A-9

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9
||| ||| |||
DB 10 GGTGGCGCT 2

RESULT 99
US-10-033-145-1209/c
; Sequence 1209, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18

; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1209
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1209

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
 |||||
 DB 10 TGGAGAAGG 2

RESULT 100
 US-10-033-145-1502/c
 ; Sequence 1502, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1502
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1502

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
 |||||
 DB 10 GCTGTGGG 2

RESULT 101
 US-10-033-145-1908
 ; Sequence 1908, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1908
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1908

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
 |||||
 DB 2 GCTGTGGG 10

RESULT 102
 US-10-033-145-2103
 ; Sequence 2103, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2103
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-2103

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
 |||||
 DB 2 GCGCTGTGG 10

RESULT 103
 US-10-330-627-279
 ; Sequence 279, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 279
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-330-627-279

Query Match 38.9%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
 |||||
 DB 2 GCGCTGTGG 10

RESULT 104
 US-10-330-627-280
 ; Sequence 280, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:

```
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-280

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      5 GCGCTGTGG 13
Db      2 GCGCTGTGG 10

RESULT 105
US-10-330-627-447/c
; Sequence 447, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-447

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      6 CGCTGTGGC 14
Db      9 CGCTGGGC 1

RESULT 106
US-10-330-627-586/c
; Sequence 586, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 586
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-586

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      6 CGCTGTGGC 14
Db      10 CGCAGTGGC 2

RESULT 107
US-10-330-627-734/c
; Sequence 734, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 734
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-734

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      11 TGGCGAAGG 19
Db      10 TGGAGAAGG 2

RESULT 108
US-10-330-627-1025
; Sequence 1025, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1025
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1025

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      7 GCTGTGGCG 15
```

```

Db      1  GCTGTGGC  9
||||| |||
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 205
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-205

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GGTGCGCGT  9
||||| |||
Db      10  GGTGCGCGT  2
||||| |||

RESULT 112
US-10-723-940-92/c
; Sequence 92, Application US/10723940
; Publication No. US20040185468A1
; GENERAL INFORMATION:
; APPLICANT: Leonard, Sherry
; APPLICANT: Freeman, Robert
; TITLE OF INVENTION: Promoter Variants in the Alpha-7 Nicotinic Acetylcholine Receptor
; TITLE OF INVENTION: Gene
; FILE REFERENCE: VARD-07989
; CURRENT APPLICATION NUMBER: US/10/723,940
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 08/956,518
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-723-940-92

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8  CTGTGCGGA  16
||||| |||
Db      10  CTGTGCGGA  2
||||| |||

RESULT 113
US-10-487-934-14
; Sequence 14, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429

```

```

Db      1  GCTGTGGC  9
||||| |||
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 00107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1064
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1064

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11  TGGCGAAGG  19
||||| |||
Db      2  TGGTGAAGG  10
||||| |||

RESULT 110
US-10-197-019-109/c
; Sequence 109, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MWH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-109

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2  GTCGCGCTG  10
||||| |||
Db      9  GTAGCGCTG  1
||||| |||

RESULT 111
US-10-293-222-205/c
; Sequence 205, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:

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; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-487-934-14

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
Db 2 TGGCAAAGG 10

RESULT 114
US-10-487-934-123/c
; Sequence 123, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-487-934-123

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCCGGCT 9
Db 9 GGTCCGGCT 1

RESULT 115
US-10-487-934-184
; Sequence 184, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805

; CURRENT APPLICATION NUMBER: US/10/487,934
; Sequence 23, Application US/10987549
; Publication No. US20050191656A1
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/10/987,549
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/09/479,608
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 10
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-29

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 CTGTGGCGCA 16
Db      10 CTGTGGCGCA 2

RESULT 118
US-10-987-549-30/c
; Sequence 30, Application US/10987549
; Publication No. US20050191656A1
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/10/987,549
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/09/479,608
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-30

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 CTGTGGCGCA 16
Db      9 CTGTGGCGCA 1

RESULT 119
US-11-035-899-259/c
; Sequence 259, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Jennifer C. Learnmont
; APPLICANT: Dale A. McPhee
; APPLICANT: Suzanne Crowe
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-11-035-899-259

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 GTGGCGCAAG 18
Db      10 GTGGCGTAAG 2

RESULT 120
US-11-035-899-260/c
; Sequence 260, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Jennifer C. Learnmont
; APPLICANT: Dale A. McPhee
; APPLICANT: Suzanne Crowe
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)

```

```

; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PNO284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 260:
US-11-035-899-260

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAG 18
Db      9 GTGGCTAAG 1

RESULT 121
US-09-867-262-5
; Sequence 5, Application US/09867262
; Patent No. US20020119457A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DEVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-867-262-5

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
Db      4 CGCGCTG 10

RESULT 122
US-09-885-551A-6
; Sequence 6, Application US/09885551A
; Patent No. US20020146762A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsoetne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/09/885,551A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-885-551A-6

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
Db      1 CGCGCTG 7

RESULT 123
US-09-990-186-92
; Sequence 92, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-92

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GCGGAAG 18
Db      4 GCGGAAG 10

RESULT 124
```


US-09-990-186-93
 ; Sequence 93, Application US/09990186
 ; Publication No. US20030068675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: 8325-0011.21 / S11-US3
 ; CURRENT APPLICATION NUMBER: US/09/990,186
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 93
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: example target
 ; OTHER INFORMATION: DNA
 US-09-990-186-93

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGGAG 18
 |||||
 Db 4 GCGGAG 10

RESULT 125

US-09-990-186-1278
 ; Sequence 1278, Application US/09990186
 ; Publication No. US20030068675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: 8325-0011.21 / S11-US3
 ; CURRENT APPLICATION NUMBER: US/09/990,186
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1278
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: example target
 ; OTHER INFORMATION: DNA
 US-09-990-186-1278

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
 |||||
 Db 4 GCTGTGG 10

RESULT 126

US-09-990-186-1653
 ; Sequence 1653, Application US/09990186
 ; Publication No. US20030068675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: 8325-0011.21 / S11-US3
 ; CURRENT APPLICATION NUMBER: US/09/990,186
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1653
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: example target
 ; OTHER INFORMATION: DNA
 US-09-990-186-1653

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGG 7
 |||||
 Db 3 GGTGCGG 9

RESULT 127

US-09-990-186-1654
 ; Sequence 1654, Application US/09990186
 ; Publication No. US20030068675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: 8325-0011.21 / S11-US3
 ; CURRENT APPLICATION NUMBER: US/09/990,186
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1654
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: example target
 ; OTHER INFORMATION: DNA
 US-09-990-186-1654

Query Match 36.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGG 7
 |||||
 Db 3 GGTGCGG 9

RESULT 128

US-09-990-186-1667
 ; Sequence 1667, Application US/09990186
 ; Publication No. US20030068675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: 8325-0011.21 / S11-US3
 ; CURRENT APPLICATION NUMBER: US/09/990,186
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1667
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: example target
 ; OTHER INFORMATION: DNA
 US-09-990-186-1667

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGG 7
|||||
Db 3 GGTGCGG 9

RESULT 129

US-09-989-994-92
; Sequence 92, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-92

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGGAAG 18
|||||
Db 4 GCGGAAG 10

RESULT 130

US-09-989-994-93
; Sequence 93, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-93

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGGAAG 18
|||||
Db 4 GCGGAAG 10

RESULT 131

US-09-989-994-1278
; Sequence 1278, Application US/09989994

Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1278

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13
|||||
Db 4 GCTGTGG 10

RESULT 132

US-09-989-994-1653
; Sequence 1653, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1653
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1653

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGG 7
|||||
Db 3 GGTGCGG 9

RESULT 133

US-09-989-994-1654
; Sequence 1654, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1654

```

; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-1654

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCG 7
Db 3 GGTGCG 9

RESULT 134
US-09-989-994-1667
; Sequence 1667, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: TRIPLETS BY ZINC FINGERS
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1667
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-1667

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCG 7
Db 3 GGTGCG 9

RESULT 135
US-10-087-426-6
; Sequence 6, Application US/10087426
; Publication No. US20020142394A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-11-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-11-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31

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; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-1654

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGCGCTG 10
Db 1 CGCGCTG 7

RESULT 136
US-10-033-145-299
; Sequence 299, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 299
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-299

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CGCTGTG 12
Db 1 CGCTGTG 7

RESULT 137
US-10-033-145-527/c
; Sequence 527, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 527

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```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-527

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
        |||||
Db       9 CTGTGGC 3

RESULT 138
US-10-033-145-1855/c
; Sequence 1855, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1855
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1855

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
        |||||
Db       9 GCTGTGG 3

RESULT 139
US-10-033-145-2019
; Sequence 2019, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2019
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2019

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
        |||||

; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-077-6

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
        |||||
Db       1 CGCGCTG 7

RESULT 141
US-10-142-111-23/c
; Sequence 23, Application US/10142111
; Publication No. US20030101485A1
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/142,111
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-142-111-23

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
        |||||
Db       7 GCTGTGG 1

RESULT 142
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US-10-223-765-284
; Sequence 284, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-284

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGC 7
Db 3 GGTGCGC 9

RESULT 143
US-10-330-627-524
; Sequence 524, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 524
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-524

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
Db 4 CTGTGGC 10

RESULT 144
US-10-091-281-247/c
; Sequence 247, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:

```

```

; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 247
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative CREB/HLP.01 motif
US-10-091-281-247

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
Db 9 TGGCGAA 3

RESULT 145
US-10-422-523-28
; Sequence 28, Application US/10422523
; Publication No. US20040002103A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; TITLE OF INVENTION: SYNTHETIC LIGATION REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-15A US
; CURRENT APPLICATION NUMBER: US/10/422,523
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: 09/332,835
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-422-523-28

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10
Db 1 CGCGCTG 7

RESULT 146
US-10-029-221C-5
; Sequence 5, Application US/10029221C
; Publication No. US20040152077A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; APPLICANT: DJAVAKHISHVILI, TSOTNE D.
; APPLICANT: FREY, GERHARD J.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-21
; CURRENT APPLICATION NUMBER: US/10/029,221C
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/008,311
; PRIOR FILING DATE: 1995-12-07

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; PRIOR APPLICATION NUMBER: 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-029-221C-5

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10
Db 1 CGCGCTG 7

RESULT 147
US-10-816-079-27/c
; Sequence 27, Application US/10816079
; Publication No. US20040166527A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Beaudry, Gary A
; APPLICANT: Madden, Stephen L
; APPLICANT: Bertelsen, Arthur H
; TITLE OF INVENTION: Composition and Methods for the Identification of Lung Tumor
; TITLE OF INVENTION: Cells
; FILE REFERENCE: GA0129C2
; CURRENT APPLICATION NUMBER: US/10/816,079
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: 09/663,516
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/080,037
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SAGE tag
US-10-816-079-27

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14
Db 9 CTGTGGC 3

RESULT 148
US-10-855-595-25/c
; Sequence 25, Application US/10855595
; Publication No. US20040235057A1
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
```

```
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/855,595
; FILING DATE: 28-May-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,482
; FILING DATE: 25-Sep-2000
; APPLICATION NUMBER: 08/882,164
; FILING DATE: June 25, 1997
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 25
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25
US-10-855-595-25

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17
Db 9 TGGCGAA 3

RESULT 149
US-10-631-544-6
; Sequence 6, Application US/10631544
; Publication No. US20040248143A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTI
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/631,544
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-631-544-6

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGCGCTG 10
Db 1 CGCGCTG 7

RESULT 150

US-10-855-532-25/c
; Sequence 25, Application US/10855532
; Publication No. US20040259074A1
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/855,532
; FILING DATE: 28-May-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,482
; FILING DATE: 25-Sep-2000
; APPLICATION NUMBER: 08/882,164
; FILING DATE: June 25, 1997
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 25
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGCGGAA 17
Db 9 TGCGGAA 3

RESULT 151

US-10-688-489-166/c
; Sequence 166, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen

; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 166
; LENGTH: 10
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(10)
; OTHER INFORMATION: 2'-OME nucleotide analogs
; US-10-688-489-166

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GCGAAGG 19
Db 10 GCGAAGG 4

RESULT 152

US-10-398-271-14
; Sequence 14, Application US/10398271
; Publication No. US20050124010A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Fu, Pengcheng
; APPLICANT: Latterich, Martin
; APPLICANT: Wei, Jing
; APPLICANT: Levin, Michael
; TITLE OF INVENTION: WHOLE CELL ENGINEERING BY MUTAGENIZING A
; TITLE OF INVENTION: SUBSTANTIAL PORTION OF A STARTING GENOME, COMBINING
; TITLE OF INVENTION: MUTATIONS, AND OPTIONALLY REPEATING
; FILE REFERENCE: 09010-060051
; CURRENT APPLICATION NUMBER: US/10/398,271
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: PCT/US01/31004
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/US01/19367
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/279,702
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/677,584
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polynucleotide sequence of a restriction site
; US-10-398-271-14

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGCGCTG 10

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Db          1  CGCGCTG 7
|||||
QY          8  CTGTGGC 14
|||
Db          7  CTGTGGC 1

Search completed: May  9, 2006, 15:51:35
Job time : 0.001 secs

RESULT 153
US-10-987-549-31/c
; Sequence 31, Application US/10987549
; Publication No. US20050191656A1
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/10/987,549
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/09/479,608
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-31

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8  CTGTGGC 14
|||
Db          8  CTGTGGC 2

RESULT 154
US-10-987-549-32/c
; Sequence 32, Application US/10987549
; Publication No. US20050191656A1
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/10/987,549
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/09/479,608
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-32

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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